

From: Bunner, Bridget
Sent: Wednesday, April 06, 2005 2:00 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:

1. the nucleic acid sequence of SEQ ID NO: 2
2. the nucleic acid sequence of SEQ ID NO: 3

CRFE

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Result No.	Score	Query Match	Length	DB	ID	Description
1	2689.2	99.8	3137	4	US-09-590-304-1	Sequence 1, Appli
2	2681.2	99.5	3074	4	US-09-613-148-1	Sequence 1, Appli
3	2625.2	97.4	2772	4	US-09-825-147-1	Sequence 1, Appli
4	2625.2	97.4	3111	4	US-09-825-147-3	Sequence 3, Appli
5	518.4	19.2	2196	4	US-09-949-016-1823	Sequence 1823, Ap
6	518.4	19.2	2235	4	US-09-492-361-1	Sequence 1, Appli
7	516	19.2	2273	3	US-09-177-650-88	Sequence 88, Appl
8	510	18.9	2169	3	US-09-105-058C-22	Sequence 22, Appl
9	509.8	18.9	582	4	US-09-495-050A-303	Sequence 303, Appl
10	465.4	17.3	896	3	US-09-105-058C-1	Sequence 1, Appli
11	464	17.2	2814	3	US-09-177-650-90	Sequence 90, Appl
12	460.8	17.1	2565	3	US-09-105-058C-26	Sequence 26, Appl
13	460.8	17.1	2914	3	US-09-177-650-6	Sequence 6, Appli
14	452	16.8	575	4	US-09-495-050A-305	Sequence 305, Appl
15	425	15.8	3287	3	US-09-105-058C-19	Sequence 19, Appl
16	423.4	15.7	3232	3	US-09-177-650-1	Sequence 1, Appli
17	423.4	15.7	3237	3	US-09-177-650-95	Sequence 95, Appl
18	421.4	15.6	900	3	US-09-105-058C-3	Sequence 3, Appli
19	420.6	15.6	900	3	US-09-105-058C-5	Sequence 5, Appli
20	363.8	13.5	930	3	US-09-105-058C-17	Sequence 17, Appl
21	334.2	12.4	735	3	US-09-105-058C-7	Sequence 7, Appli
22	276.4	10.3	284	4	US-09-495-050A-304	Sequence 304, Appl
23	267.8	9.9	2028	3	US-09-634-920-1	Sequence 1, Appli
24	267.8	9.9	2028	4	US-09-840-125-1	Sequence 1, Appli
25	267.8	9.9	3181	3	US-09-135-021-1	Sequence 1, Appli
26	267.8	9.9	3181	3	US-09-135-020-1	Sequence 1, Appli
27	267.8	9.9	3181	3	US-09-135-010A-1	Sequence 1, Appli

Db	1141	GCCTCAAGTTGGCTCTTTGATCCTCGGAGTTCGTCATGATTTGTCGTTGGAGTTC	420	Db	1441	CCACCACCTTAAAACTGTCTCATTCGAGCTATCAGAAATTTAGAAATTTTCATGTTGCAAAACGG	1500
Qy	421	ATCATTCGAATCTGGTCTGGGTTGCTGTTGTCGATATAGAGATGGCAAGAACACTG	480	Qy	1501	AAGTTTAAAGGAAACGTTACGTTCCATATGATCTAAAGATGTCATTTGAACAATATTTCTGCT	1560
Db	421	ATCATTCGAATCTGGTCTGGGTTGCTGTTGTCGATATAGAGATGGCAAGAACACTG	480	Db	1501	AAGTTTAAAGGAAACATTTACGTTCCATATGATGTTAAAGATGTCATTTGAACAATATTTCTGCT	1560
Qy	481	AGGTTTCTCGAAGCCCTCTGTTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540	Qy	1561	GGTCATCTGGACATGTTGTTAGAAATTTAAAGCCCTTCAAAACACGTTGTTGATCAAAATCTT	1620
Db	481	AGGTTTCTCGAAGCCCTCTGTTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540	Db	1561	GGTCATCTGGACATGTTGTTAGAAATTTAAAGCCCTTCAAAACACGTTGTTGATCAAAATCTT	1620
Qy	541	GTGTTTCTCGAAGAACCTCAGGTTAATATTTTGGCCACGTCGCACTCAGAACTCTCCGT	600	Qy	1621	GGAAAAGGCGCAATCACATCAGATGAAGAGCCGAGAGAAAATAACACGAGAACATCAG	1680
Db	541	GTGTTTCTCGAAGAACCTCAGGTTAATATTTTGGCCACGTCGCACTCAGAACTCTCCGT	600	Db	1621	GGAAAAGGCGCAATCACATCAGATGAAGAGCCGAGAGAAAATAACACGAGAACATCAG	1680
Qy	601	TTCTCAGATCTCCGATGTTGCGATGACGACGAGGAGGAGGACCTTGGAAATTAATG	660	Qy	1681	ACCAAGAGCGATCTCAGTATGCTCGGTGGGTGTCGAGGTTGAAAGAACAGTACAGTCC	1740
Db	601	TTCTCAGATCTCCGATGTTGCGATGACGACGAGGAGGAGGACCTTGGAAATTAATG	660	Db	1681	ACCAAGAGCGATCTCAGTATGCTCGGTGGGTGTCGAGGTTGAAAGAACAGTACAGTCC	1740
Qy	661	GGTTCAAGTGTATGCTCAGCAAGGAAATTAATCAAGCTTGGTACATAGGATTTTG	720	Qy	1741	ATAGAGTCCAAAGCTGGACTGCTTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	1800
Db	661	GGTTCAAGTGTATGCTCAGCAAGGAAATTAATCAAGCTTGGTACATAGGATTTTG	720	Db	1741	ATAGAGTCCAAAGCTGGACTGCTTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	1800
Qy	721	GTTCTTATTTTTCGTTCTTCTTCTGTTGTAAGGAGGATGCAATTAAGAGTTT	780	Qy	1801	GGCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	1860
Db	721	GTTCTTATTTTTCGTTCTTCTTCTGTTGTAAGGAGGATGCAATTAAGAGTTT	780	Db	1801	GGCTCAGCCCTCGCTTTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	1860
Qy	781	TCTACATATGATGCTCTCTGTTGGGCAAAATTAATGACAACTATTTGGCTATGGA	840	Qy	1861	GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCGCAAAACAGTGGCTGC	1920
Db	781	TCTACATATGATGCTCTCTGTTGGGCAAAATTAATGACAACTATTTGGCTATGGA	840	Db	1861	GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCGCAAAACAGTGGCTGC	1920
Qy	841	GACAAAACCTCCCTAACTTGGCTGGAGATGCTTTCTGAGGCTTTTGCACCTCTTGGC	900	Qy	1921	TTATCCAGATCAACTAGTGGCCAACTCTCGAGAGGCTCGAGTTCAITCTGACGCCAAAT	1980
Db	841	GACAAAACCTCCCTAACTTGGCTGGAGATGCTTTCTGAGGCTTTTGCACCTCTTGGC	900	Db	1921	TTATCCAGATCAACTAGTGGCCAACTCTCGAGAGGCTCGAGTTCAITCTGACGCCAAAT	1980
Qy	901	ATTTCTTTTCTGTTGCTTCTGCTGCGGATCTTCTGCTCAGGTTTGTGATTTAAAGTACAA	960	Qy	1981	GAGTTCAAGTGGCCAGACTTTCTAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG	2040
Db	901	ATTTCTTTTCTGTTGCTTCTGCTGCGGATCTTCTGCTCAGGTTTGTGATTTAAAGTACAA	960	Db	1981	GAGTTCAAGTGGCCAGACTTTCTAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG	2040
Qy	961	GAAACAACCCGCAAGAACACTTTGAGAAAGAGAGAACCCAGCTGCGCAACCTCAITCAG	1020	Qy	2041	GTCCCAATTAGTCAAAAGCGATGCTCAGCAGTGGGACCAACCAACCACTTGCAGAACCA	2100
Db	961	GAAACAACCCGCAAGAACACTTTGAGAAAGAGAGAACCCAGCTGCGCAACCTCAITCAG	1020	Db	2041	GTCCCAATTAGTCAAAAGCGATGCTCAGCAGTGGGACCAACCAACCACTTGCAGAACCA	2100
Qy	1021	TGTTGTTGCGTGTAGTACGAGCTGATCAGAAATCTGTTTCCATTGCAACTGGAAGCCA	1080	Qy	2101	ATAAATACGGCACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2160
Db	1021	TGTTGTTGCGTGTAGTACGAGCTGATCAGAAATCTGTTTCCATTGCAACTGGAAGCCA	1080	Db	2101	ATAAATACGGCACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2160
Qy	1081	CACTTTGAAGGCTTGCACACCTGCAAGCCCTTACCAAGAAAGAACAGGGAAGCATCAAGC	1140	Qy	2161	GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGA	2220
Db	1081	CACTTTGAAGGCTTGCACACCTGCAAGCCCTTACCAAGAAAGAACAGGGAAGCATCAAGC	1140	Db	2161	GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGA	2220
Qy	1141	AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGGGCCAGATTT	1200	Qy	2221	AGCATTTCTGACGTCAACCTGCTGCTTGGCTCCAGGAAAATGTTCAAGTTGCACAG	2280
Db	1141	AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGGGCCAGATTT	1200	Db	2221	AGCATTTCTGACGTCAACCTGCTGCTTGGCTCCAGGAAAATGTTCAAGTTGCACAG	2280
Qy	1201	AGAGCCGCAAGCTCAGTAGTGCACAGAGGTCCTCCAGCACGACATCACAGCCGAG	1260	Qy	2281	TCAATCTCAGGAGGACCGTTCTATGAGGAAAAGCTTTTGCATGGAGAGAAACTCTG	2340
Db	1201	AGAGCCGCAAGCTCAGTAGTGCACAGAGGTCCTCCAGCACGACATCACAGCCGAG	1260	Db	2281	TCAATCTCAGGAGGACCGTTCTATGAGGAAAAGCTTTTGCATGGAGAGAACTCTG	2340
Qy	1261	GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCGGGCC	1320	Qy	2341	TTGTCTGTCTGCTCCATGCTGCGGAGGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2400
Db	1261	GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCGGGCC	1320	Db	2341	TTGTCTGTCTGCTCCATGCTGCGGAGGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2400
Qy	1321	TGCTGCGGCTCAAGTTCTCAGCCAAACAGTATAGTGTGACACAGCCCTTGGC	1380	Qy	2401	ATCAGGTCGACCGAGGAACTGAATATACATTTTTCAGGAGTGTGATCAAGTGGCTCCAGA	2460
Db	1321	TGCTGCGGCTCAAGTTCTCAGCCAAACAGTATAGTGTGACACAGCCCTTGGC	1380	Db	2401	ATCAGGTCGACCGAGGAACTGAATATACATTTTTCAGGAGTGTGATCAAGTGGCTCCAGA	2460
Qy	1381	ACTGATGATGATATGATGAAAGAGGATCCAGTGTGATGATCAGTGGAGACCTCACC	1440	Qy	2461	GGCAGCCAAAGATTTTATACCCCAATGAGGGAATCCAAATTTGTTTATATGATGAAGAG	2520
Db	1381	ACTGATGATGATATGATGAAAGAGGATCCAGTGTGATGATCAGTGGAGACCTCACC	1440	Db	2461	GGCAGCCAAAGATTTTATACCCCAATGAGGGAATCCAAATTTGTTTATATGATGAAGAG	2520
Qy	1441	CCACCACTTAAACTGTCTATTCAGGCTATCAGAAATTTATGAAATTTTCATGTTGCCAGGAA	1500	Qy	2521	GTGGGTCCGGAAGAGACAGAGACAGACACTTTTGTATGCCGACCGCAGCTTGCAGGAA	2580
Db	1441	CCACCACTTAAACTGTCTATTCAGGCTATCAGAAATTTATGAAATTTTCATGTTGCCAGGAA	1500	Db	2521	GTGGGTCCGGAAGAGACAGAGACAGACACTTTTGTATGCCGACCGCAGCTTGCAGGAA	2580

Accession	Sequence	Position
Qy	GCTGCCTTTGCATCAGAGCTCTAAAGACTGGAAGGTACGATCATCTCAGAGCATTTGT	2640
Db	GCTGCCTTTGCATCAGAGCTCTAAAGACTGGAAGGTACGATCATCTCAGAGCATTTGT	2640
Qy	AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATCTCAAACTGAAATAA	2694
Db	AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATCTCAAACTGAAATAA	2694

RESULT 2

US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-813-148-1

Query Match	99.5%	Score 2681.2	DB 4	Length 3074
Best Local Similarity	99.7%	Pred. No. 0		
Matches 2686	Conservative 0	Mismatches 8	Indels 0	Gaps 0
Qy	1	ATGAAGATGTGGAGTCGGCCGGGGCAGAGGTGCTGCTGAAC	TCGGCAGCGCCACGAGGGC	60
Db	215	ATGAAGATGTGGAGTCGGCCGGGGCAGAGGTGCTGCTGAAC	TCGGCAGCGCCACGAGGGC	274
Qy	61	GACGGCTGTACTGCTGGGCACCCGCGCGSCACAGCTTGGTGGCGCGCGGTGGGCTG	120	
Db	275	GACGGCTGTACTGCTGGGCACCCGCGCGSCACAGCTTGGTGGCGCGCGGTGGGCTG	334	
Qy	121	AGGAGAGCCGCGGGGCAAGCAGAGGGGGCCGGATGAGCCTGCTGGGGAAAGCCGCTCTCT	180	
Db	335	AGGAGAGCCGCGGGGCAAGCAGAGGGGGCCGGATGAGCCTGCTGGGGAAAGCCGCTCTCT	394	
Qy	181	TACACGATGACGAGCTGCGCGCGCAAGCTCAAGTACCGCGGGTGCGAGACTACCTG	240	
Db	395	TACACGATGACGAGCTGCGCGCGCAAGCTCAAGTACCGCGGGTGCGAGACTACCTG	454	
Qy	241	TACAACTGTCTGGAGACACCCCGGGCTGGGCGTTCACTACCAACGCTTTCGTTTTCCTC	300	
Db	455	TACAACTGTCTGGAGACACCCCGGGCTGGGCGTTCACTACCAACGCTTTCGTTTTCCTC	514	
Qy	301	CTTGCTTTTGGTGTGATTTTGTCAAGTGTTTTCTACCATCCCTGAGCACACAAATTG	360	
Db	515	CTTGCTTTTGGTGTGATTTTGTCAAGTGTTTTCTACCATCCCTGAGCACACAAATTG	574	
Qy	361	GCCTCAAAGTGCCTTTGATCTCGAGTTCGTGATGATTCGTCTTTTGGTGGAGTTC	420	
Db	575	GCCTCAAAGTGCCTTTGATCTCGAGTTCGTGATGATTCGTCTTTTGGTGGAGTTC	634	
Qy	421	ATCATTCGAATCTGGCTTCGGGTTGCTTTGTCGATATAGAGATGCGCAAGAGACTG	480	
Db	635	ATCATTCGAATCTGGCTTCGGGTTGCTTTGTCGATATAGAGATGCGCAAGAGACTG	694	

Qy	481	AGTTTGTCTCGAAAGCCCTTCTGTGTTATATAGATACCAATTGTTCTTATTCGCTTCAATAGCA	540
Db	695	AGGTTTGTCTCGAAAGCCCTTCTGTGTTATATAGATACCAATTGTTCTTATATTCGTTTCAATAGCA	754
Qy	541	GTGTGTTTCTCGAAAAACTCAGGAGTAATATTTTTTGCCACGTCGACATCAGAAGTCTCCGT	600
Db	755	GTGTGTTTCTCGAAAAACTCAGGAGTAATATTTTTTGCCACGTCGACATCAGAAGTCTCCGT	814
Qy	601	TTCTCAGAGATCTCTCGCATGSGTGCAGATGGACCGAAGGGGAGGCACCTTGGAATAATCTG	660
Db	815	TTCTCAGAGATCTCTCGCATGSGTGCAGATGGACCGAAGGGGAGGCACCTTGGAATAATCTG	874
Qy	661	GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATACATAGATTTTTTG	720
Db	875	GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATACATAGATTTTTTG	934
Qy	721	GTTCCTATTTTTTTCGTTCTTTCCTTGTCTATCTCGTGGAAAAGATGCCAATAAAGAGTTT	780
Db	935	GTTCCTATTTTTTTCGTTCTTTCCTTGTCTATCTCGTGGAAAAGATGCCAATAAAGAGTTT	994
Qy	781	TCTACATATGCAGATGCTCTCTGGTGGGGCACAAATACATTTGACAACTATTGGCTATGGA	840
Db	995	TCTACATATGCAGATGCTCTCTGGTGGGGCACAAATACATTTGACAACTATTGGCTATGGA	1054
Qy	841	GACAAAACCTCCCTTAACCTTGGCTGGGAAGATTCGCTTTCGACGGCTTTGCATCTCTTGGC	900
Db	1055	GACAAAACCTCCCTTAACCTTGGCTGGGAAGATTCGCTTTCGACGGCTTTGCATCTCTTGGC	1114
Qy	901	ATTCTTCTTCTTTCGCACTTCTCTGCGGCATTTCTTGGCTCAGGTTTTCGATTTAAAGATCAA	960
Db	1115	ATTCTTCTTCTTTCGCACTTCTCTGCGGCATTTCTTGGCTCAGGTTTTCGATTTAAAGATCAA	1174
Qy	961	GAACAAACACCGCCAGAAAAACATTTTGAAAAAGAAAGAACCCAGCTGCCAACCTCATTCAG	1020
Db	1175	GAACAAACACCGCCAGAAAAACATTTTGAAAAAGAAAGAACCCAGCTGCCAACCTCATTCAG	1234
Qy	1021	TGTGTTTGGGTAGTTACGAGCTGATAGAAATCTGTTTCCATTTGCAATGCGAAGCCCA	1080
Db	1235	TGTGTTTGGGTAGTTACGAGCTGATAGAAATCTGTTTCCATTTGCAATGCGAAGCCCA	1294
Qy	1081	CACCTGAAGCCCTTGACACCTTCGACCCCTTACCAAGAAAGAAACAAGGGGAAGCATCAAGC	1140
Db	1295	CACCTGAAGCCCTTGACACCTTCGACCCCTTACCAAGAAAGAAACAAGGGGAAGCATCAAGC	1354
Qy	1141	AGTCAGAAGCTAAAGTTTAAAGACGAGTCGCGCATGGCTAGCCCTCAGGGGCCAGAGTATT	1200
Db	1355	AGTCAGAAGCTAAAGTTTAAAGACGAGTCGCGCATGGCTAGCCCTCAGGGGCCAGAGTATT	1414
Qy	1201	AAGAGCCGCAAGCCCTCAGTAGGTGACAGAGAGTCCCCAAGACCGGACATCAGACCGAG	1260
Db	1415	AAGAGCCGCAAGCCCTCAGTAGGTGACAGAGAGTCCCCAAGACCGGACATCAGACCGAG	1474
Qy	1261	GGCAGTCCCAACAAAGTCGAGAGAGCTGGAGCTTCAACGACCGAACCCCGCTTCCGGCCC	1320
Db	1475	GGCAGTCCCAACAAAGTCGAGAGAGCTGGAGCTTCAACGACCGAACCCCGCTTCCGGCCC	1534
Qy	1321	TCGCTGGCCCTCAAAAGTTCTCAGCCAAAACACCAAGTATAGATGCTGACACAGCCCTTGGC	1380
Db	1535	TCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCAAGTATAGATGCTGACACAGCCCTTGGC	1594
Qy	1381	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGGAAGACCTCAAC	1440
Db	1595	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGGAAGACCTCAAC	1654
Qy	1441	CCACCCTTAAACTGTCTTTCAGCTATCAGAAATTTATGNAATTTTCAATGTTGCAAAACGG	1500
Db	1655	CCACCCTTAAACTGTCTTTCAGCTATCAGAAATTTATGNAATTTTCAATGTTGCAAAACGG	1714
Qy	1501	AAGTTTAAAGAAACGTTTACGTCCTATGATGATAAAGATGCTCATTTGAACAATATTTCTGCT	1560
Db	1715	AAGTTTAAAGAAACATTTACGTCCTATGATGATAAAGATGCTCATTTGAACAATATTTCTGCT	1774
Qy	1561	GGTCATCTGACATGTTGTGTAGAAATTTAAAGCCCTTCAAAACAGCTGTTGATCAAAATTCCT	1620

QY 601 TTCTACAGATCCTCGCATGTGGCGATGAGCCGAAGGGGAGGACATTTGGAAATTAATCTG 660
DB 706 TTCTACAGATCCTCGCATGTGGCGATGAGCCGAAGGGGAGGACATTTGGAAATTAATCTG 765
QY 661 GGTTCAGTGGTTATGCTCACAGCAAGAAATTAATACAGCTTGTGTACATAGATTTTGG 720
DB 766 GGTTCAGTGGTTATGCTCACAGCAAGAAATTAATACAGCTTGTGTACATAGATTTTGG 825
QY 721 GTTCTTATTTTTCGCTTCTTCCTGCTATCTGCTGGAAGAAAGATGCCAATAAAGATTT 780
DB 826 GTTCTTATTTTTCGCTTCTTCCTGCTATCTGCTGGAAGAAAGATGCCAATAAAGATTT 885
QY 781 TCTACATATGAGATGCTCTCTGCTGGGGCACAATTAATGACAACTATTGGCTATGGA 840
DB 886 TCTACATATGAGATGCTCTCTGCTGGGGCACAATTAATGACAACTATTGGCTATGGA 945
QY 841 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTGCACTCTCTGGC 900
DB 946 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTGCACTCTCTGGC 1005
QY 901 ATTTCTTTCTTTCGCTTCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 1006 ATTTCTTTCTTTCGCTTCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1065
QY 961 GAAACAACCCGCGAGAAACATTTTCAGAAAAAGAAAGAAACCCAGCTGCGCAACCTCAATTCAG 1020
DB 1066 GAAACAACCCGCGAGAAACATTTTCAGAAAAAGAAAGAAACCCAGCTGCGCAACCTCAATTCAG 1125
QY 1021 TGTGTTTGGCTGATGAGTATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCCA 1080
DB 1126 TGTGTTTGGCTGATGAGTATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCCA 1185
QY 1081 CACTTGAAGGCTTCCACACCTGACGCTTACCAAGAAAGAAACAGGAGGAGCATCAAGC 1140
DB 1186 CACTTGAAGGCTTCCACACCTGACGCTTACCAAGAAAGAAACAGGAGGAGCATCAAGC 1220
QY 1141 AGTCAGAAAGCTTAAGTTTAAAGAGGAGTGGCTAGCTGCTAGCTGCTGCTGCTGCTGCTGCT 1200
DB 1221 --TCAGAAAGCTTAAGTTTAAAGAGGAGTGGCTAGCTGCTAGCTGCTGCTGCTGCTGCT 1278
QY 1201 AAGAGCCGCAAGACCTCAGTATGAGTATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCCA 1260
DB 1279 AAGAGCCGCAAGACCTCAGTATGAGTATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCCA 1338
QY 1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGCAACCGCTTCCGGCCC 1320
DB 1339 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGCAACCGCTTCCGGCCC 1398
QY 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAACCCAGTGATAGTGTGACACAGCCCTTGGC 1380
DB 1399 TCGCTGCGCTCAAAAGTTCTCAGCCAAACCCAGTGATAGTGTGACACAGCCCTTGGC 1458
QY 1381 ACTGATGATATGATGAAAGAGTGCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1459 ACTGATGATATGATGAAAGAGTGCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1518
QY 1441 CCACACCTTAAACTGCTATTCGAGCTATCAGAAATTAATGAAATTTCAATTTGTCGCAAGCG 1500
DB 1519 CCACACCTTAAACTGCTATTCGAGCTATCAGAAATTAATGAAATTTCAATTTGTCGCAAGCG 1578
QY 1501 AAGTTTAAAGGAAACCTGCTCATATGATGTAAGAAAGTGTCAATTTGAAACAATATTCTGCT 1560
DB 1579 AAGTTTAAAGGAAACCTGCTCATATGATGTAAGAAAGTGTCAATTTGAAACAATATTCTGCT 1638
QY 1561 GGTCACTGGAATGTTGTGATGAAATTAAGAGCTTCAAGCAAGCTGTTGATCAAAATCTT 1620
DB 1639 GGTCACTGGAATGTTGTGATGAAATTAAGAGCTTCAAGCAAGCTGTTGATCAAAATCTT 1698
QY 1621 GGAAAGGCGCAATCAGATCAGATGAGAGGCGGAGAGAAATTAACAGCAGACATGAG 1680
DB 1699 GGAAAGGCGCAATCAGATCAGATGAGAGGCGGAGAGAAATTAACAGCAGACATGAG 1758

QY 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
DB 1759 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818
QY 1741 ATAGAGTCCAGCTGGACTGCTCTAGACATCTATCAACAGGTCTTTGGAAGAGCTCT 1800
DB 1819 ATAGAAATCCAGCTGGACTGCTCTAGACATCTATCAACAGGTCTTTGGAAGAGCTCT 1878
QY 1801 GCCTCAGCCCTCGCTTTCGCTTTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
DB 1879 GCCTCAGCCCTCGCTTTCGCTTTCAGATCCACCTTTTGAATGTGAACAGACATCT 1938
QY 1861 GACTATCAAGCCCTGCTGATAGCAAGATCTTTTCGGGTTCGCAACAAACAGTGGCTGC 1920
DB 1939 GACTATCAAGCCCTGCTGATAGCAAGATCTTTTCGGGTTCGCAACAAACAGTGGCTGC 1998
QY 1921 TTATCCAGATCAATCTAGTGGCAACATCTCGAGAGGCTTGCAGTTCATTTCTGACGCAAT 1980
DB 1999 TTATCCAGATCAATCTAGTGGCAACATCTCGAGAGGCTTGCAGTTCATTTCTGACGCAAT 2058
QY 1981 GAGTTCAGTGGCCAGACTTTCTAGCGCTTACCGCTTATGTCAGTTCAGTTCAGACACAG 2040
DB 2059 GAGTTCAGTGGCCAGACTTTCTAGCGCTTACCGCTTATGTCAGTTCAGTTCAGACACAG 2118
QY 2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACCATTTGCAAAACCA 2100
DB 2119 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACCATTTGCAAAACCA 2178
QY 2101 ATAAATACGGCAACCAAGCCAGAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
DB 2179 ATAAATACGGCAACCAAGCCAGAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2238
QY 2161 GCCATCAAGCATCTGCCAGGCGCAAGAACTCTGACCCCTTAACCCCTGCGAGGCTTACAGGA 2220
DB 2239 GCCATCAAGCATCTGCCAGGCGCAAGAACTCTGACCCCTTAACCCCTGCGAGGCTTACAGGA 2298
QY 2221 AGCATTTCTGACGTCACCACTGCTTGTGCTTCAAGGAAATTTGTCAGGTTGCACAG 2280
DB 2299 AGCATTTCTGACGTCACCACTGCTTGTGCTTCAAGGAAATTTGTCAGGTTGCACAG 2358
QY 2281 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTCTG 2340
DB 2359 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTCTG 2418
QY 2341 TTGTCTGTCTGCTCCATGCTGCGAAGCACTTGGCBAATCTTTGCTGTGCAABACCTG 2400
DB 2419 TTGTCTGTCTGCTCCATGCTGCGAAGCACTTGGCBAATCTTTGCTGTGCAABACCTG 2478
QY 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTGGCTTCCAGA 2460
DB 2479 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTGGCTTCCAGA 2538
QY 2461 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAATCTGATGAAGAG 2520
DB 2539 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAATCTGATGAAGAG 2598
QY 2521 GTGGGTCCGAGAGACAGACACACTTTTGTATGCGCAGCCGACGCTGCCAGGGA 2580
DB 2599 GTGGGTCCGAGAGACAGACACACTTTTGTATGCGCAGCCGACGCTGCCAGGGA 2658
QY 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGCATCATCTCAGAGCAATTTGT 2640
DB 2659 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGCATCATCTCAGAGCAATTTGT 2718
QY 2641 AAGCAGGAGAAAGTACAGATGCGCTCAGCTTGGCTCATGTCAAACCTGAAATAA 2694
DB 2719 AAGCAGGAGAAAGTACAGATGCGCTCAGCTTGGCTCATGTCAAACCTGAAATAA 2772

RESULT 4

US-09-825-147-3

; Sequence 3, Application US/09825147

; Patent No. 6767736

Patent No. 6794161
GENERAL INFORMATION:
APPLICANT: JENTSCH, Thomas J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
FILE OF INVENTION: POTASSIUM CHANNELS
FILE REFERENCE: 2815-127P
CURRENT APPLICATION NUMBER: US/09/492,361
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2335
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2335)
NAME/KEY: CDS
LOCATION: (83)..(2170)
US-09-492-361-1
Query Match 19.2%; Score 518.4; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 1.3e-143; Indels 165; Gaps 8;
Matches 1103; Conservative 0; Mismatches 566;
217 TACCGCGGGTGCAGAACTTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGTTTC 276
Db TACCGCGGGTGCAGAACTTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGTTTC 379
277 ATCTACCAAGCTTTCGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 336
Db ATCTACCAAGCTTTCGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 439
380 GTCTACCAAGCTTTCGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 499
381 GTCTACCAAGCTTTCGTTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 456
397 ATTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 559
500 ATCGTGTTCGCTTGGAGTACATCGTCCGGGTCTGGTCCGGCGGATGCTGCTGCGCG 516
457 TATAGAGGATGCAAGAGAGTCTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 619
560 TACGAGGATGCGAGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 576
517 ATTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 679
620 ATCGTGTTCGCTTGGAGTACATCGTCCGGGTCTGGTCCGGCGGATGCTGCTGCGCG 636
577 AGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 739
680 ACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 696
637 AGGAGGAGCTTGGAAATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 799
740 CGCGCGGACCTTGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 756
697 ACAGCTTGGTACATAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 859
800 ACCGCTTGGTACATAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 816
757 GAAAGAGTGCATAAAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 919
860 GAGAGGAGGAGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 876
817 ACATTGACAACTATTTGGCTATGGAGACAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 979
920 ACATTGACAACTATTTGGCTATGGAGACAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 936
877 TCTGAGGCTTGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1039
980 GCTGCTGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT

1057 GTTTCATTCGAACTGGAAGCAGCACTTGAAGGCTTGCACACCTGACG 1107
Db GTTTCATTCGAACTGGAAGCAGCACTTGAAGGCTTGCACACCTGACG 1080
1021 GCCTTACCTGACAGCAGCTTGTACTATGACAGTATCTCCATCTTCAAGAGCTG 1152
1108 CCTACCAAGAAAGAAAGGAGGAGCATCAAGCAGTCAAGAGCTA 1140
Db CCTACCAAGAAAGAAAGGAGGAGCATCAAGCAGTCAAGAGCTA 1152
1081 GCCCTCTTGTGACACAGTGCACGGGCCGCAATGGGGCTCAGGCGCTGGAGTG 1200
1153 ----- 1167
1141 CGGCGGCGCGGTACCCGAGGAGCACCTCCCGTTACCCCGCGTGCACCTCCAC 1260
1153 -----AGTTTAAAGGAGCA 1260
1201 CGGCGGCGGAGCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1221
1168 GTGCGCATGGCTAGCCCGAGGCGCAGA-----GTATTAGAGCGGACCAAGCTCAGTA 1260
Db GTGCGCATGGCTAGCCCGAGGCGCAGA-----GTATTAGAGCGGACCAAGCTCAGTA 1320
1261 ATCCGATGGCAGCTCCAGCGGCGGAGCGGTCTTCCAGGAGCATCTGGCACCTCCA 1278
1222 GGTGACAGGAGGTCCCAAGCAGCAGCATCACAGCGAGG---GCAGTCCACCAAGTG 1380
1321 ACAATGCCACCTCCCAAGCAGCAGCAGGTGGTGGGCGGATCTCTGAGACTC-----1434
1279 CAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGGGCTCGCTGCGCTCAAAAGT 1398
Db CAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGGGCTCGCTGCGCTCAAAAGT 1458
1381 CAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCTCGCTGAGACTC-----1542
1339 TCTAGCCAAACACAGTATGATGCTGACACAGCCTTGGACCTGATGATATGAT 1518
1435 -----AACCCCGCACCTTCTGAGGATGCCC---CCTCAGAGGAGTATGACAG 1602
1399 GAAAGAGTGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1578
1483 GAGAAGAGTACACAGTGTGAGCTACGCTGAGCAGCATCATGCTGCTGAGACAGTC 1662
1459 ATTGAGCTATCAGAAATTTATGAAATTTATGTTGCAAAACGAGTGTAAAGAACTGTA 1635
1543 ATCCGCTCCATCAGGATCTCAAGTCTTCTGTTGGCCAAAGAAATCAAGGAGACACTG 1722
1519 CGTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1695
1603 CGACCGTACGCTGAGGAGCTCATGAGCAGTACTGAGCAGTACTGAGCAGTACTGAGCAGTACT 1782
1579 TGTAGAAATTAAGAGCTTCAAAACAGCTGTTGATCAAAATTTCTTGGAAAGGCG---AAATC 1755
1663 GCGCGGATCAAGAGCTGCAAACTCGGCTGGACCAAAATTTGGGTGCGGGGCGCGGAGC 1842
1636 ACATCAGATAGAGAGCGGAGGAGAAATACAGCAGAGACATGAGACACAGACCATCTC 1815
1723 AGGAAGCGCGGAGAGGCGGAGCAAGGGGCTCTCGAGCGGAGGTGTGATGAAATC 1896
1696 AGTATGCTCGTGGGTGGTCAAGGTTGAAAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1909
1783 AGCATGATGAGCGGCTGAGTCAAGTGGAGAGCAGTGCAGTCCATCAGCAGCAAGTGT 1990
1756 GACTGCTTACTAGACATCTATCAAGCTTCTTGGAAAGGCTTCTGCTCAGCCCTCGCT 1875
1843 GACCTGCTTGGCTTCTATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1956
1816 TTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1909
1897 CTGGGCGCGTGAAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1990
1876 GTGATAGCAAGATCTTCTGCGGTTCGCAAAA 1909
1957 GTGACCAAGGAGCATCTCGTCTCGGACAGA 1990

Db 547 CTGGTCTGGTTCCTCCAGGCAATGTCTTTGGCACAATCTGCGCTTCGGAGCTTGGGGTTC 606
Qy 604 CTACAGATCTCCGCGATGTCGCGATGGACCCGAAGGGAGGCACCTTGGAAATTAATCTGGGT 663
Db 607 TTGCAATCTTCGGGATGATCGTATGGACCGGGGGTGGCACCTTGGAAAGCTCTTGGGA 666
Qy 664 TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTATACATAGGAATTTTGGTT 723
Db 667 TCGGTAGTCTACGCTCACAGCAAGAGCTGGTGACTGCGCTGTATACATTTGGCTTCTCTGC 726
Qy 724 CTTATTTTCT 783
Db 727 CTCATCTCTGGCCCTCAATTTCTGGTGTACTTTGGCAGAAAGGGTGAAGATGACCACTTTGAC 786
Qy 784 ACATATGAGATGCTCTCTGGTGGGCGCAATTAATGACAACTATTGGCTATGAGAC 843
Db 787 ACCTAGCAGATGCACTCTGGTGGGCTGTGATCACCTGACCACTATGGCTACGGGGAC 846
Qy 844 AAAAATCCCTAACCTTGGCTGGGAAGATTTCTTCTGCAAGCTTTTGCACCTCTTGGCAAT 903
Db 847 AAGTACCCTCAGACCTGGAACGGAGGCTGTGGCAGCGACCTTTACCTCTCATTTGGTGT 906
Qy 904 TCTTTCTTTGCACTTCTCGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGTACAAGAA 963
Db 907 TCGTTCTTTGCTCTTCTGCTGGCATTTTGGGATCGGCTTTGGCCTGAAAGTCCAAGAG 966
Qy 964 CAACACCGCCAGAAACACTTTGAGAAAGAGAAAGCCAGCTGCGCACTCATTCAGTGT 1023
Db 967 CAGCATCGGCAAAACACTTTGAGAAAGCGCGCAACCTTGGCGAGGCTGTATCAGTCT 1026
Qy 1024 GTTTGGCGTAGTTACGCACTGATGAGAAAT----- 1054
Db 1027 GCCTGAGATCTATGCTACTTAACCTCTACGCAAGGACCTGCACTCCAGCTGGCAGTAC 1086
Qy 1055 -----CTGTTTCCATTTGCAACCTGGAAGCCACCTTGAAGGCTTGGAC 1098
Db 1087 TACGAGCGGACAGTCACTGTCTCCCATGTACAGACTCATCCCACTCTGAAACCAAGCTGGAG 1146
Qy 1099 ACCTCAGCCCTACCAAGA----- 1131
Db 1147 CTGCTGAGATCTCAAGAGCAAAATCTGCACTCACTCAGAAAGGAGCCACAGCCAGAG 1206
Qy 1132 GCATCAAGCAGTCAGAAAGTAAAGTAAAGGAGCGAG---TCGCGATGGCTAGCCCGCAGG 1188
Db 1207 CCATCAACCAAGTCAGAGTCAAGTAAAGATCGTGTCTCTCCAGCCCGGCGCATG 1266
Qy 1189 GGCCAGAGTATTAAGAGCCGAACAAGCTCAGTAGGTGACAGAGGTCCCAAGCAAGCAAC 1248
Db 1267 GCTGCAAGGAAAGGGGTCTCCCGAGGCCAGAGCGGTCCGCGGTCCCGCAGTCCGGAT 1326
Qy 1249 ATCAGAGCGAGGCGAGTCCCAACCAAGTGAAGAGAGTGGAGCTTCAACGACCGAACC 1308
Db 1327 CAGAGTCTTGTATGACAGCCGAGCAAGGTGCCAAGAGCTGGAGCTTTGGTGAACGCGAGC 1386
Qy 1309 CGCTTCCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAAACCAAGTATAGATGCTGAC 1368
Db 1387 CGCACAGCCAGGCTTCCGATCAAGGTGTGATCCCGCAGAAATTCAGAACCAAGC 1446
Qy 1369 ACAGCCCTTGGACCTGATGATATATGATGAAAGAGATGCCAGTGTGATGATGATGATG 1428
Db 1447 C---TCCCTGGGGAGGACATCGTAGAGCAACAAGAGCTGTAACTGGAGTTTGTGACT 1503
Qy 1429 GAAGACCTCACCCCACTTAAACTGTCTTCGAGCTATCAGAAATTAATGAAATTTTCAAT 1488
Db 1504 GAAGATCTTACCCCTGGCCCTCAAGTTAGCATCAGAGCTGTGTGTTATGGGTTCTTG 1563
Qy 1489 GTTGCAAAACGGAAGTTTAAAGAAACGTTTACGTCATATGATGATGATGATGATGATGATG 1548
Db 1564 GTATCTAAGCGAAAGTTCAAGAGAGTCTGCGCCCATATGATGATGATGATGATGATGATG 1623
Qy 1549 CAATATCTGCTGTGATCTGAGCATGTTGTGTAGAAATTAAGGCTTCAAAACAGCTGTT 1608

Db 1624 CAGTACTCGGCTGGACACTTGGATATGTTGTCCGCATCAAGAGCCTGCAGTCCAGAGTG 1683
Qy 1609 GATCAAAATCTTGGAAAGGGCAATCATCATCAGATAAGAGCGGAGAGAAATAACA 1668
Db 1684 GACCAGATTTGGGGGGGGGGCCCAACAATAACGATTAAGGA---TCGCACCAAGGCCCA 1740
Qy 1669 GCAGAAATGAGACACACAGCATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAA 1728
Db 1741 GCGGAAACGGAGCTGCCCGAAGACCCAGCATGATGGGACGGCTTGGGAAGGTGGAGAA 1800
Qy 1729 CAGGTACAGTCCATAGATGTCAGCTGACCTACTAGACATCTATCAACAG 1782
Db 1801 CAGGTCTTGTCCATGGAAGAAAGCTCGACTTCTTGGTGGATCTATACACAG 1854

RESULT 9
US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; PRIORITY FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIORITY FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1
US-09-495-050A-303

Query Match 18.9%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.8e-141;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1621 GGAAAGGGCAATTCACATCAGATAAGAGCGGAGAGAAATAACAGCAGAAATGAG 1680
Db 1 GAAAGGGCAATTCACATCAGATAAGAGCGGAGAGAAATAACAGCAGAAATGAG 60
Qy 1681 ACCAGACGATCTCAGTATGCTCGGTGCGGTGAGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db 61 ACCAGACGATCTCAGTATGCTCGGTGCGGTGAGTCAAGGTTGAAAAACAGGTACAGTCC 120
Qy 1741 ATAGAGTCAAGCTGGAGTGGCTACTAGACATCTATCAACAGCTCCTTCGGAAGGCTCT 1800
Db 121 ATAGAAATCAAGCTGGAGTGGCTACTAGACATCTATCAACAGCTCCTTCGGAAGGCTCT 180
Qy 1801 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
Db 181 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGACATCT 240
Qy 1861 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTGGGTCCGCAAAAAACAGTGGCTGC 1920
Db 241 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTGGGTCCGCAAAAAACAGTGGCTGC 300
Qy 1921 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTTGCAGTTCATTTGACGCCAAT 1980
Db 301 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTTGCAGTTCATTTGACGCCAAT 360
Qy 1981 GAGTTAGTCCGAGACTTTCTAGCGCTTAGCCCTACTATGTCAGAGTCAAGCAACAG 2040
Db 361 GAGTTAGTCCGAGACTTTCTAGCGCTTAGCCCTACTATGTCAGAGTCAAGCAACAG 420
Qy 2041 GTGCCAATTAGTCAAGAGCGATGGCTCAGCAGTGGCAGCCCAACACCAATTTGCAAAACAA 2100

Db	429	ATYYTEGSGATGMTSCGBATGGACCGGMRGGHGGCACCTGGAAAGCTBYTGGMTCDGYV	488
Qy	670	GTUATGCTCACAGCAAGAAATTAATCAAGCTTGGTACATAGGATTTTGGTTCATT	729
Db	489	RTCTRYGVCACAGCAARGACTSRTSACKGCGTGGTACATYGGYTCTTBSHCTCATC	548
Qy	730	TTTTGTCCTTTCCTGTCTACTCTGGTGGAAAGAGTACCATAAAGATTTTCTACATAT	789
Db	549	CTKKCYTCRTTYCTKGTSTACTYTTGGYWGABAAASDGAWRBGAYSMTTYGASACCTAY	608
Qy	790	GCAGATGCTCTCTGGTGGGCGACAAATTACATATGACAACCTATGGCTATGGAGACAAAAC	849
Db	609	GCRGATGCMCTGGTGGGGYCTGATCACVCTGRCVACCATGGCTAYGGRGACAAGMM	668
Qy	850	CCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTCACCTCTGGCATTTCTTTC	909
Db	669	CCYNARACTGGRANGSGMKCSHTDGCVCVACSTTYWCYTMAITYGGYGTCTCTVTT	728
Qy	910	TTTGCACTTCTCGCGGCATCTTGGCTCAGGTTTTCGATTAAGATCAAGAACACAC	969
Db	729	TTYGCBCTKCGWCGDGGCATVYTGGRCTCYGSGYTKGCGCTSAARGTBCARGAGCARCY	788
Qy	970	CGCCAGAAACACTTTTGAAAGAAGGAAACCCAGCTGCCACCTCATTCACTGTGTTTGG	1029
Db	789	MGKCAARACACTTTGAAARMGGMGAABCCDGDGCGWRBCTSATYCAGKCKGCCTGG	848
Qy	1030	CGTAGTTACGCAGCTGA	1046
Db	849	AGRTWYTRAYGCVAYAA	865

RESULT 11

US-09-177-650-90

; Sequence 90, Application US/09177650

; Patent No. 6413719

; GENERAL INFORMATION:

; APPLICANT: Leppert, Mark F.

; APPLICANT: Singh, Nanda

; APPLICANT: Charlier, Carole

; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE

; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)

; TITLE OF INVENTION: AND OTHER EPILEPSIES

; FILE REFERENCE: 2323-134

; CURRENT APPLICATION NUMBER: US/09/177,650

; CURRENT FILING DATE: 1998-10-23

; EARLIER APPLICATION NUMBER: 60/063,147

; EARLIER FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 129

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 90

; LENGTH: 2814

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (202)..(2811)

US-09-177-650-90

	Query Match	17.2%	Score 464;	DB 3;	Length 2814;
	Best Local Similarity	57.9%;	Prd.No. 2.5e-127;	Indels 66;	Gaps 5;
	Matches 952;	Conservative	Mismatches 623;		
Qy	15	GTGGGGCGGGGAGGGTCTGCTGAATCGGCGACGCCACAGGGCGGACGGCGCTGCTACT	74		
Db	294	GGCGGTGGCCGCGCACAGAGCGGAAAGTGGGGCTGGCGCAGAGAGACGTGGAGCAAGT	353		
Qy	75	GCTGGGCACCCGCGCGCCACGCTTGGTGGCGGCGCGGCTGGCTGAGGGAGAGCGCGCG	134		
Db	354	CACCTTGGCGCTAGGGGCGGGACCCGACAAAGACGGGACCCCTGCTGCTGGAGGGCGGTGG	413		
Qy	135	GGCGACAGGGGGCCCGATAGCTGTGGGGAAGCCGCTTCTTACAGAGTAGCCA	194		
Db	414	CCGCGAAGAGGGGACAGAGGAGGACCCCGCAGGGCATCGGGCTCTGGGCAAGACCCCCCT	473		

[illegible][illegible]

QY 195 GAGCTGCC-----GGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACTCTGACAA 245
DB 474 GAGCGCGCCAGTCAAGAGGAAACAACGCAAGTACAGGCGCATCCAACTTTCATCA 533
QY 246 CGTGTGAGAGACCCCGCGCTGGCGGTTCATCTACACGCTTTCGTTTTCCTGCT 305
DB 534 CGCCCTGGAGAGACCGCGGGCTGGCGGTCTACACGCGCTTGTCTCTGATTTGT 593
QY 306 CTTTGGTGTCTGATTTTGTCACTGTTTCTACCATCCCTGAGCACACAAAATGCGCTC 365
DB 594 CTTGGATGCTTGTCTGGCGTCTCACCCTTCAAGGAATATGAGACTGTGTCTGG 653
QY 366 AAGTGTCCCTTGTGATCTGGAGTTCGTGATGATGCTGCTTTCGTTTGGAGTTCATCAT 425
DB 654 AGACTGGCTTTTGTCTGGAAACATTTGCTATTTTCATCTTTGAGCTGAGTTGCTTT 713
QY 426 TCGAATCTGCTGCGGGTGTCTGTTGCGATATGAGATGCGAAGAGACTGAGGTT 485
DB 714 GAGGATCTGGCTGAGGATGTTGCTGTCATACAAAGGCTGGCGTGGACGGCTAAAGTT 773
QY 486 TCTCGAAAGCCCTTCTGTTTATAGATACCACTTCTTATCGCTTCAATAGACTGTTGT 545
DB 774 TGCCAGGAGCCCTGTGCAATGTTGGACATCTTCGTACTGATGCTCTGTGCCAGTGGT 833
QY 546 TTCTGCAAAAACCTCAGGGTAATATTTTGGCCACGCTGTCACCTCAGAAAGTCTCCGTTTCT 605
DB 834 TGCCGTGGGAACACGAGCAATGTTTGGCCACCT--CCCTGCGAAGCCTTCGCTTCT 890
QY 606 ACAGATCTCCGATGTTGCGCATGGACGGAAGGGAGGACCTTGGAAATACTGGGTTCT 665
DB 891 GCGATCTCCGCGATGCTTCGAATGGATAGAGGGGTGGCACCTGGAAGCTCTCGGCTC 950
QY 666 AGTGTGTTATGCTCACAGCAAGAAATTAATCACACCTTGGTACATAGGATTTTGGTTCT 725
DB 951 GGCTATCTGTGCCACAGCAAGAACTCATCACTGCTGCTGATAGGCTTCTGACACT 1010
QY 726 TATTTTTCCTTCTTCTTCTGCTATCTGTTGGAAGGATG----- 766
DB 1011 CATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1070
QY 767 -----CCATAAAGAGTTTTCATATGACATGCTCTCTGTTGGGACAAAT 815
DB 1071 AGGAGAGAGATGAAGGAGGATTTGAGACCTATGACATGCTCTGTTGGGCGCTGAT 1130
QY 816 TACATTGACAACTATTGCTATGAGACAAAACTCCCTAACTTGGCTGGGAAGTCTCT 875
DB 1131 CACACTGGCCACCTATGTTATGAGACRAGACCTAAACCTGGGAAGGACGCTCTGAT 1190
QY 876 TTCTGAGGCTTTGCACTCCTTGGCATTTCTTTTTCACCTTCTGCGGCACTTCTTGG 935
DB 1191 TGCTGCCACCTTTCTTTAATCGCGCTCTCTTTTGGCTTCTCGGCGAGCATCTTGG 1250
QY 936 CTCAGGTTTTCATTTAAAGTACAGAAACAACCGCCAGAAAACCTTTGAGAAAAGAG 995
DB 1251 CTCAGGACTGGCACTGAAGGTTTCAAGAGCAGCAGCCTGAGAGCACTTTGAGAGAGA 1310
QY 996 GAACCCAGCTGCAACCTCATCTACGTGTTGGGTAGTTACGAGCTGATGAGAAATC 1055
DB 1311 GAAGCCAGCTGGGAACCTATCCAGGCTGCTGGAGATATTATGCTACCAACCCCAACAG 1370
QY 1056 TGTTTCCATTGCAACTGGAAAGCCACACTTGAAGGCTTTGACACCTTCAGCCCTTACCAA 1115
DB 1371 GTTGGATCTGGTGGCAACTGGAGATCTTATGAATCAGTTGTCTCTTTCCATCTTTCAG 1430
QY 1116 GAAAGAACAGGGGAAGCATCAAGCAGTACAGAACTAAGTTTAAAGGAGCGAGTCCGAT 1175
DB 1431 GAAAGAACAACTGGAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1490
QY 1176 GGCTAGCCCCAGGGCCAGAGTATTAAAGCGCCGACAAAGCCTCAGTAGGTGACAGGATC 1235
DB 1491 TTCTAATCTCTGTGTAGCAATACTAA-----AGGAAGCTATTATTAC 1532

QY 1236 CCCAAGCACCGACATCAAGCGGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGGAGCTT 1295
DB 1533 CCCTCTGAATGTAGATGCCATAGAAGAGCCCTTCCAAAGAGCCAAAGCCTTGTGGCTT 1592
QY 1296 CAACGACGAACCCCGCTTCCGCGCTTCCGCTGCGCTCAAAAGTTTCTAGCCAAACCACT 1355
DB 1593 AAACAATAAAGAGCGTTTCCGACCGCTTCCGATGAAGCCTACGCTTCTTGGCAGAG 1652
QY 1356 GATAGATCTCACACAGCCCTTGGCAGCTGATGATATATGATGATAAAGGATGCCAGTG 1415
DB 1653 WTCTGAAGATGCTGGGACAGGAGCC-----CATGGCAGAAAGAGGGGCTATGGAA 1706
QY 1416 TGATGTATCAGTGGAGAGCTCACCCACCACTTAAACTGTCTATTCAGAGCTATCAGAA 1475
DB 1707 TGACWTCTCATTTGAGACATGATCCCTTCCCTTAAAGCTGCCATCCGAGCTGTGAGAT 1766
QY 1476 TATGAATTTTCTGTTGCAAAACGGAAGTTTAAAGAAAGCTTACCTCATATGATGATAA 1535
DB 1767 TCTACAGTTCGCTCTATATAAATAAAGTTTCAAGGAGAGCTTGAAGGCTTATGATGTA 1826
QY 1536 AGATGTCTTCAACAATAATTTCTGCTGCTCATCTGGACATGTTGTAGAAATTTAAAGCT 1595
DB 1827 AGATGTGATGAGCAGTATTCGCGGACATCTTGACATGCTTTCCAGATAAAGTACCT 1886
QY 1596 TCAACACGCTGTTGATCAAAATCT 1619
DB 1887 ACAGACAAGATAGATATGATTTT 1910

RESULT 12

US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCON POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR FILING DATE: 1998-05-59
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

Query Match 17.1%; Score 460.8; DB 3; Length 2565;
Best Local Similarity 57.9%; Pred. No. 2.2e-126;
Matches 953; Conservative 0; Mismatches 627; Indels 56; Gaps 5;
QY 13 GAGTGGGCGCGGCGAGGCTGCTGAACTCGGCGAGCCGCGAGGGGCGAGCGCTGCTA 72
DB 43 GCGGCGGCGCGCGGCGAGGAGCGGAAAGTGGGGCTGGCGCGCGCGGCGAGCGA 102
QY 73 CTGCTGGGCACTCCGCGGCGCCACGCTTGGTGGCGCGCGGCTGGCTTGGAGAGCGCG 132
DB 103 GTCACTTGGCGCTCGGGGCGCGAGCCGACAAAGACCGGACCTGCTCTGGAGGGCGCG 162
QY 133 CGGGCAAGCAGGCGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTTACACGAGTAGC 192
DB 163 GCGCGCAGAGGCGGCGGAGGAGCCCGCAGGCGCATCGGCTCTTGGCCAGAGCCCG 222
QY 193 CAGAGCTGCC-----GGCGCAAGCTCAAGTACCGGCGGCTGCAGAACTTACTGTAC 243

Db 223 CTGAGCGCCAGCTCAAGAGAACAAACGCAAGTACCGGCGCATCCAAACTTTGATCTAC 282
Qy 244 AAGTGTGTGAGAGACCCCGCGCTGGCGTTTCATCTACACGCTTTTCGTTTTCCTCTT 303
Db 283 GAGCGCTGAGAGACCGCGCGCTGGCGTCTTTTACACGCTGTGTCTCTGAT 342
Qy 304 GTCTTTGTTGCTTGTATTTTGTTCAGTGTGTTTCTACCATCCCTGAGCACACAAATTTGGCC 363
Db 343 GTCTGCGGTGCTTGTATTTCTGCTGTCTCTGACACACATTCAGGAGTATGAGACTGTCTCG 402
Qy 364 TCAAGTTTGCCTCTTGTATCTTGTGAGTTCGTGATGATGCTTTGTTGGTTTGGATTCATC 423
Db 403 GGAGACTGGCTTCTGTTACTTGGAGACATTTGCTATTTTCTATTTTGGAGCCGAGTTTGT 462
Qy 424 ATTGCAATCTGCTCGGGTGTGCTGTGTCGATATAGAGATGGCAAGAGACTGAGG 483
Db 463 TTGAGGATCTGGGTGTGATGTTGTCTGCGATACAAAGCTGGCGGGCCGACTGAAG 522
Qy 484 TTTGCTGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATGCTTCAATAGAGATT 543
Db 523 TTTGCGAGGAGCCCTGTGATCTTGGACATCTTTGTGCTGATTTGCTCTGTGCCAGTG 582
Qy 544 GTTCTGCAAAAACCTCAGGGTAATATTTTGGCACGCTGCACTCAGAACTCTCCGTTTC 603
Db 583 GTTGTGTGGGAAACCAAGGCAATGTTCTGGCCACCT---CCCTGGCAAGCCTGCGCTTC 639
Qy 604 CTACAGATCTCCGATGCTGCGATGGACCGAAGGGGAGGCACTTGGAAATTAATCTGGGT 663
Db 640 CTGCGAGATCTTGGGATGCTGCGATGTTGTCTGCGATACAAAGCTGGCGGGCCGACTTCTGGC 699
Qy 664 TCAGTGGTTTATGCTCAGCAAGAAATTAATCAAGCTTGGTACATAGATTTTGGTT 723
Db 700 TCAGCACTGTGCGCCACAGCAAGAACTATCAAGGCTGGTACATCGGTTTCTGCA 759
Qy 724 CTTATTTTCTGCTTCTCTGCTATCTGCTGTTGAAAGAGATGCC----- 768
Db 760 CTCATCTCTTCTCAATTTCTTCTTCTTCTGCTGTTGAAAGAGCTCCAGAGGTGGATGCA 819
Qy 769 -----AATAAGAGTTTCTACATGAGATGCTCTCTCTGTTGGGAGATG 813
Db 820 CAAGGAGAGAGATGAAGAGAGTTTGAGACCTATGAGATGCTCTGTTGGGCGCTG 879
Qy 814 ATTACATTGACAACTATTGGCTATCGGACAAACTCCCTTAATCTGCTGGGAGATG 873
Db 880 ATCACATCGCCACCATTTGGCTATGAGACAAGACACCAACAACTGGGAAGCCGCTG 939
Qy 874 CTTTCTGAGGCTTTCACCTCTTGGCATTTCTTTTGTGCACTTCTCTTCTGCGGCAATCTT 933
Db 940 ATTGCGCCACCTTTTCTTAAATTTGGGCTCTCTTTTGTGCGCTTCCAGCGGCACTCTG 999
Qy 934 GGCTCAGGTTTTCATTAAGATTAAGAAACACACCGCCAGAAACACTTTGAGAAAGA 993
Db 1000 GGCTCCGGGTGCGCCCTCAAGGTGAGGAGCAACCCGTCAGAGCACTTTGAGAAAGG 1059
Qy 994 AGGAAACCACTGCGCACTTCTTCACTGTTGTTGGCTGAGTTTACGAGCTGATGAGAA 1053
Db 1060 AGGAGCGAGCTGCTGAGCTCATTTAGGCTGCTGAGGTATTTATGCTACCAACCCCAAC 1119
Qy 1054 TCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCTTGGACCTGAGGCGCTTACC 1113
Db 1120 AGGATTGACCTGTGGGCGACATGAGATTTTATGAATCAGTCTCTCTTTCTTTCTTC 1179
Qy 1114 AAGAAAGCAAGGGGAGAGATCAAGCAGTCAGAGCTAAGTTTAAAGGAGGAGTGGCC 1173
Db 1180 AGGAAAGCAAGCTGGAGGAGGATCCAGCCAAAGCTGGTCTCTTGTATGGGTTCCG 1239
Qy 1174 ATGCTAGCCCGCCAGGGCCAGAGATTTAAGAGCCGCAAGCTTCAGTGTGAGGAGG 1233
Db 1240 CTTTCTTAACTCTGCTGTAGCAATACTAA-----AGGAAAGCTATTT 1281
Qy 1234 TCCCAAGCAGCCAGCATACAGCGGAGGCTCCCAACCAAGCTGCAAGAGAGCTGGAG 1293
Db 1282 ACCCTCTGATGTAGATGCGATAGAAGAGTCTTCTTAAGAACCAAGAGCTGTGGC 1341

Qy 1294 TTAAACGACGAACCCGCTTCGGCCCTCGCTCGCTCAAAAGTTCTCAGCCAAAACCA 1353
Db 1342 TTAAACAAATAAAGAGCGTTTTCGGACCGCTTCGGATGAAAGCCT-----ACGCTTTC 1395
Qy 1354 GTGATAGATGCTGACACAGCCCTTTGGCACTGATGATGATATATGATGAAAAAGATGCCAG 1413
Db 1396 TGGCAGAGTTCTGAAGATGCGGACAGAGTGACCCCATGGCGAAGACAGGGGCTATGGG 1455
Qy 1414 TGTGATGATCAGTGAAGACCTCACCCACCACTTAAACTTAAACTGTCTCCAGCTATCAGA 1473
Db 1456 AATGACTTCCCATCGAAGACATGATCCCAACCCCTGAAGCGCGCATCCGAGCGCTCAGA 1515
Qy 1474 ATTATGAATTTCTGTTGCAAAACGGAAGTTTAAAGAAACGTTTACGTCCATATGATGTA 1533
Db 1516 ATTTACAAATTCGCTCTCTATAAAAAAATTCAGGAGACTTTGAGGCTTTACGATGTG 1575
Qy 1534 AAAGATGTCATTGAACAATATTTCTGCTGGTCACTGGACATGTTGTGTAGNAATTTAAAGC 1593
Db 1576 AAGATGTTGATGAGCAGTATTTCTGCGGCGCATCTCGACATGCTTCCAGGATAAGTAC 1635
Qy 1594 CTTCAAAACAGTGTGATCAAAATTTCT 1619
Db 1636 CTTCAAGCAGAAATAGATATGATTTT 1661

RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.

FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

Query Match 17.1%; Score 460.8; DB 3; Length 2914;
Best Local Similarity 57.9%; Pred. No. 2.4e-126;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

QY 13 GAGTCGGGCGGGGAGGAGTGTCTGAACCTGGCAGCCGCGCAGGGGCGACGGCTGTCTA 72
DB 115 GCGGGCGGCGCGCGACAGAGAGCGGAAAGTGGGCTGGCCCGCGACGTGGAGCAA 174

QY 73 CTGCTGGGCAACCGCGCGCGCGCTTGGTGGCGGCGGCTGGCTGAGGGAGAGCGCG 132
DB 175 GTCACTTGGCGCTCGGGGCGGAGCGCGACAAGACGGACCTGTCTGTGAGGGCGGC 234

QY 133 CGGGGCAAGAGGGGCGCGGATGAGCTGTCTGGGAAAGCGCTCTCTTACAGAGTAGC 192
DB 235 GCGCGGACAGGGGCGCGGAGGACCGCGCAGGGCATCGGCTCTCTGGCCAAGACCGCG 294

QY 193 CAGAGCTGCC-----GGCGCAACGTCAAGTACCGGCGGGTGCAGAACTACCTGTAC 243
DB 295 CTGAGCGGCCAGTCAAGAGAAACAAACGCCAAGTACCGGGCGATCCAACTTTGATCTAC 354

QY 244 AACGTCTGAGAGACCCCGCGCTGGGCTTCACTACACGCTTTGGTTTTCTCTT 303
DB 355 GACGCGCTGGAGAGCCGCGGCGCTGGGCTGTCTTACGCGTTGGTGTCTCTGATT 414

QY 304 GTCTTTGGTGTGATTTTGTCAAGTGTCTTACCATCCCTGAGCACAAAAATTGGCC 363
DB 415 GTCTGGGCTGTGATTCTGGCTGTCTGACCACTTCAAGGAGTATGAGACTGTCTCG 474

QY 364 TCAAGTGTCTTGTGATCTGAGATTCGTGATGATTTGCTGTTGGTTGGAGTTTATC 423
DB 475 GGAGACTGTGCTTGTGATCTGAGAGATTTGTGATTTTTCATCTTTGGAGCGGTTTGT 534

QY 424 ATTGCAATCTGTCTGGCGTGTCTGTCTGATATAGAGGATGCAAGAGAGCTGAGG 483
DB 535 TTGAGATCTGGGCTGTGATTTGTCTCCGATACAAAGGCTGGCGGGCGCATGGAAG 594

QY 484 TTTGCTCGAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCAGTT 543
DB 595 TTTGCCAGGAAGCCCTGTGCTGATTTGGACATCTTTGTCTGATTGCTCTGTGCCAGTG 654

QY 544 GTTCTGCAAAACTCAGGGTAATTTTGGCACTGTGCACTCAGAACTCCGTTTC 603
DB 655 GTTGTGTGGGAAACCAAGGCAATGTTCTGGCCACCT---CCCTGCAAGCCCTGGGCTTC 711

QY 604 CTACAGATCTCGCATGTGCGCATGGACCGAAGGGAGGCACTTGGAAATTTACTGGCT 663
DB 712 CTGCAATCTGGGATGCTGGATGGAACCGAGGAGTGGCACCTGGAAGCTTCTGGGC 771

QY 664 TCAGTGGTTTATCTCACAGCAAGGAATTAATCACAGCTTGGTATAGAGATTTTGGTT 723
DB 772 TCAGCCATCTGTGCCACAGCAAGAACTCATCAGCGCTGTGTACATCGTTTCTGTACA 831

QY 724 CTTATTTTCTCTTCT 768
DB 832 CTATCTCTTCT 891

QY 769 -----AATAAGATTTTCTACATATGACAGATGCTCTCTGGTGGGCGACA 813
DB 892 CAAGAGAGGAGATGAAGAGAGTTTGAGACTATGACAGATGCTCTGTGGTGGGCGCTG 951

QY 814 ATTACATTGACAACTATTGGCTATGGAGCAAACTCCCTTAACCTTGGCTGGGAAAGTTG 873
DB 952 ATCACATGCGCCACCATTTGGCTATGGAGACAGACACCAAAACGTGGGAAGCGCTGTG 1011

QY 874 CTTTCTGAGGCTTTGCACTCTTGGCACTTTCTTTTGTGCACTTCTCTGCGGCAATCTT 933
DB 1012 ATTGGCGGCACCTTTTCTTAAATTGGCGTCTCTCTTTTGGCCCTTCCAGCGGCACTCTG 1071

QY 934 GSCTCAGGTTTTTGCAATTAAGTCAAGAACCAACCGCCAGAACACCTTTTGAGAAAGA 993
DB 1072 GGTCCGGGCTGGCCCTCAAGGTGAGGAGCAACACCGTCAAGAGCACTTTGAGAAAGG 1131

QY 994 AGGAACCCAGCTGCCAACCTCATTCAGTGTGTGTGGCGTAGTTACGACAGCTGATGAGAA 1053
DB 1132 AGGAAGCCAGCTGCTGAGCTCATTCAGGCTGCTGAGGATTTATGCTACCAACCCCAAC 1191

QY 1054 TCTGTTTTCCATTGCAACCTGGNAGCCACACTTGAAGGCTTGCACACCTGACGACCTTACC 1113
DB 1192 AGGATGTACCTGGTGGCGACATGGAGATTTTATGAATCAGTCGTCTCTCTTTCTTTC 1251

QY 1114 AAGAAAGAACCAAGGGGAAAGCATCAAGCAGTCAAGAGCTAAAGTTTAAAGGAGCGAGTGC 1173
DB 1252 AGGAAGAACAGCTGGAGCGACATCCAGCCAAAGCTGGGTCTCTTGGATCGGTTCCG 1311

QY 1174 ATGGCTAGCCCGAGGGCCAGAGTATTAAAGACCGCAAGCCTCAGTAGGTGACAGGAGG 1233
DB 1312 CTTTCTAATCTCGTGGTAGCAATACTAA-----AGGAAAGCTATTT 1353

QY 1234 TCCCAAGCAGCAGCATCACAGCCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGGAGC 1293
DB 1354 ACCCTCTGAATGTAGATGCCATAGAGAAAGTCTCTTAAAGAACCAAGCCCTGTGGC 1413

QY 1294 TTCAAGCAGCCGAACCCGCTTCGGGCTTCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCA 1353
DB 1414 TTAAACAATAAGAGCGTTTCGACGCGCTTCGCGCATGAAGCCCT-----ACGCTTTC 1467

QY 1354 GTGATAGATGTCACAGCCCTTGGCACTGATGATGATATGATGAAGGAGGATGCCAG 1413
DB 1468 TGGCAGAGTTCTGAAGATGCGGGACAGGTGACCCCATGGCGGAAGACAGGGGCTATGG 1527

QY 1414 TGTGATGATCAGTGGAGAGCTCACCCCAACCACTTAAACTGTCTATTCGACGTATCAGA 1473
DB 1528 AATGACTTCCCATCGAAGACATGATCCCACTTGAAGGCGCCATCCGAGCCGCTCAGA 1587

QY 1474 ATATGAATTTCAATGTTGCAAAACGGAAGTTTAAAGGAAACGTTACGTCCATATGATGA 1533
DB 1588 ATTTCAATTTCCGTCTCTATATAAATAAATTCAGAGAGACTTTCAGGCGCTTACGATGTG 1647

QY 1534 AAGATGTCATTGAACAAATTTCTGCTGCTCATCTGGAATGTTGTGTAGAAATTAAGAGC 1593
DB 1648 AAGATGTCATTGAGCAGTATTCTGCGGGCATCTCGACATGCTTCCAGGATAAAGTAC 1707

QY 1594 CTTCAACACAGTGTGATCAAAATTTCT 1619
DB 1708 CTTCAAGCAGAGATAGATATGATTTT 1733

RESULT 14
US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118, 318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 305
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006F6

NAME/KEY: unsure
LOCATION: 486, 510, 552, 573
OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

Query Match 16.8%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 3.2e-124;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

1621 GGAAGGGGCAATCAGATCAGATAGAGAGCGGAGAGAAATAACAGCAGAAATGAG 1680
1 GGAAGGGGCAATCAGATCAGATAGAGAGCGGAGAGAAATAACAGCAGAAATGAG 60
1681 ACCACAGACCATCTCAGTATGCTCGGTTCGGTCAAGGTTGAAAGAAAGAGTACAGTCC 1740
61 ACCACAGACCATCTCAGTATGCTCGGTTCGGTCAAGGTTGAAAGAAAGAGTACAGTCC 120
1741 ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGAAAGGCTCT 1800
121 ATAGAAATCCAAAGCTGGAGTGCCTACTAGACATCTATCAACAGGTCTTCGAAAGGCTCT 180
1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCACCTTTGAAATGTGAACAGCATCT 1860
181 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCACCTTTGAAATGTGAACAGCATCT 240
1861 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGACAAAACAGTGGCTGC 1920
241 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGACAAAACAGTGGCTGC 300
1921 TTATCCAGATCAATAGTGGCAACATCTCGAGAGGCTGCAAGTTCATTTGACGCCAAAT 1980
301 TTATCCAGATCAATAGTGGCAACATCTCGAGAGGCTGCAAGTTCATTTGACGCCAAAT 359
1981 GAGTTCAGTGGCCAGACTTTCTACGGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2040
360 GAGTTCAGTGGCCAGACTTTCTA--CGCTTAGCTTATGACAGTCAAGCAACACAG 417
2041 GTGCCAAATAGTCAAAAGCGATGGCTCAGCAGTGGGAGCGACCAACAATTTGAAACCA 2100
418 GTGCCAA--TAGTCAAAAGCGATGGCTCAGCAGTGGGAGCGACCAACAATTTGAAACCA 475
2101 ATAAATAGGCAACCAAGCCAGCAGCCCAACACTTTTACAGATCCCACTCTCTCT 2156
476 ATAAATAGGCAACCAAGCCAGCAGCCCAACACTTTTACAGTCTCTCTCTCTCTCT 531

RESULT 15
US-09-105-058C-19
Sequence 19, Application US/09105058C
Patent No. 6403360
GENERAL INFORMATION:
APPLICANT: Blumar, Michael A.
APPLICANT: Dworetzky, Steven
APPLICANT: Grikoff, Valentin K.
APPLICANT: Levesque, Paul C.
APPLICANT: Little, Wayne A.
APPLICANT: Neubauer, Michael G.
APPLICANT: Yang Wen-Pin
TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
FILE REFERENCE: 3053-4052
CURRENT APPLICATION NUMBER: US/09/105,058C
CURRENT FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 60/055,599
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 3287
TYPE: DNA
ORGANISM: Homo sapiens
US-09-105-058C-19

15 88. score 425: DB 3: Length 3287:

Search completed: April 11, 2005, 21:46:20

Job time : 446.638 secs



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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2694	100.0	2694	6	AX322509	Sequence
2	2689	99.8	3137	6	AX430568	Sequence
3	2689	99.8	3137	6	AX056817	Sequence
4	2689	99.8	3137	9	AF202977	Homo sapi
5	2681.2	99.5	3074	6	AX393778	Sequence
6	2681.2	99.5	3074	6	AX253254	Sequence
7	2681.2	99.5	3074	6	AX456864	Sequence
8	2681.2	99.5	3074	9	AF249278	Homo sapi
9	2625.2	97.4	2772	6	AX565635	Sequence
10	2625.2	97.4	2772	6	AX268474	Sequence
11	2625.2	97.4	3111	6	AX565636	Sequence
12	2625.2	97.4	3111	6	AX368476	Sequence
13	2585	96.0	2832	6	BD275572	Novel Hum
14	2571.6	95.5	2832	9	AF263835	Homo sapi
15	2217.4	82.3	3108	10	AF263836	Mus muscu
16	1548.8	57.5	1552	6	CQ720576	Sequence
17	1142	42.4	1508	9	BC050689	Homo sapi
18	963.4	35.8	1691	9	AF272519	Homo sapi
19	963.4	35.8	120846	9	AL365232	Human DNA

181 TACACGAGTAGCAGAGCTCCCGGCGCAACGTCACGACCGGGGTGCAGAACTACCTG 240 Db
241 TACAACGTGCTGGAGAGACCCCGGGCTGGCGCTTCATCTACACGCTTTCCCTTTCTC 300 Qy
241 TACAACGTGCTGGAGAGACCCCGGGCTGGCGCTTCATCTACACGCTTTCCCTTTCTC 300 Db
301 CTGTCTTTGGTTGCTTGTATGTTGTGTCAGTGTCTTTTACCATCCCTCAGACACAAATG 360 Qy
301 CTGTCTTTGGTTGCTTGTATGTTGTGTCAGTGTCTTTTACCATCCCTCAGACACAAATG 360 Db
361 GCCTCAAGTTGCCCTTCATGCTGGAGTTCTGTGATGATGCTCTTTGGTTGGAGTTC 420 Qy
361 GCCTCAAGTTGCCCTTCATGCTGGAGTTCTGTGATGATGCTCTTTGGTTGGAGTTC 420 Db
421 ATCAATTCGAATCTGGTCTGGGTTGCTGTGTCGATATAGAGATGGCAAGCAACTG 480 Qy
421 ATCAATTCGAATCTGGTCTGGGTTGCTGTGTCGATATAGAGATGGCAAGCAACTG 480 Db
481 AGGTTTGTCTCGAAGCCCTTCGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 540 Qy
481 AGGTTTGTCTCGAAGCCCTTCGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 540 Db
541 GTTGTCTCTGCAAAACTCAGGGTAATATTTTCCGACGCTGCACCTCAGAGTCTCCGT 600 Qy
541 GTTGTCTCTGCAAAACTCAGGGTAATATTTTCCGACGCTGCACCTCAGAGTCTCCGT 600 Db
601 TTCCTACAGATCCCTCGGATGGTGGCATGCACCGAAGGGGAGGCACTTGGAAATTA 660 Qy
601 TTCCTACAGATCCCTCGGATGGTGGCATGCACCGAAGGGGAGGCACTTGGAAATTA 660 Db
661 GGTTCAGTGGTTTATGCTCACAAGCAAGAAATTAATCAAGCTTGGTACATAGGATTTT 720 Qy
661 GGTTCAGTGGTTTATGCTCACAAGCAAGAAATTAATCAAGCTTGGTACATAGGATTTT 720 Db
721 GTTCTTATTTTTCGTTCTCTCTCTATCTGTTGGAAGAAAGGATGCCAATAAAGAGTT 780 Qy
721 GTTCTTATTTTTCGTTCTCTCTCTATCTGTTGGAAGAAAGGATGCCAATAAAGAGTT 780 Db
781 TCTACATATGCAGATGCTCTCTGTTGGGCAACAATTAATCAAGCTTGGTATGGA 840 Qy
781 TCTACATATGCAGATGCTCTCTGTTGGGCAACAATTAATCAAGCTTGGTATGGA 840 Db
841 GACAAACTCCCTTAATCTGCTGGAGATGCTTCTGCAAGGCTTGGCACTCCCTGGC 900 Qy
841 GACAAACTCCCTTAATCTGCTGGAGATGCTTCTGCAAGGCTTGGCACTCCCTGGC 900 Db
901 ATTTCTTTCTTGCACTTCTGCGGCAATTTTGGCTCAGGTTTGGATTAAGTACAA 960 Qy
901 ATTTCTTTCTTGCACTTCTGCGGCAATTTTGGCTCAGGTTTGGATTAAGTACAA 960 Db
961 GAAACAACCGCCAGAAACAATTTGAAAGAAAGAAAGGAAAGGCTGCCAACCCTTCA 1020 Qy
961 GAAACAACCGCCAGAAACAATTTGAAAGAAAGAAAGGAAAGGCTGCCAACCCTTCA 1020 Db
1021 TGTGTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCA 1080 Qy
1021 TGTGTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCA 1080 Db
1081 CACTTTGAAGGCTTGCACCTGAGCCCTTACCAAGAAAGAAAGGAAAGGCTCAAGC 1140 Qy
1081 CACTTTGAAGGCTTGCACCTGAGCCCTTACCAAGAAAGAAAGGAAAGGCTCAAGC 1140 Db
1141 AGTCAGAGCTAAGTTTATAGGAGCTGCGATGCTAGCCCGGAGGAGGCTAGATTT 1200 Qy
1141 AGTCAGAGCTAAGTTTATAGGAGCTGCGATGCTAGCCCGGAGGAGGCTAGATTT 1200 Db
1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGTTCCTCAAGCAAGGCTCAGCCGAG 1260 Qy
1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGTTCCTCAAGCAAGGCTCAGCCGAG 1260 Db
1261 GGCAGTCCCAAAAGTGCAGAGGCTTGAAGCTTCAACGACCAAGGCTTCCGCGCC 1320 Qy
1261 GGCAGTCCCAAAAGTGCAGAGGCTTGAAGCTTCAACGACCAAGGCTTCCGCGCC 1320 Db

1321 TCGTGTGGCTCAAAAGTTCTCAGCCAAACACAGTGTATAGATGCTGACACAGCCCTTGGC 1380 Qy
1321 TCGTGTGGCTCAAAAGTTCTCAGCCAAACACAGTGTATAGATGCTGACACAGCCCTTGGC 1380 Db
1381 ACTCATCATGTATATGATAAAGGATGCCAGTGTGTATATCAGTGGAGACCTTCACC 1440 Qy
1381 ACTCATCATGTATATGATAAAGGATGCCAGTGTGTATATCAGTGGAGACCTTCACC 1440 Db
1441 CCACCCTTAAACTGTCAITTCGAGCTTATCAGAAATTAATGAAATTTCAATTTGCAAAACGG 1500 Qy
1441 CCACCCTTAAACTGTCAITTCGAGCTTATCAGAAATTAATGAAATTTCAATTTGCAAAACGG 1500 Db
1501 AAGTTAAGGAAAGCTTACGTCCTATATGATGTAAGAGATGTCATTTGAAACAATTTCTGCT 1560 Qy
1501 AAGTTAAGGAAAGCTTACGTCCTATATGATGTAAGAGATGTCATTTGAAACAATTTCTGCT 1560 Db
1561 GGTCTATCTGGAATGTTGTGTAGAAATTAAGGCTTCAACACGCTTGTGATCAAAATTTCT 1620 Qy
1561 GGTCTATCTGGAATGTTGTGTAGAAATTAAGGCTTCAACACGCTTGTGATCAAAATTTCT 1620 Db
1621 GGAAGGAGGCAATCAATCAGATGTAAGAGAGCCGAGGAAATAACAGCAGAAACATGAG 1680 Qy
1621 GGAAGGAGGCAATCAATCAGATGTAAGAGAGCCGAGGAAATAACAGCAGAAACATGAG 1680 Db
1681 ACCACAGAGATCTCAGTATGCTCGGTGGGTGTTCAAGTTGAAATGTAAGAGATGTCAT 1740 Qy
1681 ACCACAGAGATCTCAGTATGCTCGGTGGGTGTTCAAGTTGAAATGTAAGAGATGTCAT 1740 Db
1741 ATAGAGTCAAGCTGGAGTCTGCTACTAGACATCTATCAACAGGCTCTTCGAAAGGCTCT 1800 Qy
1741 ATAGAGTCAAGCTGGAGTCTGCTACTAGACATCTATCAACAGGCTCTTCGAAAGGCTCT 1800 Db
1801 GCTCAGCCCTCGCTTGGCTTCAITTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1860 Qy
1801 GCTCAGCCCTCGCTTGGCTTCAITTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1860 Db
1861 GACTATCAAGGCTTGGATAGCAAGATCTTTGGGTCCGCAACAAACAGTGGCTGTC 1920 Qy
1861 GACTATCAAGGCTTGGATAGCAAGATCTTTGGGTCCGCAACAAACAGTGGCTGTC 1920 Db
1921 TTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTTCAGTTCATTTGACGCAAAAT 1980 Qy
1921 TTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTTCAGTTCATTTGACGCAAAAT 1980 Db
1981 GAGTTCAGTGGCCAGACTTTCTACGCGCTTACGCTTACAGTCAAGTCAAGCAACAG 2040 Qy
1981 GAGTTCAGTGGCCAGACTTTCTACGCGCTTACGCTTACAGTCAAGTCAAGCAACAG 2040 Db
2041 GTGCCAATTTAGTCAAGCGATGGCTCAGCGTGGCAGCCCAACCAACCACTTGCACCA 2100 Qy
2041 GTGCCAATTTAGTCAAGCGATGGCTCAGCGTGGCAGCCCAACCAACCACTTGCACCA 2100 Db
2101 ATAAATACGGCAGCCCAAGCCAGCAGCCCAACCACTTACAGATCCACCTCTCTCCCA 2160 Qy
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RESULT 2
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LOCUS AR430568 3137 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6649371.
ACCESSION AR430568
VERSION AR430568.1 GI:40191384
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3137)
AUTHORS Jentsch, T.J.
TITLE Potassium channel KCNQ5 and sequences encoding the same
JOURNAL Patent: US 6649371-A 1 18-NOV-2003;
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Location/Qualifiers
source 1..3137
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ORIGIN

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Tue Apr 12 17:15:10 2005

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DEFINITION member 5 (KCNQ5) mRNA, complete cds.
ACCESSION AF202977
VERSION AF202977.1 GI:7798695
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3137)
Schroeder, B.C., Hechenberger, M., Weinreich, F., Kubisch, C. and
Jentsch, T.J.,
KCNQ5, a novel potassium channel broadly expressed in brain,
mediates M-type currents
J. Biol. Chem. 275 (31), 24089-24095 (2000)
JOURNAL MEDLINE 20379054
PUBMED 10816588
REFERENCE 2 (bases 1 to 3137)
Schroeder, B.C., Hechenberger, M., Weinreich, F., Kubisch, C. and
Jentsch, T.J.,
Direct Submission
Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse
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199.8%; Score 2689.2; DB 9; Length 3137;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DEFINITION Sequence 1 from Patent WO0170811.
ACCESSION AX253254
VERSION AX253254.1 GI:16073802
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Lerche, C., Scherer, C., Seebohm, G., Busch, A. and Steinmeyer, K.
TITLE Potassium channel protein kcnq5, a target for diseases of central
nervous system and cardiovascular system
JOURNAL Patent: WO 0170811-A 1 27-SEP-2001;
Aventis Pharma Deutschland GmbH (DE)
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ORIGIN
Query Match 99.5%; Score 2681.2; DB 6; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 121 AGGAGAGCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Db 335 AGGAGAGCCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 394
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Db 395 TACAGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 454
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VERSION					
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LOCUS AR565635 2772 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6767736.
ACCESSION AR565635
VERSION AR565635.1 GI:53981668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2772)
AUTHORS Hu, Y., Kieck, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G.,
Zambrowicz, B. and Sands, A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;
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DEFINITION Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1.
AUTHORS Hu,Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
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Location/Qualifiers
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Best Local Similarity 98.9%; Pred. No. 0;
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QY	2341	TTGTCTGTCTG	TCCCATG	TGTCGCGAGGACTTGGGCA	AAATCTTTTGTCTGTGCAAAACCTG	2400
DB	2419	TTGTCTGTCTG	TCCCATG	TGTCGCGAGGACTTGGGCA	AAATCTTTTGTCTGTGCAAAACCTG	2478
QY	2401	ATCAGTGC	ACCGAGAACTGA	ATATACATTTTCAGGAGT	AGTCAAGTGGCTCCAGA	2460
DB	2479	ATCAGTGC	ACCGAGAACTGA	ATATACATTTTCAGGAGT	AGTCAAGTGGCTCCAGA	2538
QY	2461	GGCAGCC	ACAGATTTTTTAC	CCCCAAATGGAGGAA	ATCCAAATTTGTTTAACTGATGAAGAG	2520
DB	2539	GGCAGCC	ACAGATTTTTTAC	CCCCAAATGGAGGAA	ATCCAAATTTGTTTAACTGATGAAGAG	2598
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Db	705	GTTCGTTCTTCGAAAACTCAGGGTAAATATTTTTGGCCACGCTCGCATCAGAAAGTCTCCGT	764
Qy	601	TTCCCTACAGATCCTCCGCGATGGTCGCATCGACCGAAGGGGAGGCATCTGGAATTAATCTG	660
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Db	825	GGTTCACTGGTTTATAGTCTCACAGCAAGGAATTAATCAACAGCTTTGGTACATAGGATTTTTG	884
Qy	721	GTTCCTTATTTTTTCGTCCTCTTTCCTTGTCTACTCTGCTGGAAGAGATGCCAATAAAGAGTTT	780
Db	885	GTTCCTTATTTTTTCGTCCTCTTTCCTTGTCTACTCTGCTGGAAGAGATGCCAATAAAGAGTTT	944
Qy	781	TCTACATATGAGATGCTCTCTGCTGGGGCAGCAATTAATGACCACTATTTGGCTATGGA	840
Db	945	TCTACATATGAGATGCTCTCTGCTGGGGCAGCAATTAATGACCACTATTTGGCTATGGA	1004
Qy	841	GACAAAACTCCCCTAACTTGGCTGGGAAGATTTGCTTTCTCGAGGCTTTGCACTCCTTTGGC	900
Db	1005	GACAAAACTCCCCTAACTTGGCTGGGAAGATTTGCTTTCTCGAGGCTTTGCACTCCTTTGGC	1064
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Db	1065	ATTTCTTTCTTTTGCACTCTCTGCTGGCGGCAATCTTTGGCTCAGGTTTGCATTTAAAGTACAA	1124
Qy	961	GAACAACACCGCCAGAAACACTTTGAAAAGAGGAACCCAGCTGCCACCTCATCTCAG	1020
Db	1125	GAACAACACCGCCAGAAACACTTTGAAAAGAGGAACCCAGCTGCCACCTCATCTCAG	1184
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Db	1185	TGTGTTTGGGCTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTTGCAACTCTGGAAGCCA	1244
Qy	1081	CACTTGAAGGCTTTGCAACACTGTCAGGCGCTTACCAAGAAAGAAACAAGGGGAAGCATCAAGC	1140
Db	1245	CACTTGAAGGCTTTGCAACACTGTCAGGCGCTTACCAAGGCGCTTACCAAGGCGCGCTTACCAAG	1279
Qy	1141	AGTCAGAAAGCTAGTTTTTAAGGAGCGAGTCGGCATGGCTAGCCAGCCAGGGGCCAGAGTATT	1200
Db	1280	- -TCAGAAAGCTAGTTTTTAAGGAGCGAGTCGGCATGGCTAGCCAGGGGCCAGAGTATT	1337
Qy	1201	AAGAGCCGACAAAGCCTCAGTAGGTGACAGAGAGTCCCAAGACACCGACATCAAGCCGAG	1260
Db	1338	AAGAGCCGACAAAGCCTCAGTAGGTGACAGAGAGTCCCAAGACACCGACATCAAGCCGAG	1397
Qy	1261	GGCAGTCCCAACAAAGTGCAGAGAGTGGAGCTTCAACGACCGAACCCGCTTCCGCGCC	1320
Db	1398	GGCAGTCCCAACAAAGTGCAGAGAGTGGAGCTTCAACGACCGAACCCGCTTCCGCGCC	1457
Qy	1321	TCGCTGGCGCTCAAAAGTTCTCAGCCAAAACCGATGATAGATGCTGACACAGGCCCTTGGC	1380
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LOCUS BD275572 3718 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Human Voltage-Gated Potassium Channel.
ACCESSION BD275572
VERSION BD275572.1 GI:33085340
KEYWORDS JP 2002543768-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 3718)
AUTHORS Metzker, M.L., Li, W., Petrukhin, K. and Caskey, T. C.
TITLE Novel Human Voltage-Gated Potassium Channel
JOURNAL Patent: JP 2002543768-A 2 24-DEC-2002;
COMMENT Merck and Co Inc
OS Homo sapiens
PN JP 2002543768-A/2
PD 24-DEC-2002
PF 10-APR-2000 JP 2000611548
PR 14-APR-1999 US 60/129274
PI michael l metzker, wen li, konstantin petrukhin, thomas c caskey
CC
FH
FEATURES
source
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Query Match 96.0%; Score 2585; DB 6; Length 3718;
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AUTHORS		Kniazeva, M. and Han, M.	
TITLE		Direct Submission	
JOURNAL		Submitted (04-MAY-2000) MCD, University of Colorado at Boulder,	
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 LOCUS Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
 DEFINITION partial cds.
 ACCESSION AF263836
 VERSION AF263836.1 GI:8132998
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3108)
 AUTHORS Kniazeva, M. and Han, M.
 TITLE A new gene of the voltage-gated potassium channel KCNQ family.
 KCNQ5, is a candidate gene for retinal disorders
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3108)
 AUTHORS Kniazeva, M. and Han, M.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA
 FEATURES
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 /sex="male"
 /tissue_type="brain"
 /dev_stage="9-11 weeks"
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 /db_xref="GI:8132998"
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 AVNSAQTCQNI FATSALRSURFQILRNVRMDRGGTVKLLGSVVAHSEKELITAMG
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 gene
 CDS

ORIGIN

	Query Match	82.3%;	Score 2217.4;	DB 10;	Length 3108;
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Qy	57	GGGCGACGGCTGTACTGTGGGCACC	CGCGGCCACGTTTGGTCGGCGCGGTGG	116	
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Tue Apr 12 17:15:10 2005

Qy	2397	CCTGATCAGGTCGACCGAGAACTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGGCTC	2456
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Db	2401		
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Db	2461		
Qy	2577	GGAAGCTGCCTTTTGCATCAGACTCTTAAGGACTTGAAGGTACAGATCATCTCAGAGCAT	2636
Db	2521		
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Db	2581		

Search completed: April 11, 2005, 16:49:33
Job time : 13351.3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:07:42 ; Search time 1379.41 Seconds
(without alignments)
11561.287 Million cell updates/sec

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Perfect score: 2694
Sequence: 1 atgaaggatgtggatcggg.....ctcatgtcaactgaaataa 2694

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004as: *
13: Geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	ID	Description
1	2694	100.0	2694	4	AAS14652 Human CDN
2	2694	100.0	2694	6	AAD27192 Human pot
3	2690.4	99.9	3071	4	AAS14651 Human CDN
4	2689.2	99.8	3137	4	AAC85414 Human KCN
5	2681.2	99.5	3074	4	AAB49499 Human KCN
6	2679.6	99.5	3074	10	ADB78684 Human pot
7	2630	97.6	2667	4	AAS14653 Human CDN
8	2625.2	97.4	3111	5	AAB43633 Human ion
9	2625.2	97.4	3111	5	AAB43634 Human ion
10	2585	96.0	3718	3	AAC64371 Human KCN
11	963.4	35.8	125910	3	AAC64370 Human KCN
12	518.4	19.2	2335	3	AAA47618 Human KCN
13	518.4	19.2	2335	10	ADE31698 Human KCN
14	516	19.2	2273	2	AAH57140 Mouse KCN
15	510	18.9	2169	2	AAH57140 Mouse KCN
16	509.8	18.9	582	8	ACA04855 cDNA enco
17	500.6	18.6	7407	10	ADB78688 Human pot
18	500.6	18.6	7407	10	ADB78686 Human pot
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21	500.6	18.6	7411	10	ADD29557 Human tum
22	500.6	18.6	7420	11	ADN38963 Cancer/an
23	500.6	18.6	7420	11	ADP65810 Human mRN
24	500.6	18.6	7420	11	ADP65731 Human pot
25	500.6	18.6	7420	12	ADL06495 Human tum
26	500.6	18.6	7863	10	ADJ56529 Human CDN
27	499	18.5	7407	10	ADB78685 Human pot
28	480.6	17.8	7413	5	AAS74832 DNA enco
29	478.4	17.8	7413	5	ADSI7851 Rattus no
30	477	17.7	2565	2	AAH81548 Human bra
31	477	17.7	3195	5	AAH81548 Human bra
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33	465.8	17.3	2766	13	ADSI7849 Rattus no
34	465	17.3	548	6	ABA90234 Human ORF
35	464	17.2	2814	2	AAS57141 Mouse KCN
36	460.8	17.1	2565	2	AAH26596 Nucleotid
37	460.8	17.1	2914	2	AAH57059 Human KCN
38	460.8	17.1	2926	10	ADB78690 Human pot
39	460.8	17.1	2926	10	ADB78682 Human pot
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43	455.8	16.9	1848	12	ADH51119 Potassium
44	455.8	16.9	1848	12	ADM77995 KCNQ2-15b
45	454.2	16.9	4512	10	ADJ56528 Rat cDNA

ALIGNMENTS

RESULT 1
AAS14652
ID AAS14652 standard; cDNA; 2694 BP.
XX
AC AAS14652;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-1.
XX
KW Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
PH Key
CDS Location/Qualifiers
FT 1..2994
FT /*tag= a
FT /product= "hKCNQ5-1"
XX

WO200170759-A1.
XX
XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US009328.
XX
XX 21-MAR-2000; 2000US-0190954P.
XX
XX (ICAG-) ICAGEN INC.
XX
XX Jegla TJ;
XX
XX WPI; 2001-611467/70.
XX P-PSDB; AAU09020.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
XX identifying a compound modulating ion flux in eukaryotic cell or cell
XX membrane expressing the protein, comprises KCNQ approximatelya- subunits.
PS Claim 5; Page 62-63; 78pp; English.

XX	The invention relates to an isolated polypeptide comprising an alpha-
CC	subunit of a KCNQ potassium channel, with a subsequence having 65%
CC	sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC	and forms a KCNQ potassium channel having the characteristic of voltage-
CC	gating with at least an additional KCNQ alpha-subunit. Also included in
CC	the scope of the invention are the nucleic acids encoding hKCNQ5
CC	(including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC	vectors encoding them, antibodies against them, the use of 3-dimensional
CC	computer modelling to identify molecules that bind to a KCNQ containing
CC	potassium channel and modulate ion flux through the channel. The KCNQ
CC	polypeptide is useful for identifying a compound that increases or
CC	decreases ion flux through a potassium channel expressed in an eukaryotic
CC	host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC	used in gene therapy) is useful as a pharmaceutical agent for treating
CC	diseases involving abnormal ion flux, such as disorders of the central
CC	nervous system, such as epilepsy, migraines, hearing and vision problems,
CC	psychotic disorders, seizures, learning and memory disorders, stroke and
CC	pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC	human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC	computer databases to find variants of the sequence which are associated
CC	with disease states, is useful for screening mutations of KCNQ5. The
CC	present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-1
XX	
SQ	Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;
	Query Match 100.0%; Score 2694; DB 4; Length 2694;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	61 GACGGCTGTACTGTCTGGGCACCGCGCGCCACCGTTGTGTGGCGCGCGGTGGCGCTG 120
Qy	121 AGGGAGAGCCGCGGGGCAAGCAGGGGGCCGGATGAGCTGTGTGGGAAGCCGCTCTCT 180
Db	121 AGGGAGAGCCGCGGGGCAAGCAGGGGGCCGGATGAGCTGTGTGGGAAGCCGCTCTCT 180
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Qy	301 CTGTGCTTTGGTTGCTTGATTTTTGTTCAGTGTGTTTCTACCATCCCTGAGCACAAAAATTG 360
Db	301 CTGTGCTTTGGTTGCTTGATTTTTGTTCAGTGTGTTTCTACCATCCCTGAGCACAAAAATTG 360
Qy	361 GCCTCAAGTTGCTCTTTGATCCTGGAGTTTCGTGTGATGATTTGTCGTCTTTGGTTGAGTTTC 420
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Qy	421 ATCATTTCGAATCTGFTCTCGGGTTGCTGTTGTCGNATATAGAGTAGGCAAGAGACACTG 480
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 Db 421 ATCAATTCGAATCTCGTCTGGGTTGCTTGTTCGATATAGAGGATGCGCAAGGAGACTG 480
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 Db 721 GTTCATTTTTCGCTCTTCTGCTATCTGTTGGAAGGATGCGCAATTAAGAGATT 780
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 Db 841 GACAAACTCCCTAACTTGGCTGGAGATGCTTTCGAGGCTTTGCACTCCTTGGC 900
 Qy 901 ATTTCTTTTTCGCTCTTCTGCTGCTTCTGCTCAGTTCGATTTTGAAGTACAA 960
 Db 901 ATTTCTTTTTCGCTCTTCTGCTGCTTCTGCTCAGTTCGATTTTGAAGTACAA 960
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 Db 1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
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 Db 1441 CCACCACTTAAACCTGTCTCAGCTATCAGAAATTAAGAAATTTCAATTTGATGATGATGATG 1500
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 Db 1501 AAGTTTAAAGGAAACGTTACGCTCCATATGATGATGATGATGATGATGATGATGATGATGATG 1560
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 Db 1621 GGAAGGAGGCAATCAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
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 Db 1681 ACCACAGAGATCTCAGTATGCTCGTTCGGTGGTCAAGTTTGAAGGATGATGATGATGATGATG 1740
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 Db 1741 ATAGAGTCCAAAGCTGAGCTGCTTACTAGATCATCTATCAACAGGCTCTTGGAAAGGCTCT 1800
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 Qy 1861 GACTATCAAAAGCCTGTTGATAGCAAGATCTTTCGGGTTCCGCAAAACAGTGGCTGC 1920
 Db 1861 GACTATCAAAAGCCTGTTGATAGCAAGATCTTTCGGGTTCCGCAAAACAGTGGCTGC 1920
 Qy 1921 TTATCCAGATCAATGATGCTCAATCTCGAGAGGCTGAGTTTCAATTTGATGATGATGATGATGATG 1980
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 Db 2221 AGCATTTCTGAGCTCAACCTGCTTGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2280

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Qy	2401	ATCAGGTCTGACCGAGGAACTGAATATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2460	
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Qy	2461	GGCAGCCCAAGATTTTATCCCAATATGGAGGGAATCCAAATCTTTTAACTGATGAAGAG	2520	
Db	2461	GGCAGCCCAAGATTTTATCCCAATATGGAGGGAATCCAAATCTTTTAACTGATGAAGAG	2520	
Qy	2521	GTGGTCTCCGAAAGACAGAGACAGACACTTTTGTATGCCGACCGCAGCTGCCACGGAA	2580	
Db	2521	GTGGTCTCCGAAAGACAGAGACAGACACTTTTGTATGCCGACCGCAGCTGCCACGGAA	2580	
Qy	2581	GCTGCCTTTTGCATCAGACTCTCTAAGGACTTGGAGGTTCAGATCATCTCAGAGCATTTGT	2640	
Db	2581	GCTGCCTTTTGCATCAGACTCTCTAAGGACTTGGAGGTTCAGATCATCTCAGAGCATTTGT	2640	
Qy	2641	AAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAATGAATAA	2694	
Db	2641	AAGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAATGAATAA	2694	

RESULT 3

AAAS14651	
ID	AAAS14651 standard; cDNA; 3071 BP.
XX	
XX	AAAS14651;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Human cDNA for voltage gated potassium channel hKVNQ5.
XX	
KW	Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
KW	cerebroprotective; neurotropic; analgesic; vision disorder;
KW	central nervous system disorder; epilepsy; migraine; hearing disorder;
KW	psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW	pain; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200170759-A1 ..
XX	
PD	27-SEP-2001.
XX	
PF	20-MAR-2001; 2001WO-US009328.
XX	
PR	21-MAR-2000; 2000US-0190954P.
XX	
PA	(ICAG-) ICAGEN INC.
PI	Jegla TJ;
XX	
XX	WPI; 2001-611467/70.
XX	
PT	Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT	identifying a compound modulating ion flux in eukaryotic cell or cell
PT	membrane expressing the protein, comprises KCNQ approximatelya- subunits
XX	
PS	Claim 5; Page 61-62; 78pp; English.
XX	
CC	The invention relates to an isolated polypeptide comprising an alpha-
CC	subunit of a KCNQ potassium channel, with a subsequence having 65%
CC	sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC	and forms a KCNQ potassium channel having the characteristic of voltage-
CC	gating with at least an additional KCNQ alpha-subunit. Also included in
CC	the scope of the invention are the nucleic acids encoding hKCNQ5

730 GTTCTTATTTTTCGTCCTTCTTGTCTATCTCGTGGAAAGGATGCCAATAAAGAGTTT 789
781 TCTACATATCAGATGCTCTCGTGGGGCACAATATACATTGACAACTATTGGCTATGGA 840
790 TCTACATATCAGATGCTCTCGTGGGGCACAATATACATTGACAACTATTGGCTATGGA 849
841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGACGGCTTTGCACTCTTGGC 900
850 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGACGGCTTTGCACTCTTGGC 909
901 ATTTCTTTCTTGGCACTTCTGCGGCATTTCTGGCTCAGGTTTGCATTTAAAGATACAA 960
910 ATTTCTTTCTTGGCACTTCTGCGGCATTTCTGGCTCAGGTTTGCATTTAAAGATACAA 969
961 GAACAAACACGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCAACCTCATTCAG 1020
970 GAACAAACACGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCAACCTCATTCAG 1029
1021 TGTGTTGGGGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACTGGAAGCCA 1080
1030 TGTGTTGGGGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACTGGAAGCCA 1089
1081 CACTTGAAGGCTTTGCACACCTGAGCCCTACCAAGAAAGAAACAGGGGAGCATCAAGC 1140
1090 CACTTGAAGGCTTTGCACACCTGAGCCCTACCAAGAAAGAAACAGGGGAGCATCAAGC 1149
1141 AGTCAGAAGCTTAAGTTTAAAGAGCGAGTGGCATGCTAGCCCAAGGGGCCAGATATT 1200
1150 AGTCAGAAGCTTAAGTTTAAAGAGCGAGTGGCATGCTAGCCCAAGGGGCCAGATATT 1209
1201 AAGAGCCGACAAAGCTCAGTAGTGTACAGAGGTCCCAAGCAGCAGCATCACAGCCGAG 1260
1210 AAGAGCCGACAAAGCTCAGTAGTGTACAGAGGTCCCAAGCAGCAGCATCACAGCCGAG 1269
1261 GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGCCC 1320
1270 GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGCCC 1329
1321 TCGTTCGCCCTCAAAAGTTCTCAGCCAAAACAGTGTATGATGTATCAGTGGAAAGACTCAC 1380
1330 TCGTTCGCCCTCAAAAGTTCTCAGCCAAAACAGTGTATGATGTATCAGTGGAAAGACTCAC 1389
1381 ACTGATGATGTATGATGAAAGAGTGCAGTGTATGATGTATCAGTGGAAAGACTCAC 1440
1390 ACTGATGATGTATGATGAAAGAGTGCAGTGTATGATGTATCAGTGGAAAGACTCAC 1449
1441 CCACCACTTAAACCTGCTCAATTCGAGCTATCAGAAATTTAAGAAATTTCAATTTGCAAAACGG 1500
1450 CCACCACTTAAACCTGCTCAATTCGAGCTATCAGAAATTTAAGAAATTTCAATTTGCAAAACGG 1509
1501 AAGTTTAAAGAAACGTTACGTCATATGATGTAAAGATGTCATTTGAAATATTTCTGCT 1560
1510 AAGTTTAAAGAAACGTTACGTCATATGATGTAAAGATGTCATTTGAAATATTTCTGCT 1569
1561 GGTCACTGGAATGCTGTGTAGAAATTAAGAGCCCTTCAAAACGCTGTTGATCAAAATCTT 1620
1570 GGTCACTGGAATGCTGTGTAGAAATTAAGAGCCCTTCAAAACGCTGTTGATCAAAATCTT 1629
1621 GGAAAGGGCAAAATCACATCAGATCAGATGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1680
1630 GGAAAGGGCAAAATCACATCAGATCAGATGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1689
1681 ACCACAGAGATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAGAGAGAGTACAGTCC 1740
1690 ACCACAGAGATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAGAGAGAGTACAGTCC 1749
1741 ATAGAGTCCAAAGCTGAGCTGCTTACTAGACATCTATCAACAGGTCCTTCCGAAAGGCTCT 1800
1750 ATAGATCCAAAGCTGAGCTGCTTACTAGACATCTATCAACAGGTCCTTCCGAAAGGCTCT 1809
1801 GCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTCAGTGTGAAAGAGATCT 1860
1810 GCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTCAGTGTGAAAGAGATCT 1869

QY 1861 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 1920
Db 1870 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 1929
QY 1921 TTATCCAGATCAATAGTGCACCAATCTCGAGAGGCTTCGAGTTTCAATTCGACGCCAAAT 1980
Db 1930 TTATCCAGATCAATAGTGCACCAATCTCGAGAGGCTTCGAGTTTCAATTCGACGCCAAAT 1989
QY 1981 GAGTTTCAGTGGCCAGACTTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2040
Db 1990 GAGTTTCAGTGGCCAGACTTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2049
QY 2041 GTGCCAAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCACCACCAACCATTCGAAACCAA 2100
Db 2050 GTGCCAAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCACCACCAACCATTCGAAACCAA 2109
QY 2101 ATAAATACGGCAACCAAGCCAGCAGCCCCAACCAACTTTACAGATCCCACTCTCTCCCA 2160
Db 2110 ATAAATACGGCAACCAAGCCAGCAGCCCCAACCAACTTTACAGATCCCACTCTCTCCCA 2169
QY 2161 GCATCAAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCCCTGACGGCTTACAGGAA 2220
Db 2170 GCATCAAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCCCTGACGGCTTACAGGAA 2229
QY 2221 AGCATTTCTGAGCTCACCACCTGCTTGTGCTTCAAGGAAAATGTTTCAGGTTGCACAG 2280
Db 2230 AGCATTTCTGAGCTCACCACCTGCTTGTGCTTCAAGGAAAATGTTTCAGGTTGCACAG 2289
QY 2281 TCAAAATCTCACCAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAAAATCTCTG 2340
Db 2290 TCAAAATCTCACCAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAAAATCTCTG 2349
QY 2341 TTGCTGCTGTGCTCCATGTCGAGGAGTGGGCAAAATCTTTGCTGTCGAAAACCTG 2400
Db 2350 TTGCTGCTGTGCTCCATGTCGAGGAGTGGGCAAAATCTTTGCTGTCGAAAACCTG 2409
QY 2401 ATCAGGTCCACCGAGGAACTGAATATACAACTTTTTCAGGGAGTGAATCAAGTGGCTCCAGA 2460
Db 2410 ATCAGGTCCACCGAGGAACTGAATATACAACTTTTTCAGGGAGTGAATCAAGTGGCTCCAGA 2469
QY 2461 GGAGCCAGATTTTTCACCAATTCGAGGAGTCCAAATGTTTATTAATGATGAAGAG 2520
Db 2470 GGAGCCAGATTTTTCACCAATTCGAGGAGTCCAAATGTTTATTAATGATGAAGAG 2529
QY 2521 GTGGTCCCGAAGACAGACAGACACTTTTGTATGTCGCGCACCGCAGGCTTCAGGGAA 2580
Db 2530 GTGGTCCCGAAGACAGACAGACACTTTTGTATGTCGCGCACCGCAGGCTTCAGGGAA 2589
QY 2581 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCTCAGAGCATTTGT 2640
Db 2590 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCTCAGAGCATTTGT 2649
QY 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAAACTGAAATAA 2694
Db 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAAACTGAAATAA 2703

RESULT 4
AAC85414

ID AAC85414 standard; cDNA; 3137 BP.

XX AAC85414;

AC AC

DT 20-APR-2001 (first entry)

XX Human KCNQ5 potassium channel subunit coding sequence.

Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
compulsive behaviour; dementia; depression; Huntington's disease; mania;
memory impairment; memory dysfunction; spinal cord damage; phobia;

1381 ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGTATCATCTAGTGAAGACCTCAC 1440
1441 CCACCACTTAAACTGTCTATTCAGAGTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1500
1441 CCACCACTTAAACTGTCTATTCAGAGTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1500
1501 AAGTTTAAAGAAAGCTTTACGTCCATATGATGTAAGAGTGTCAATGCAAAATTTCTGCT 1560
1501 AAGTTTAAAGAAAGCTTTACGTCCATATGATGTAAGAGTGTCAATGCAAAATTTCTGCT 1560
1561 GGTCAATCTGGACATGTTGTGTAGAAATTTAAAGAGCTTTCAAAACAGTGTGATCAAAATTTCT 1620
1561 GGTCAATCTGGACATGTTGTGTAGAAATTTAAAGAGCTTTCAAAACAGTGTGATCAAAATTTCT 1620
1621 GGAAAGGGCAAAATCACATCAGATGAAAGAGCGGAGAGAAATTAACAGCAGAACATGAG 1680
1621 GGAAAGGGCAAAATCACATCAGATGAAAGAGCGGAGAGAAATTAACAGCAGAACATGAG 1680
1681 ACCACAGCATCTCAGTATGCTCGGTGGGTGCTCAAGTTGAAAGAGGTACAGTCC 1740
1681 ACCACAGCATCTCAGTATGCTCGGTGGGTGCTCAAGTTGAAAGAGGTACAGTCC 1740
1741 ATAGAGTCCAGCTGGAGTCTACTAGACATCTATCAACAGGTCTCTTCGAAAGGCTCT 1800
1741 ATAGAGTCCAGCTGGAGTCTACTAGACATCTATCAACAGGTCTCTTCGAAAGGCTCT 1800
1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
1801 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 1920
1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 1920
1921 TTATCCAGATCAACTAGTGCACAACTCTGAGAGGCTGCAAGTTCATTCTGACGCCAAAT 1980
1921 TTATCCAGATCAACTAGTGCACAACTCTGAGAGGCTGCAAGTTCATTCTGACGCCAAAT 1980
1981 GAGTTGAGTCCAGACCTTTCTAGCGCTTACGCTTATGCAAGTCAAGCAACAG 2040
1981 GAGTTGAGTCCAGACCTTTCTAGCGCTTACGCTTATGCAAGTCAAGCAACAG 2040
2041 GTGCCAATTTAGTCAAGAGGATGGCTCAGAGTGGGAGCCACCAACCACTTTGCAACCA 2100
2041 GTGCCAATTTAGTCAAGAGGATGGCTCAGAGTGGGAGCCACCAACCACTTTGCAACCA 2100
2101 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
2101 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
2161 GGCATCAAGCATCTGCCAGGCGAGAACTCTGACCCCTTAACCCCTGCAAGGTTACAGGA 2220
2161 GGCATCAAGCATCTGCCAGGCGAGAACTCTGACCCCTTAACCCCTGCAAGGTTACAGGA 2220
2221 AGCATTTCTGAGTCAACCACTGCTTGTGCTTCCAGGAAATGTTTCAAGTTCACAG 2280
2221 AGCATTTCTGAGTCAACCACTGCTTGTGCTTCCAGGAAATGTTTCAAGTTCACAG 2280
2281 TCAATCTCACCAGGACCGTCTATGAGGAAAGCTTTGATCGGGAGGAAACTCTG 2340
2281 TCAATCTCACCAGGACCGTCTATGAGGAAAGCTTTGATCGGGAGGAAACTCTG 2340
2341 TTGCTGTCTGCTCCATGTCGGAAGGACTTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2400
2341 TTGCTGTCTGCTCCATGTCGGAAGGACTTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2400
2401 ATCAGGTTCGACCGGAGAACTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAG 2460
2401 ATCAGGTTCGACCGGAGAACTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAG 2460
2461 GGCAGCCAGATTTTACCCCAATCGGGGATCCAAATTTGTTTATTAATCTGATGAAG 2520
2461 GGCAGCCAGATTTTACCCCAATCGGGGATCCAAATTTGTTTATTAATCTGATGAAG 2520

2521 GTGGGTCCGGAAGAGACAGACAGACACTTTTGTATGCGCACCGCAGCCTGCCAGGAA 2580
2521 GTGGGTCCGGAAGAGACAGACAGACACTTTTGTATGCGCACCGCAGCCTGCCAGGAA 2580
2581 GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
2581 GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
2641 AAGGCAGGAGAAAGTACAGATGCTCTGCTTGCCTCATGTCAAACTGAATAA 2694
2641 AAGGCAGGAGAAAGTACAGATGCTCTGCTTGCCTCATGTCAAACTGAATAA 2694

RESULT 5
AAH49499
ID AAH49499 standard; DNA; 3074 BP.
XX
AC AAH49499;
XX
DT 11-DEC-2001 (first entry)
XX
DE Human KCNQ5 DNA.
XX
KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
KW anticonvulsant; excitability modulator; membrane potential; neuron;
KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
KW screening; central nervous system disease; cardiovascular disease; ds.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 110..2908
FT /*tag= a
FT /product= "KCNQ5"
XX
XX DE10013732-Al.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2000; 2000DE-01013732.
XX
XX 21-MAR-2000; 2000DE-01013732.
XX
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX
XX Steinmeyer K, Lerche C, Scherer C, Seebohm G, Busch AE;
XX
XX WPI; 2001-571700/65.
XX
XX P-PSDB; AAB86979.
XX
XX New DNA sequence encoding potassium channel KCNQ5, useful in screening
XX for specific modulators, potential agents for treating central nervous
XX system and cardiovascular diseases.
XX
XX Claim 2a; Page 9-10; 20pp; German.
XX
XX This invention describes a novel DNA sequence (I) encoding: (i) a
XX polypeptide (II) with potassium channel KCNQ5 activity; (ii) a
XX polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
XX the invention have neurological, cardiovascular and anticonvulsant
XX activity and act as modulators of the voltage-dependent KCNQ5 potassium
XX channel, a key regulator of membrane potential and modulator of
XX excitability of electrically activated cells such as neurons and
XX cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
XX are used to screen for compounds that modulate the activity of KCNQ5,
XX potentially useful for treating central nervous system (e.g. epilepsy)
XX and cardiovascular diseases. This sequence encodes the human potassium
XX channel KCNQ5 protein described in the invention
XX
XX Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;
XX
XX Query Match 99.5%; Score 2681.2; DB 4; Length 3074;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	1	ATGAGGATGAGTCGGGCGGGGAGGTCCTGAACTCGCGAGCGCCAGGGGC	60
Db	215	ATGAGGATGTCGAGTCGGGCGGGGAGGTCCTGAACTCGCGAGCGCCAGGGGC	274
QY	61	GACGGCTGCTACTGTCGGGACCCCGCGGCAAGCTTGGTGGGCGGGGCGGCTG	120
Db	275	GACGGCTGCTACTGTCGGGACCCCGCGGCAAGCTTGGTGGGCGGGGCGGCTG	334
QY	121	AGGAGAGCGCGCGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAAGCGCTCTCT	180
Db	335	AGGAGAGCGCGCGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAAGCGCTCTCT	394
QY	181	TACAGAGTAGCAGAGTCGGCGGCGCAACGTCAGTACCGGGGGTGCAGAACTACCTG	240
Db	395	TACAGAGTAGCAGAGTCGGCGGCGCAACGTCAGTACCGGGGGTGCAGAACTACCTG	454
QY	241	TACAACTGCTGGAGAGACCCCGCGGCTGCGGCTTCATCTACAGCGCTTTCGTTTCTC	300
Db	455	TACAACTGCTGGAGAGACCCCGCGGCTGCGGCTTCATCTACAGCGCTTTCGTTTCTC	514
QY	301	CTTGCTTTGGTGTGATTTTGTAGTGTTCAGTGTTCCTACCATCCCTGAGCACACAAATG	360
Db	515	CTTGCTTTGGTGTGATTTTGTAGTGTTCAGTGTTCCTACCATCCCTGAGCACACAAATG	574
QY	361	GCCTCAAGTGTCTCTGATCTGGAGTCGTCGATGTCGTCCTTGGTTGGAGTTC	420
Db	575	GCCTCAAGTGTCTCTGATCTGGAGTCGTCGATGTCGTCCTTGGTTGGAGTTC	634
QY	421	ATCATTCGAATCTGCTCGCGGTTGCTGTCGATATAGAGGATGCGAAGAACTG	480
Db	635	ATCATTCGAATCTGCTCGCGGTTGCTGTCGATATAGAGGATGCGAAGAACTG	694
QY	481	AGGTTTGTCTGAAAGCCCTTCGTGTATAGATACATTTGTTCTTATCGCTTCAATAGCA	540
Db	695	AGGTTTGTCTGAAAGCCCTTCGTGTATAGATACATTTGTTCTTATCGCTTCAATAGCA	754
QY	541	GTGTTTCTGCAAAACTCAGGTAATATTTTGCACGTCGCTCAGAGTCTCCGT	600
Db	755	GTGTTTCTGCAAAACTCAGGTAATATTTTGCACGTCGCTCAGAGTCTCCGT	814
QY	601	TTCTACAGATCCTCGCATGTGCGCATGGAACCGAGGGAGGCACTTGGAAATTA	660
Db	815	TTCTACAGATCCTCGCATGTGCGCATGGAACCGAGGGAGGCACTTGGAAATTA	874
QY	661	GGTTCAGTGGTTTATGCTCAGCAGGAAGGAATTAATCAGCTTGTGTAATAGGATTTTG	720
Db	875	GGTTCAGTGGTTTATGCTCAGCAGGAAGGAATTAATCAGCTTGTGTAATAGGATTTTG	934
QY	721	GTTCATATTTTTCGTCCTTCTCTCTATCTGGTGGAAAGGATGCCAATAAGAGTTT	780
Db	935	GTTCATATTTTTCGTCCTTCTCTCTATCTGGTGGAAAGGATGCCAATAAGAGTTT	994
QY	781	TCTACATATGAGATGCTCTCGTGGGCAAAATTAATGACAACTATTGGCTATGGA	840
Db	995	TCTACATATGAGATGCTCTCGTGGGCAAAATTAATGACAACTATTGGCTATGGA	1054
QY	841	GACAAACTCCCTAACTTGGCTGGGAAGATTTCTGCAAGGCTTTGCACTCCTTGGC	900
Db	1055	GACAAACTCCCTAACTTGGCTGGGAAGATTTCTGCAAGGCTTTGCACTCCTTGGC	1114
QY	901	ATTTCTTTTTCGTCCTTCTCTCTATCTGGTGGAAAGGATGCCAATAAGATGAA	960
Db	1115	ATTTCTTTTTCGTCCTTCTCTCTATCTGGTGGAAAGGATGCCAATAAGATGAA	1174
QY	961	GAAACACCGCAGAAACACTTTGAGAAAAGAAAGAAACCCAGCTGCCAACTCTTCCAG	1020
Db	1175	GAAACACCGCAGAAACACTTTGAGAAAAGAAAGAAACCCAGCTGCCAACTCTTCCAG	1234
QY	1021	TGTGTTTGGGTTAGTCAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCCA	1080
Db		TGTGTTTGGGTTAGTCAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCCA	

Db	1235	TGTGTTTGGGTTAGTCAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCCA	1294
QY	1081	CACTTGAAGGCTTGCACACCTGACACCTTACCAGAAAGAACAGGGAAGCATCAAGC	1140
Db	1295	CACTTGAAGGCTTGCACACCTGACACCTTACCAGAAAGAACAGGGAAGCATCAAGC	1354
QY	1141	AGTCAGAAAGCTTAAGTATTAAGGAGCGAGTCGCGCATGGCTAGCCCCAGGGGCCAGAGTATT	1200
Db	1355	AGTCAGAAAGCTTAAGTATTAAGGAGCGAGTCGCGCATGGCTAGCCCCAGGGGCCAGAGTATT	1414
QY	1201	AAGAGCGACAAAGCCCTCAGTAGGTGACAGAGAGGTCGCCAAGCAACCGACATCAACAGCCGAG	1260
Db	1415	AAGAGCGACAAAGCCCTCAGTAGGTGACAGAGAGGTCGCCAAGCAACCGACATCAACAGCCGAG	1474
QY	1261	GGCAGTCCCAACCAAGTCAGAAAGCTGGAAGCTTCAACGACCGAACCCGCTTCCGGCCC	1320
Db	1475	GGCAGTCCCAACCAAGTCAGAAAGCTGGAAGCTTCAACGACCGAACCCGCTTCCGGCCC	1534
QY	1321	TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCCAGTATAGATGCTGACACAGCCCTTGGC	1380
Db	1535	TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCCAGTATAGATGCTGACACAGCCCTTGGC	1594
QY	1381	ACTGATGATGATATGATGAAAGGATGCGCAGTGTGATGATATCAGTGGGAAGACCTCACC	1440
Db	1595	ACTGATGATGATATGATGAAAGGATGCGCAGTGTGATGATATCAGTGGGAAGACCTCACC	1654
QY	1441	CCACCACCTTAAACCTGTCATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG	1500
Db	1655	CCACCACCTTAAACCTGTCATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG	1714
QY	1501	AAGTTTAAAGGAAACGTTACGTCCTATGATGTAAGAGATGTCATTTGAAACAAATTTCTGCT	1560
Db	1715	AAGTTTAAAGGAAACGTTACGTCCTATGATGTAAGAGATGTCATTTGAAACAAATTTCTGCT	1774
QY	1561	GGTCATCTGGAGATGTTGTTAGAAATTAAGAGCTTCAAAACGCTGTTGATCAAAATTTCTT	1620
Db	1775	GGTCATCTGGAGATGTTGTTAGAAATTAAGAGCTTCAAAACGCTGTTGATCAAAATTTCTT	1834
QY	1621	GGAAAGGGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAAACATGAG	1680
Db	1835	GGAAAGGGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAAACATGAG	1894
QY	1681	ACCACAGACGATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1740
Db	1895	ACCACAGACGATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1954
QY	1741	ATAGAGTCCAGCTGGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	1800
Db	1955	ATAGAAATCCAAAGCTGGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	2014
QY	1801	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT	1860
Db	2015	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT	2074
QY	1861	GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTGGGTTCGCAACAAAAACAGTGGCTGC	1920
Db	2075	GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTGGGTTCGCAACAAAAACAGTGGCTGC	2134
QY	1921	TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTGCGAGTTTCATTTCTGACGCCAAAT	1980
Db	2135	TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTGCGAGTTTCATTTCTGACGCCAAAT	2194
QY	1981	GAGTTCAGTGGCCAGACTTTCTACGCTTAGCCCTACTATGCAAGTCAAGCAACACAG	2040
Db	2195	GAGTTCAGTGGCCAGACTTTCTACGCTTAGCCCTACTATGCAAGTCAAGCAACACAG	2254
QY	2041	GTGCCAAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGGCAACCAA	2100
Db	2255	GTGCCAAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGGCAACCAA	2314
QY	2101	ATAAATACGGCAACCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2160
Db	2315	ATAAATACGGCAACCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA	2374

QY	2161	GCCATCAAGCATCTGCCCGAGGCAGAAACTCTGCAACCTTAACCCCTCAGGCTTTACAGGAA	2220
Db	2375	GCCATCAAGCATCTGCCCGAGGCAGAAACTCTGCAACCTTAACCCCTCAGGCTTTACAGGAA	2434
QY	2221	AGCATTTCTGACGTCAACACCTGCTTGGCTTCGAAGAAAATGTTCHGGTTGCACAG	2280
Db	2435	AGCATTTCTGAGGTCAACACCTGCTTGGCTTCGAAGAAAATGTTCHGGTTGCACAG	2494
QY	2281	TCAAATCTCACCAAGGACCGTTCTATCAGAGAAAGCTTTGCATCGGAGAGAAAACTCTG	2340
Db	2495	TCAAATCTCACCAAGGACCGTTCTATCAGAGAAAGCTTTGCATCGGAGAGAAAACTCTG	2554
QY	2341	TTGTCTGTCTGTCCCATGTGTCGGAAGGACTTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2400
Db	2555	TTGTCTGTCTGTCCCATGTGTCGGAAGGACTTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2614
QY	2401	ATCAGGTGCGACCGAGGAACCTGAATATACAACCTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2460
Db	2615	ATCAGGTGCGACCGAGGAACCTGAATATACAACCTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2674
QY	2461	GGCAGCCGAAGATTTTTATCCCCAAATGGAGGAAATCCAAATTTGTTATACTGATGAAGAG	2520
Db	2675	GGCAGCCGAAGATTTTTATCCCCAAATGGAGGAAATCCAAATTTGTTATACTGATGAAGAG	2734
QY	2521	GTGGGTCCCGAAGACAGACAGACAGACACTTTTGAATGCCGACCGGAGCCTGCCAGGGAA	2580
Db	2735	GTGGGTCCCGAAGACAGACAGACAGACACTTTTGAATGCCGACCGGAGCCTGCCAGGGAA	2794
QY	2581	GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGGTCACCATCATCTCAGAGCATTTGT	2640
Db	2795	GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGGTCACCATCATCTCAGAGCATTTGT	2854
QY	2641	AAGGCAGAGAAAGTACAGATGCCCTCAGTTGCCCTCATGTCAAACCTGAATAA	2694
Db	2855	AAGGCAGAGAAAGTACAGATGCCCTCAGTTGCCCTCATGTCAAACCTGAATAA	2908

RESULT 6	Best Local Similarity	99.7%	Indels	9%	Mismatches	0%	Gaps	0%
ADB78684	ADB78684 standard; cDNA; 3074 BP.							
XX	AC	ADB78684;						
XX	DT	04-DEC-2003 (first entry)						
XX	DE	Human potassium channel subunit mutant cDNA SEQ ID NO:55.						
XX	ss;	gene; mutant; ion channel; ion channel subunit; ICs; nootropic;						
KW	KW	neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;						
KW	KW	antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;						
KW	KW	nephrotropic; antidiabetic; ophthalmological; epilepsy;						
KW	KW	ion channel dysfunction; human.						
XX	OS	Synthetic.						
OS	OS	Homo sapiens.						
XX	PN	WO2003008574-A1.						
XX	XX	30-JAN-2003.						
XX	XX	08-JUL-2002; 2002WO-AU000910.						
XX	XX	18-JUL-2001; 2001AU-00006452.						
PR	PR	05-MAR-2002; 2002AU-00000910.						
PR	PR	13-MAY-2002; 2002AU-00002292.						
XX	XX	(BION-) BIONOMICS LTD.						
PA	PA	(WALL-) WALLACE R W.						
XX	XX	Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;						
PI	PI	Berkovic SF, Scheffer IE;						

QY 481 AGGTTTGTCTGGAAGCCCTTCGTGTATAGATACCAITTTCTTATCGCTTCAATAGCA 540
DB |||||
QY 695 AGGTTTGTCTGGAAGCCCTTCGTGTATAGATACCAITTTCTTATCGCTTCAATAGCA 754
DB |||||
QY 541 GTTGTCTTCTGCAAAACTCAGGGTAATATTTTGGCAAGTCTGCACTCAGAAAGTCTCCGT 600
DB |||||
QY 755 GTTGTCTTCTGCAAAACTCAGGGTAATATTTTGGCAAGTCTGCACTCAGAAAGTCTCCGT 814
DB |||||
QY 601 TTCTTACAGATCCTCGCATGTGGCATGGAACCGAAGGGAGGCACCTTGGAAATTTACTG 660
DB |||||
QY 815 TTCTTACAGATCCTCGCATGTGGCATGGAACCGAAGGGAGGCACCTTGGAAATTTACTG 874
DB |||||
QY 661 GTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGT 720
DB |||||
QY 875 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGT 934
DB |||||
QY 721 GTTCTTATTTTTCGTCTTCTTCTGCTATCTGCTGGAAAGGATGCCAATAAAGAGTTT 780
DB |||||
QY 935 GTTCTTATTTTTCGTCTTCTTCTGCTATCTGCTGGAAAGGATGCCAATAAAGAGTTT 994
DB |||||
QY 781 TCTACATATGAGATGCTCTCTGCTGGGGCACAATTTACATTCACAACATATTGGCTATGGA 840
DB |||||
QY 995 TCTACATATGAGATGCTCTCTGCTGGGGCACAATTTACATTCACAACATATTGGCTATGGA 1054
DB |||||
QY 841 GACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCCTTGGC 900
DB |||||
QY 1055 GACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCCTTGGC 1114
DB |||||
QY 901 ATTTCTTTCTTGGCATCTTCTCGGGCATTTCTTGGCTCAGGTTTGGCATTTAAAGTACAA 960
DB |||||
QY 1115 ATTTCTTTCTTGGCATCTTCTCGGGCATTTCTTGGCTCAGGTTTGGCATTTAAAGTACAA 1174
DB |||||
QY 961 GAAACAACCCGCGAGAACACTTTTCAGAAAGAAAGGAAACCCAGCTGCCAACCCTCATTGAG 1020
DB |||||
QY 1175 GAAACAACCCGCGAGAACACTTTTCAGAAAGAAAGGAAACCCAGCTGCCAACCCTCATTGAG 1234
DB |||||
QY 1021 TGTGTTTGGCTGATGAGCACTGATGAGAAATCTGTTTCCATTTGCAACCTTGGAAAGCA 1080
DB |||||
QY 1235 TGTGTTTGGCTGATGAGCACTGATGAGAAATCTGTTTCCATTTGCAACCTTGGAAAGCA 1294
DB |||||
QY 1081 CACTTGAAGGCCCTTGACACCTTGACAGCCCTTACCAAGAAAGAACCAAGGGAGGATCAAGC 1140
DB |||||
QY 1295 CACTTGAAGGCCCTTGACACCTTGACAGCCCTTACCAAGAAAGAACCAAGGGAGGATCAAGC 1354
DB |||||
QY 1141 AGTCAGAAAGTAAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCGCCAGGGGCCAGAGTATT 1200
DB |||||
QY 1355 AGTCAGAAAGTAAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCGCCAGGGGCCAGAGTATT 1414
DB |||||
QY 1201 AAGAGCCGACAAAGCCTCAGTAGGTGACAGAGGTCCTCCCAAGCACCCGACATCAAGCCGAG 1260
DB |||||
QY 1415 AAGAGCCGACAAAGCCTCAGTAGGTGACAGAGGTCCTCCCAAGCACCCGACATCAAGCCGAG 1474
DB |||||
QY 1261 GGCAGTCCCAACAAAGTCGAGAGCTGGAGCTTCAACGACCGAACCCTTCCGGCCC 1320
DB |||||
QY 1475 GGCAGTCCCAACAAAGTCGAGAGCTGGAGCTTCAACGACCGAACCCTTCCGGCCC 1534
DB |||||
QY 1321 TCGCTGCGCTCCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGC 1380
DB |||||
QY 1535 TCGCTGCGCTCCTCAAAAGTTCTCAGCCAAACCAAGTATGATGCTGACACAGCCCTTGGC 1594
DB |||||
QY 1381 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGAT 1440
DB |||||
QY 1595 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGAT 1654
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QY 1441 CCACACTTAAACTGTCATTCGAGCTATCAGAAATTTGAAATTTGATGTTGCAAAACGG 1500
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DB |||||
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DB |||||
QY 1715 AAGTTTAAAGGAACCTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1774
DB |||||
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DB |||||

DB |||||
QY 1775 GGTCAATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAACACAGGTGTTGATCAAAATCTCT 1834
DB |||||
QY 1621 GGAAAGGGCAAAATCACATCAGATAAGAGAGCGGAGAGAAATTAACACAGAGCAATGAG 1680
DB |||||
QY 1835 GGAAAGGGCAAAATCACATCAGATAAGAGAGCGGAGAGAAATTAACACAGAGCAATGAG 1894
DB |||||
QY 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1740
DB |||||
QY 1895 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1954
DB |||||
QY 1741 ATAGAGTCCAAGCTGGACTGCTTACATAGACATCTATCAACAGGTCCTTTCGAAAGGCTCT 1800
DB |||||
QY 1955 ATAGAAATCCAAGCTGGACTGCTTCTAGACATCTATCAACAGGTCCTTTCGAAAGGCTCT 2014
DB |||||
QY 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
DB |||||
QY 2015 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
DB |||||
QY 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC 1920
DB |||||
QY 2075 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC 2134
DB |||||
QY 1921 TTATCCAGATCAACTAGTGGCCAAACATCTCGAGAGGCTGCGAGTTCAATCTTGACGCCAAT 1980
DB |||||
QY 2135 TTATCCAGATCAACTAGTGGCCAAACATCTCGAGAGGCTGCGAGTTCAATCTTGACGCCAAT 2194
DB |||||
QY 1981 GAGTTTCAGTGGCCAGACTTTCTACGCGTTAGCCCTTACTATGACAGTCAAGACACAG 2040
DB |||||
QY 2195 GAGTTTCAGTGGCCAGACTTTCTACGCGTTAGCCCTTACTATGACAGTCAAGACACAG 2254
DB |||||
QY 2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCACCAACACCATTTGCAAAACCA 2100
DB |||||
QY 2255 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCACCAACACCATTTGCAAAACCA 2314
DB |||||
QY 2101 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2160
DB |||||
QY 2315 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2374
DB |||||
QY 2161 GCCATCAGCATCTGCCAGCCAGCAAACTCTGCACCTTAACCTTCCGAGGCTTACAGGA 2220
DB |||||
QY 2375 GCCATCAGCATCTGCCAGCCAGCAAACTCTGCACCTTAACCTTCCGAGGCTTACAGGA 2434
DB |||||
QY 2221 AGCATTTCTGACGTCAACCACTGCTTCTGCTCCCAAGGAAATGTTTTCAGGTTGCACAG 2280
DB |||||
QY 2435 AGCATTTCTGACGTCAACCACTGCTTCTGCTCCCAAGGAAATGTTTTCAGGTTGCACAG 2494
DB |||||
QY 2281 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTGT 2340
DB |||||
QY 2495 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTGT 2554
DB |||||
QY 2341 TTGTCTGTCTGCCATGGTCCGAGGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2400
DB |||||
QY 2555 TTGTCTGTCTGCCATGGTCCGAGGACTTGGGCAATCTTTGTCTGTGCAAAACCTG 2614
DB |||||
QY 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTGGCTCCAGA 2460
DB |||||
QY 2615 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTGGCTCCAGA 2674
DB |||||
QY 2461 GGCAGCCAAAGATTTTATCCCAATGGAGGAAATCCAAATTTGTTTATTAATGATGAAGAG 2520
DB |||||
QY 2675 GGCAGCCAAAGATTTTATCCCAATGGAGGAAATCCAAATTTGTTTATTAATGATGAAGAG 2734
DB |||||
QY 2521 GTGGGTCGAGAGACAGACAGACTTTTGAATGCCGACCGCAGCTGCCAGGGA 2580
DB |||||
QY 2735 GTGGGTCGAGAGACAGACAGACTTTTGAATGCCGACCGCAGCTGCCAGGGA 2794
DB |||||
QY 2581 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGGTCAAGCATCATCTCAGAGCAATTTGT 2640
DB |||||
QY 2795 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGGTCAAGCATCATCTCAGAGCAATTTGT 2854
DB |||||
QY 2641 AAGCGAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTGAAATAA 2694
DB |||||

Db	2855	AAGCAGGAGAACTACAGATGCCCTCAGCTTGCTGCTCATGTCAAACTGAATAA	2908	Best Local Similarity 99.0%; Pred. No. 0; Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
RESULT 7				
AAAS14653				
ID	AAAS14653	standard; cDNA; 2667 BP.		
XX	AAAS14653;			
AC				
XX	18-DEC-2001	(first entry)		
DT				
XX		Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.		
DE				
XX		Human; ss; voltage-gated potassium channel; KCNQ5-2; nototropic; cerebrotective; neurotropic; analgesic; vision disorder; central nervous system disorder; epilepsy; migraine; hearing disorder; psychotic disorder; seizure; learning disorder; memory disorder; stroke; pain; gene therapy; splice variant.		
KW				
KW				
KW				
KW				
KW				
XX				
OS		Homo sapiens.		
XX				
XX				
FT	Key	Location/Qualifiers		
FT	CDS	1..2967		
FT		/*tag= a		
FT		/product= "hKCNQ5-2"		
XX				
PN	WO200170759-A1.			
XX				
PD	27-SEP-2001.			
XX				
PF	20-MAR-2001; 2001WO-US009328.			
XX				
XX	21-MAR-2000; 2000US-0190954P.			
PR				
XX	(ICAG-) ICAGEN INC.			
PA				
XX	Jegla TJ;			
PI				
XX				
DR	WPI; 2001-611467/70.			
DR	P-PSDB; AAU09021.			
XX				
PT	Polypeptides and polynucleotides of potassium channel KCNQ5 for identifying a compound modulating ion flux in eukaryotic cell or cell membrane expressing the protein, comprises KCNQ approximately alpha-subunits.			
PT				
PT				
PT				
PT				
XX	Claim 5; Page 63-64; 78pp; English.			
PS				
XX	The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in the scope of the invention are the nucleic acids encoding hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modelling to identify molecules that bind to a KCNQ containing potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2			
XX				
XX	Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;			
SQ				
	Query Match	97.6%;	Score 2630; DB 4; Length 2667;	

Db 1021 TGTGTTGGCGTAGTACGACGCTGATGAGAAATCTGTTCCATGCAACCTGGAAGCCA 1080
Qy 1081 CACTTGAAGGCTTCACACCTGACGCTTACCAAGAAAGAACAGGGAAGCATCAAGC 1140
Db 1081 CACTTGAAGGCTTCACACCTGACGCTTACCAAGAAAGAACAGGGAAGCATCAAGC 1115
Qy 1141 AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCTAGCGCTAGCCCGAGGGGCCAGAGTATT 1200
Db 1116 --TCAGAGCTAAGTTTAAAGAGCGAGTGGCTAGCGCTAGCCCGAGGGGCCAGAGTATT 1173
Qy 1201 AAGAGCCGACAGCCTCAGTAGTGTACAGAGAGTCCCAAGCAGCAGCATCACAGCCGAG 1260
Db 1174 AAGAGCCGACAGCCTCAGTAGTGTACAGAGAGTCCCAAGCAGCAGCATCACAGCCGAG 1233
Qy 1261 GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1320
Db 1234 GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1293
Qy 1321 TCGTGGCGCTCAAAAGTCTCAGCCAAACCAAGTGTAGTGTGACACAGCCCTTGGC 1380
Db 1294 TCGTGGCGCTCAAAAGTCTCAGCCAAACCAAGTGTAGTGTGACACAGCCCTTGGC 1353
Qy 1381 ACTGATGATGTATGATGAAAGAGTGCAGTGTGATGTATCAGTGGAGAGCTCACC 1440
Db 1354 ACTGATGATGTATGATGAAAGAGTGCAGTGTGATGTATCAGTGGAGAGCTCACC 1413
Qy 1441 CCACACTTAAACCTGTCAATTCGAGCTATCAGAAATTGAAATTTCAATGTTGCAAAACGG 1500
Db 1414 CCACACTTAAACCTGTCAATTCGAGCTATCAGAAATTGAAATTTCAATGTTGCAAAACGG 1473
Qy 1501 AAGTTTAAGGAAACGTTACGTCATATGATGTAAGAGTGCATTGAAACAATATTCTGCT 1560
Db 1474 AAGTTTAAGGAAACGTTACGTCATATGATGTAAGAGTGCATTGAAACAATATTCTGCT 1533
Qy 1561 GGTCACTGGAATGTTGTAGATTTAAAGCCTTCAACACGCTGTTGATCAAAATCTT 1620
Db 1534 GGTCACTGGAATGTTGTAGATTTAAAGCCTTCAACACGCTGTTGATCAAAATCTT 1593
Qy 1621 GGAAAGGGCAATCACAATCAGATGAAGAGCGGAGAGAAATAACAGCAGAACATGAG 1680
Db 1594 GGAAAGGGCAATCACAATCAGATGAAGAGCGGAGAGAAATAACAGCAGAACATGAG 1653
Qy 1681 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGAGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db 1654 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGAGTCAAGGTTGAAAAACAGGTACAGTCC 1713
Qy 1741 ATAGAGTCCAGCTGGAGCTGCTACTAGACATCTATCAACAGGCTCTCGGAAAGGCTCT 1800
Db 1714 ATAGAGTCCAGCTGGAGCTGCTACTAGACATCTATCAACAGGCTCTCGGAAAGGCTCT 1773
Qy 1801 GCCTCAGCCCTCGCTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
Db 1774 GCCTCAGCCCTCGCTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT 1833
Qy 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTCCGGGTTCCGCAAAAAACAGTGGCTGC 1920
Db 1834 GACTATCAAGCCCTGTGATAGCAAGATCTTTCCGGGTTCCGCAAAAAACAGTGGCTGC 1893
Qy 1921 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCAATTCATCTGACGCCAAT 1980
Db 1894 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCAATTCATCTGACGCCAAT 1953
Qy 1981 GAGTTCAAGTCCGAGCTTTCTACCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2040
Db 1954 GAGTTCAAGTCCGAGCTTTCTACCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2013
Qy 2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACCAATTCGAAACCAA 2100
Db 2014 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACCAATTCGAAACCAA 2073
Qy 2101 ATAATACGGCCCAAGCCAGCAGCCCAACCACTTTACAGATCCCACTCTCTCCCA 2160
Db 2074 ATAATACGGCCCAAGCCAGCAGCCCAACCACTTTACAGATCCCACTCTCTCTCCCA 2133

Qy 2161 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAACCTTGAGGCTTACAGAA 2220
Db 2134 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAACCTTGAGGCTTACAGAA 2193
Qy 2221 AGCATTTCTGAGCTCACACCTGCTTGTGTCCTCCCAAGGAAATGTTTCAGGTGACAG 2280
Db 2194 AGCATTTCTGAGCTCACACCTGCTTGTGTCCTCCCAAGGAAATGTTTCAGGTGACAG 2253
Qy 2281 TCAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAAACTCTG 2340
Db 2254 TCAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAAACTCTG 2313
Qy 2341 TTGTCGTCTCTCCATGGTCCCAAGGACCTTGGGCAAAATCTTGTCTGTGCAAAACCTG 2400
Db 2314 TTGTCGTCTCTCCATGGTCCCAAGGACCTTGGGCAAAATCTTGTCTGTGCAAAACCTG 2373
Qy 2401 ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTGGCTCCAGA 2460
Db 2374 ATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTGGCTCCAGA 2433
Qy 2461 GGCAGCCCAAGATTTTACCCCAATGGAGGAAATCCAAATGTTTATAACTGATGAAGAG 2520
Db 2434 GGCAGCCCAAGATTTTACCCCAATGGAGGAAATCCAAATGTTTATAACTGATGAAGAG 2493
Qy 2521 GTGGGTCCCGAAGAGACAGACACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA 2580
Db 2494 GTGGGTCCCGAAGAGACAGACACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA 2553
Qy 2581 GCTGCTTTGATCAGACTCTTAAGGACGTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2640
Db 2554 GCTGCTTTGATCAGACTCTTAAGGACGTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2613
Qy 2641 AAGCAGGAGAACTCAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2694
Db 2614 AAGCAGGAGAACTCAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2667

RESULT 8

AAH43633

ID AAH43633 standard; cDNA; 2772 BP.

XX

AC AAH43633;

XX

DT 21-JAN-2002 (first entry)

XX

DE Human ion-channel forming protein ORF.

XX

KW Ion-channel forming protein; voltage-gated potassium channel; fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.

XX

OS Homo sapiens.

XX

PN WO200175108-A1.

XX

PD 11-OCT-2001.

XX

PF 03-APR-2001; 2001WO-US010875.

XX

PR 03-APR-2000; 2000US-0194255P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Hu Y, Kleke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B; Sands AT;

XX

DR WPI; 2001-656987/75.

XX

PT P-ESDB; AAB47678.

XX

PT New human ion channel protein and polynucleotides encoding the protein, useful in diagnosing or treating diseases, in drug screening, and in clinical trial monitoring.

XX

Claim 1: Page 34-35; 41pp; English.

The sequences in AAH43633-34 encode a novel ion-channel forming protein. The protein shares structural similarity with mammalian ion channel proteins, particularly voltage-gated potassium channel proteins. The protein is expressed in many human cell lines including fetal brain, brain, thymus, prostate, heart and skeletal muscle. The novel protein can be used in the diagnosis or treatment of diseases, in drug screening, and in clinical trial monitoring. The oligonucleotides may be used as hybridization probes for screening libraries, and assessing gene expression patterns (particularly using a micro array or high throughput chip format). The nucleic acids and novel protein can also be used in the identification, selection and validation of novel molecular targets for drug discovery, to screen collections of genetic material from patients who have a particular medical condition, to identify mutations associated with a particular disease, as a diagnostic or prognostic assay, and to screen for drugs which can be used to treat symptomatic or phenotypic manifestations of perturbing the normal function of novel human protein. The polypeptides are further used in generating antibodies

Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;

Query Match 97.4%; Score 2625.2; DB 5; Length 2772;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 17

Qy	1	ATGAAGAGATGTGGAGTCTGGGCGGGGCAAGGTGCTGTGAACCTGGCAGCCGACGAGGGC	60
Db	106	ATGAAGGATGTGGAGTCTGGGCGGGGCAAGGTGCTGTGAACCTGGCAGCCGACGAGGGC	165
Qy	61	CACGGCTGTACTGCTGGGCACCCGCGCGCCACGCTTGTGTGGCGGCGGTGGCCCTG	120
Db	166	CACGGCTGTACTGCTGGGCACCCGCGCGCCACGCTTGTGTGGCGGCGGTGGCCCTG	225
Qy	121	AGGAGAGCCGCGGGGCAAGCAGGGGGCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT	180
Db	226	AGGAGAGCCGCGGGGCAAGCAGGGGGCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT	285
Qy	181	TACACGAGTAGCCAGAGCTGCGGGCGCAACGTCGAAGTACCGGCGGGTGCAGAACTACCTG	240
Db	286	TACACGAGTAGCCAGAGCTGCGGGCGCAACGTCGAAGTACCGGCGGGTGCAGAACTACCTG	345
Qy	241	TACAA CGTCTGGAGAGACCCGCGGCTGGGGTTCATCTACACGCTTTCGTTTTCTC	300
Db	346	TACAA CGTCTGGAGAGACCCGCGGCTGGGGTTCATCTACACGCTTTCGTTTTCTC	405
Qy	301	CTTGTCCTTTGGTTCCTGATTTTGTTCAGTGTCTTTCTACCATCCCTGAGCACACAAAATTG	360
Db	406	CTTGTCCTTTGGTTCCTGATTTTGTTCAGTGTCTTTCTACCATCCCTGAGCACACAAAATTG	465
Qy	361	GCCTCAAGTTGCCTCTTGATCTCTGGAGTTCGTGATGATGTGCTTTGGTTTGGAGTTC	420
Db	466	GCCTCAAGTTGCCTCTTGATCTCTGGAGTTCGTGATGATGTGCTTTGGTTTGGAGTTC	525
Qy	421	ATCATTTGAAATCTGCTCTCGGGTTCCTGCTTCGATATAGAGGATGGCAAGAGACATG	480
Db	526	ATCATTTGAAATCTGCTCTCGGGTTCCTGCTTCGATATAGAGGATGGCAAGAGACATG	585
Qy	481	AGGTTTGTCTCGAAAGCCCTTCCTGTGTATAGATACCAATTTGTTCTTATCGCTTCAATAGCA	540
Db	586	AGGTTTGTCTCGAAAGCCCTTCCTGTGTATAGATACCAATTTGTTCTTATCGCTTCAATAGCA	645
Qy	541	GTGTGTTTCTGCAAAAACCTCAGGGTAATATTTTTTGGCCAGCTCTGCACTCAGAAGTCTCCGT	600
Db	646	GTGTGTTTCTGCAAAAACCTCAGGGTAATATTTTTTGGCCAGCTCTGCACTCAGAAGTCTCCGT	705
Qy	601	TTTCCTACAGATCCTCCGCAATGFTGCCATGGACCGAAGGGGAGGCACCTTGGAAATTACTG	660
Db	706	TTTCCTACAGATCCTCCGCAATGFTGCCATGGACCGAAGGGGAGGCACCTTGGAAATTACTG	765
Qy	661	GGTTCAAGTGGTTTATGCTCACACAAAGGAATTAATCACAGCTTTGGTACATAGAGATTTTG	720
Db	766	GGTTCAAGTGGTTTATGCTCACACAAAGGAATTAATCACAGCTTTGGTACATAGAGATTTTG	825

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QY 1801 GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
Db 1879 GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1938
QY 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCGGACAAAAAGTGGCTGC 1920
Db 1939 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCGGACAAAAAGTGGCTGC 1998
QY 1921 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCGCTGCAGTTCATTTCTGACGCCAAT 1980
Db 1999 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCGCTGCAGTTCATTTCTGACGCCAAT 2058
QY 1981 GAGTTCAAGTCCAGACTTTTACGGCTTAGCTTACTATGACAGTCAAGCAACACAG 2040
Db 2059 GAGTTCAAGTCCAGACTTTTACGGCTTAGCTTACTATGACAGTCAAGCAACACAG 2118
QY 2041 GTGCCAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAA 2100
Db 2119 GTGCCAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAA 2178
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Db 2179 ATAAATAGGGACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2238
QY 2161 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACTTAACTGCAAGCTTACAGGAA 2220
Db 2239 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACTTAACTGCAAGCTTACAGGAA 2298
QY 2221 AGCATTTCTGAGTCAACACCTGCTTGTGCTCAAGGAAATGTTCAAGTTGCACAG 2280
Db 2299 AGCATTTCTGAGTCAACACCTGCTTGTGCTCAAGGAAATGTTCAAGTTGCACAG 2358
QY 2281 TCAAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
Db 2359 TCAAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2418
QY 2341 TTGCTGTCTGTGCCATGTCGCGAGGACTTTGGGCAAACTTTTCTGTGCAAAACCTG 2400
Db 2419 TTGCTGTCTGTGCCATGTCGCGAGGACTTTGGGCAAACTTTTCTGTGCAAAACCTG 2478
QY 2401 ATCAGTTCGACCGAGGAACTGAATATACACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA 2460
Db 2479 ATCAGTTCGACCGAGGAACTGAATATACACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA 2538
QY 2461 GGCAGCAGAAATTTTACCCCAATGAGGGAATCCAAATTTTATTAATGATCAAGAG 2520
Db 2539 GGCAGCAGAAATTTTACCCCAATGAGGGAATCCAAATTTTATTAATGATCAAGAG 2598
QY 2521 GTGGTCCCGAAGACAGACAGACACTTTTGTATGCCGACCCGACGCTGCCAGGAA 2580
Db 2599 GTGGTCCCGAAGACAGACAGACACTTTTGTATGCCGACCCGACGCTGCCAGGAA 2658
QY 2581 GCTGCTTTGATCAGACTCTTAAGAGTGAAGGTACGATCATCTCAGAGCAATTTGT 2640
Db 2659 GCTGCTTTGATCAGACTCTTAAGAGTGAAGGTACGATCATCTCAGAGCAATTTGT 2718
QY 2641 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTGAAATAA 2694
Db 2719 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTGAAATAA 2772
```

RESULT 9

AAH43634

ID AAH43634 standard; cDNA; 3111 BP.

XX AAH43634;

AC AAH43634;

XX 21-JAN-2002 (first entry)

DT 21-JAN-2002 (first entry)

XX Human ion-channel forming protein coding sequence.

DE Human ion-channel forming protein coding sequence.

XX Ion-channel forming protein; voltage-gated potassium channel; fetal;

KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.

```
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 59..2831
/*tag= a
FT /product= "Human ion-channel forming protein"
FT
XX WO200175108-A1.
XX 11-OCT-2001.
XX 03-APR-2001; 2001WO-US010875.
XX 03-APR-2000; 2000US-0194255P.
XX (LEXI-) LEXICON GENETICS INC.
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI; 2001-655987/75.
XX P-PSDB; AAB47678.
XX New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.
XX Disclosure; Page 37-38; 41pp; English.
XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The polynucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.
CC The polypeptides are further used in generating antibodies
XX SQ Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;
```

Query Match 97.4%; Score 2625.2; DB 5; Length 3111;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

QY 1 ATGAAGATGTGGAGTGGGGCGGGGCGAGGGTGTCTGCTGAACCTCGGCAGCGCCAGGGGC 60

Db 165 ATGAAGATGTGGAGTGGGGCGGGGCGAGGGTGTCTGCTGAACCTCGGCAGCGCCAGGGGC 224

QY 61 GACGGCTGTCTGCTGGGCAACCGCGCGGCGCAGCTTGTGTGGCGGGCGGTGGCCCTG 120

Db 225 GACGGCTGTCTGCTGGGCAACCGCGCGGCGCAGCTTGTGTGGCGGGCGGTGGCCCTG 284

QY 121 AGGGAGAGCGCGGGGCAAGCAGGGGCGCGGATGAGCTGTGGGGAACCGCTCTCT 180

Db 285 AGGGAGAGCGCGGGGCAAGCAGGGGCGCGGATGAGCTGTGGGGAACCGCTCTCTCTCT 344

QY 181 TACACGAGTAGCCAGAGCTCGCGCGCAACGTCAAGTACCGCGGGGTGCAGAACTACCTG 240

Db 345 TACACGAGTAGCCAGAGCTCGCGCGCAACGTCAAGTACCGCGGGGTGCAGAACTACCTG 404

QY 241 TACACGAGTAGCCAGAGAGAGCCCGGGCTGGCGGCTTCATCTACCAAGCTTTGTTTTTCTC 300

Db 405 TACACGAGTAGCCAGAGAGAGAGCCCGGGCTGGCGGCTTCATCTACCAAGCTTTGTTTTTCTC 464

QY 301 CTTGCTCTTTGGTGTGCTGATTTTGTGACGTCTTTTCTACCATCCTCGAGCACACAAAATTG 360
Db |||||
QY 465 CTTGCTCTTTGGTGTGCTGATTTTGTGACGTCTTTTCTACCATCCTCGAGCACACAAAATTG 524
Db |||||
QY 361 GCCTCAAGTTGCCCTTTGATCCTGGAGTTGCTGATGATTTGCTCTCTTTGGTTTGGAGTTC 420
Db |||||
QY 525 GCCTCAAGTTGCCCTTTGATCCTGGAGTTGCTGATGATTTGCTCTCTTTGGTTTGGAGTTC 584
Db |||||
QY 421 ATCAATTCGAATCTGCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 480
Db |||||
QY 585 ATCAATTCGAATCTGCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 644
Db |||||
QY 481 AGGTTTGTCTGAAAGCCCTTCTGTTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 540
Db |||||
QY 645 AGGTTTGTCTGAAAGCCCTTCTGTTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 704
Db |||||
QY 541 GTTGTCTCTGAAAGAACTCAGGGTAATATTTTGGCAGCTCTGCACCTCAGAAGTCTCCGT 600
Db |||||
QY 705 GTTGTCTCTGAAAGAACTCAGGGTAATATTTTGGCAGCTCTGCACCTCAGAAGTCTCCGT 764
Db |||||
QY 601 TTCTACAGATCTCTCCGATGGTGGCATGGACCGAAGGGGAGGCACTTGGAAATTAAGT 660
Db |||||
QY 765 TTCTACAGATCTCTCCGATGGTGGCATGGACCGAAGGGGAGGCACTTGGAAATTAAGT 824
Db |||||
QY 661 GGTTCAGTGGTTATGCTCAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTGG 720
Db |||||
QY 825 GGTTCAGTGGTTATGCTCAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTGG 884
Db |||||
QY 721 GTTCTTATTTTTCGCTCTTCTGTTCTATCTGCTGGAAAGGATGCCAATAAGAGTTT 780
Db |||||
QY 885 GTTCTTATTTTTCGCTCTTCTGTTCTATCTGCTGGAAAGGATGCCAATAAGAGTTT 944
Db |||||
QY 781 TCTACATATGAGATGCTCTCTGTTGGGCAAAATTAATGACATTAATGAGTATGGA 840
Db |||||
QY 945 TCTACATATGAGATGCTCTCTGTTGGGCAAAATTAATGACATTAATGAGTATGGA 1004
Db |||||
QY 841 GACAAACTCCCTTAACTTGGCTGGAGATGCTTTCTGAGGCTTGGCACTCCTTGGC 900
Db |||||
QY 1005 GACAAACTCCCTTAACTTGGCTGGAGATGCTTTCTGAGGCTTGGCACTCCTTGGC 1064
Db |||||
QY 901 ATTTCTTTCTTTGCACTTCTCTGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGTACAA 960
Db |||||
QY 1065 ATTTCTTTCTTTGCACTTCTCTGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGTACAA 1124
Db |||||
QY 961 GAACAACACCGCCAGAACACTTTGAGAAAAGAGGAACCCAGCTGCACTTATTCAG 1020
Db |||||
QY 1125 GAACAACACCGCCAGAACACTTTGAGAAAAGAGGAACCCAGCTGCACTTATTCAG 1184
Db |||||
QY 1021 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db |||||
QY 1185 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1244
Db |||||
QY 1081 CACTTTGAAGGCTTGCACACCTGACGCTTACCAAGAAAGAACAAAGGGAAGCATCAAGC 1140
Db |||||
QY 1245 CACTTTGAAGGCTTGCACACCTGACGCTTACCAAGAAAGAACAAAGGGAAGCATCAAGC 1279
Db |||||
QY 1141 AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGGAGGCGCAGAGTAT 1200
Db |||||
QY 1280 --TCAGAACTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGGAGGCGCAGAGTAT 1337
Db |||||
QY 1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCAACGCCAG 1260
Db |||||
QY 1338 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCAACGCCAG 1397
Db |||||
QY 1261 GCGAGTCCCAACAAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCGGCTTCCGGCC 1320
Db |||||
QY 1398 GCGAGTCCCAACAAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCGGCTTCCGGCC 1457
Db |||||
QY 1321 TCGCTCGGCTCAAAAGTTCTCAGCCAAACACAGTGTATAGATGCTGACACAGCCCTTGGC 1380
Db |||||
QY 1458 TCGCTCGGCTCAAAAGTTCTCAGCCAAACACAGTGTATAGTGTGCTGACACAGCCCTTGGC 1517
Db |||||

QY 1381 ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATGATCAGTGGAAAGACCTCACC 1440
Db |||||
QY 1518 ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATGATCAGTGGAAAGACCTCACC 1577
Db |||||
QY 1441 CCACCACCTTAAACCTGTCAATTCGAGCTATCAGAAATTAAGAAATTTTCATGTTGCAAAACGG 1500
Db |||||
QY 1578 CCACCACCTTAAACCTGTCAATTCGAGCTATCAGAAATTAAGAAATTTTCATGTTGCAAAACGG 1637
Db |||||
QY 1501 AAGTTTAAAGAAAAGTTAGTTCAGTCCATATGATGTTAAAGATGTCATTTGAACAATTTCTGCT 1560
Db |||||
QY 1638 AAGTTTAAAGAAAAGTTAGTTCAGTCCATATGATGTTAAAGATGTCATTTGAACAATTTCTGCT 1697
Db |||||
QY 1561 GGTCAATCTGGACATGTTGTAGAAATTAAGAGCTTCAAAACAGCTGTTGATCAAAATTTCT 1620
Db |||||
QY 1698 GGTCAATCTGGACATGTTGTAGAAATTAAGAGCTTCAAAACAGCTGTTGATCAAAATTTCT 1757
Db |||||
QY 1621 GGAAGAGGCAAAATCACATCAGATTAAGAGAGCCGAGAGAAATAACAGCAGAAATGAG 1680
Db |||||
QY 1758 GGAAGAGGCAAAATCACATCAGATTAAGAGAGCCGAGAGAAATAACAGCAGAAATGAG 1817
Db |||||
QY 1681 ACCACAGAGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Db |||||
QY 1818 ACCACAGAGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1877
Db |||||
QY 1741 ATAGAGTCAAGCTCGAGTGCCTACTAGACATCTATCAACAGGCTCTTCGGAAGAGCTCT 1800
Db |||||
QY 1878 ATAGAGTCAAGCTCGAGTGCCTACTAGACATCTATCAACAGGCTCTTCGGAAGAGCTCT 1937
Db |||||
QY 1801 GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAAACAGACATCT 1860
Db |||||
QY 1938 GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTGAAACAGACATCT 1997
Db |||||
QY 1861 GACTATCAAGAGCCCTGATGATAGCAAGATCTTTTGGGTTCGCAACAAACAGTGGCTGC 1920
Db |||||
QY 1998 GACTATCAAGAGCCCTGATGATAGCAAGATCTTTTGGGTTCGCAACAAACAGTGGCTGC 2057
Db |||||
QY 1921 TTATCAGATCAACTAGTGCACAACTCTCGAGAGGCTCGAGTTCAATCTGACGCCAAAT 2117
Db |||||
QY 2058 TTATCAGATCAACTAGTGCACAACTCTCGAGAGGCTCGAGTTCAATCTGACGCCAAAT 2117
Db |||||
QY 1981 GAGTTCAGTGGCCAGACTTTCTAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
Db |||||
QY 2118 GAGTTCAGTGGCCAGACTTTCTAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2177
Db |||||
QY 2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGGACCAACCAACCACTTTCGAAACCAA 2100
Db |||||
QY 2178 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGGACCAACCAACCACTTTCGAAACCAA 2237
Db |||||
QY 2101 ATAAATACGGCACCCAGCCAGCAGCCCAACCACTTTACAGATCCACCTCTCTCCCA 2160
Db |||||
QY 2238 ATAAATACGGCACCCAGCCAGCAGCCCAACCACTTTACAGATCCACCTCTCTCCCA 2297
Db |||||
QY 2161 GCATCAAGCATCTGCCAGGCCAGAAAATCTCTGACCCCTAACCCCTGCAGGCTTACAGGAA 2220
Db |||||
QY 2298 GCATCAAGCATCTGCCAGGCCAGAAAATCTCTGACCCCTAACCCCTGCAGGCTTACAGGAA 2357
Db |||||
QY 2221 AGCATTTCTCAGCTCACCACCTGCTTGTGCTCCAGGAAAATGTTTCAGGTTGCACAG 2280
Db |||||
QY 2358 AGCATTTCTCAGCTCACCACCTGCTTGTGCTCCAGGAAAATGTTTCAGGTTGCACAG 2417
Db |||||
QY 2281 TCANATCTCAGCAGGAGCCGTTCTATGAGGAAAAGCTTTTACATGGGAGGAGAACTCTG 2340
Db |||||
QY 2418 TCANATCTCAGCAGGAGCCGTTCTATGAGGAAAAGCTTTTACATGGGAGGAGAACTCTG 2477
Db |||||
QY 2341 TTGTCTGTCTGTCCCATGGTCCGAGGAACTTGGGAAAATCTTTGTGTGTGTCGAAAACCTG 2400
Db |||||
QY 2478 TTGTCTGTCTGTCCCATGGTCCGAGGAACTTGGGAAAATCTTTGTGTGTGTCGAAAACCTG 2537
Db |||||
QY 2401 ATCAGGTTCGACCCAGGAACTGAAATATACAACTTTTCAGGAGGTGAGTCAAGTGGCTCCAGA 2460
Db |||||
QY 2538 ATCAGGTTCGACCCAGGAACTGAAATATACAACTTTTCAGGAGGTGAGTCAAGTGGCTCCAGA 2597
Db |||||
QY 2461 GGCAGCCAAAGATTTTTTACCCCAATGGAGGGAATCCAAATTTGTTTATTAACATGATGAAGAG 2520
Db |||||

Claim 3; Fig 1; 99pp; English.

PS The present sequence represents the human KCNQ5 (also called KCN6q) gene,
XX which encodes a voltage-gated potassium channel protein. Human KCNQ5 has
CC ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
CC identifying activators or inhibitors of KCNQ5 protein. These activators
CC and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC other forms of macular degeneration, deafness, epilepsy, and different
CC forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC chromosome 6q
XX

SQ Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other;

Query Match 35.8%; Score 963.4; DB 3; Length 125910;

Best Local Similarity 99.9%; Pred. No. 1.9e-272;

Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1730	AGGTACAGTCCATAGAGTCCAGCTGGAGTGGCTCTACTAGACATCTATCAACAGGTCCTTC	1789
DB	123624	AGGTACAGTCCATAGAGTCCAGCTGGAGTGGCTCTACTAGACATCTATCAACAGGTCCTTC	123683
QY	1790	GGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTG	1849
DB	123684	GGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGTG	123743
QY	1850	AACAGACATCTGACTATCAATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTCCGCACAAA	1909
DB	123744	AACAGACATCTGACTATCAATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTCCGCACAAA	123803
QY	1910	ACAGTGGCTGTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGTTCATTC	1969
DB	123804	ACAGTGGCTGTATCCAGATCAACTAGTGCACATCTCGAGAGCCCTGAGTTCATTC	123863
QY	1970	TGACGCCAAATGAGTTCAGTCCAGACTTCTAGCGGCTTAGCCCTACTATGCACAGTC	2029
DB	123864	TGACGCCAAATGAGTTCAGTCCAGACTTCTAGCGGCTTAGCCCTACTATGCACAGTC	123923
QY	2030	AGCAACACAGGTGCAATAGTCAAGGATGGCTCAGAGTGGCGACGACCAACACCA	2089
DB	123924	AGCAACACAGGTGCAATAGTCAAGGATGGCTCAGAGTGGCGACGACCAACACCA	123983
QY	2090	TTGCAACCAATATATAGGCAACCCAGCCAGCAGCCCAACACTTTACAGATCCAC	2149
DB	123984	TTGCAACCAATATATAGGCAACCCAGCCAGCAGCCCAACACTTTACAGATCCAC	124043
QY	2150	CTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTTAACCTTCGAG	2209
DB	124044	CTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTTAACCTTCGAG	124103
QY	2210	GCTTACAGAAAGCATTTCTGACGTCAACCTGCGCTTGTGCTCCAGGAAATGTTTC	2269
DB	124104	GCTTACAGAAAGCATTTCTGACGTCAACCTGCGCTTGTGCTCCAGGAAATGTTTC	124163
QY	2270	AGGTTGCACAGTCAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGAG	2329
DB	124164	AGGTTGCACAGTCAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGAG	124223
QY	2330	GAGAAACTCTGTGTCTGTCTGCCAGAGGACCTTGGGCAAACTTTTGTCTG	2389
DB	124224	GAGAAACTCTGTGTCTGTCTGCCAGAGGACCTTGGGCAAACTTTTGTCTG	124283
QY	2390	TGCAAACTGTATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAACAA	2449
DB	124284	TGCAAACTGTATCAGGTGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAACAA	124343
QY	2450	GTGGCTCCAGAGGACCAAGATTTTACCCCAATGGAGGAATCCAAATGTTTATAA	2509
DB	124344	GTGGCTCCAGAGGACCAAGATTTTACCCCAATGGAGGAATCCAAATGTTTATAA	124403

QY	2510	CTGATGAAGAGGTGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGCCGACGACG	2569
DB	124404	CTGATGAAGAGGTGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGCCGACGACG	124463
QY	2570	CTGCCAGGAAGCTGCTTTCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTC	2629
DB	124464	CTGCCAGGAAGCTGCTTTCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTC	124523
QY	2630	AGAGCATTTGTAAGGACGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGA	2689
DB	124524	AGAGCATTTGTAAGGACGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGA	124583
QY	2690	AATAA 2694	
DB	124584	AATAA 124588	
RESULT 12			
AAAA47618			
ID	AAA47618	standard; cDNA; 2335 BP.	
XX			
AC	AAA47618;		
XX			
DT	08-NOV-2000	(first entry)	
XX			
DE		KCNQ4 Potassium channel gene.	
XX			
KW		KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;	
KW		deafness; probes; treatment; therapy; transgenic animal; antibody;	
KW		agonist; antagonist; tinnitus; hearing loss; neonatal deafness;	
KW		presbycusis; affective disorder; Alzheimer's disease; anxiety; ataxia;	
KW		cognitive deficits; compulsive behavior; dementia; depression;	
KW		Huntington's disease; mania; memory impairment; motor disorders;	
KW		neurodegenerative disease; Parkinson's disease; Pick's disease;	
KW		psychosis; schizophrenia; spinal cord damage; stroke; tremor; ds.	
OS		Homo sapiens.	
XX			
PH		Location/Qualifiers	
FT		83.. 2170	
FT		/*tag= a	
FT		/product= "KCNQ4 Potassium channel polypeptide"	
XX			
PN		WO200044786-A1.	
XX			
PD		03-AUG-2000.	
XX			
PF		19-JAN-2000; 2000WO-DK000024.	
XX			
PR		26-JAN-1999; 99DK-00000076.	
PR		19-MAY-1999; 99DK-00000693.	
XX			
PA		(NEUR-) NEUROSEARCH AS.	
XX			
PI		Jentsch TJ;	
XX			
DR		WPI; 2000-548813/50.	
DR		P-PSDB; AAB01476.	
XX			
PT		Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful	
PT		e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's	
XX		diseases.	
PS		Claim 1; Page 43-48; 65pp; English.	
CC		Mutations in 3 known genes of the KCNQ branch of the potassium channel	
CC		gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy	
CC		and in some cases associated with deafness. KCNQ4 has been mapped to the	
CC		DNA2 locus for autosomal dominant hearing loss, and a dominant negative	
CC		KCNQ4 mutation that causes deafness in a DNA2 pedigree has been	
CC		identified. KCNQ4 is the first potassium channel gene underlying non-	
CC		syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ	
CC		channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4	

CC protein and the protein itself may be used in the prevention, treatment
 CC and diagnosis of diseases associated with inappropriate KCNQ4 expression.
 CC The nucleotides may also be used as DNA probes in diagnostic assays (e.g.
 CC polymerase chain reactions (PCR)) to detect and quantify the presence
 CC of similar nucleic acid sequences in samples and to identify mutations
 CC within them, and hence which patients may be in need of restorative
 CC therapy. They may also be used to study the expression and function of
 CC KCNQ4 polypeptides and their role in metabolism, for example through the
 CC production of transgenic animals. The KCNQ4 polypeptides may be used as
 CC antigens in the production of antibodies and to identify modulators
 CC (agonists and antagonists) of KCNQ4 expression and activity. The anti-
 CC KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate
 CC KCNQ4 expression and activity. They may be used in this way to treat
 CC tinnitus, loss of hearing (especially progressive hearing loss, neonatal
 CC deafness and presbycusis (deafness of the elderly)) and disease or
 CC adverse conditions of the central nervous system (CNS) such as affective
 CC disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by
 CC trauma, stroke or neurodegenerative illness, cognitive deficits, mania,
 CC compulsive behavior, dementia, depression, Huntington's disease, mania,
 CC memory impairment, memory disorders and dysfunctions, motion disorders,
 CC motor disorders, neurodegenerative diseases, Parkinson's disease,
 CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
 CC schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,
 CC antisense nucleic acid molecules may be administered to down regulate
 CC KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing
 CC their expression
 XX
 SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 19.2%; Score 518.4; DB 3; Length 2335;
 Best Local Similarity 60.1%; Pred. No. 8.5e-142; Indels 165; Gaps 8;
 Matches 1103; Conservative 0; Mismatches 566;
 217 TACCGCGCGGTGCAGAACTACTGTACAAACGCTGTGGAGAGACCCCGCGGTGGCGCTTC 276
 320 TACCGCGCGGTGCAGAACTGTGGTGTACAAACGCTGTGGAGAGACCCCGCGGTGGCGCTTC 379
 277 AFTACACAGCTTCGTTTTCCTCTGCTTTGCTGCTTTGCTGCTTTGCTGCTGCTTTCT 336
 380 GTCTACACAGCTTCATATTTTGTGCTTTTACGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
 337 ACCATCCCTGACACACAAATTTGGCTTCAAGTTCCTTGTATCTTGTATCTGCTGCTGCTG 396
 440 ATATCCAGGAGCACAGAACTTCCCAACGAGTGTCTCTCTCATCTTGGAAATTCGTGATG 499
 397 ATTGTGCTTTGTTGTTGAGTTTCAATTCGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 456
 500 ATCGTGGTTTTCGGCTTGGAGTACATCTGTCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCT 559
 457 TATAGGATGCAAGGAGACTGAGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACC 516
 560 TACCGAGGATGGAGGTCGCTTCCGCTTTCAGAAAGCCCTTCTGTGCTATCGACTTC 619
 517 ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAACATCAGGTAATATTTTGGC 576
 620 ATCGTGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679
 577 ACCTCTGCACTGAAAGTCTCGTTTCTTACAGATCCTCGCATCTGCTGCTGCTGCTGCTGCTG 636
 680 ACCTGCGCTGCTGCGAGCATGCTTCTTCCGAGATCTTCCGATGCTGCTGCTGCTGCTGCTGCT 739
 637 AGCGGAGGCACTTGGAAATTTACTGGGTTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 696
 740 CGCGCGGACCTTGGAGGCTGCTGGCTCAGTGGTCTACGCGATAGCAAGGAGCTGATC 799
 697 ACAGCTTGTGTACATAGATTTTGTGTTCTTATTTTTCGTTCTTCTGCTTCTATCTGTTG 756
 800 ACCGCTGTGTACATCGGTTTCTGCTGCTCATCTTCGCTCTCTGCTGCTTCTGCTGCTGCTG 859
 757 GAAAGGATCCCAATAAGATTTTCTACATATGACAGATGCTCTCTGCTGCTGCTGCTGCTGCT 816
 860 GAGAGGAGCGCCAACTCCGACTTCTCTCTCTACGCGCATCTGCTCTGCTGCTGCTGCTGCTG 919

QY 817 ACATTGACAACTATTGGCTATGGAGACAAAACTCCCTTAATCTGGCTGGGAAGATTGCTT 876
 DB 920 ACATTGACAACTATGGCTATGGTGAACAGAACCGCACATGGCTGGGAGGCTGCTG 979
 QY 877 TCTGAGGCTTTGGCACTCTCTTGGCATTTCTTTTTCATCTTCTGCTGCTGCTGCTGCTGCTG 936
 DB 980 GCTGCTGCTTGGCTTACTTGGCATCTCTTTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
 QY 937 TCAGTTTTCATTTAAAGTACAGAAACAAACCGCCGAGAACACTTTTGAGAAAAGAGG 996
 DB 1040 TCCGGCTTTGGCTTGAAGTCCAGAGCAGACCCGGCAGAGCACTTCAGAGCGGAGG 1099
 QY 997 AACCCAGCTGCAAACTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056
 DB 1100 ATGCGCGGAGCCAACTCATCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1159
 QY 1057 GTTTCATTTGAACTGGAAGCCACTTGAAGGCTTGCACACCTGTCAGC----- 1107
 DB 1160 GCTTACTGACAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1219
 QY 1108 CTTACCAAGAAAGAACAGGGAAGCATCAAGCAGTCAAGAGCTA----- 1152
 DB 1220 GCGCTCTTGTGAGCACTGCAAGCGGCCCAATGGGGCTTACGGGCCCTGGAGGCTG 1279
 QY 1153 ----- 1152
 DB 1280 CGCGGGCGCGGTACCCGAGCGAGCACCTCCCTGCTTACCCGCGCTTGCACCTGCCAC 1339
 QY 1153 -----AGTTTAAAGAGCGA 1167
 DB 1340 CGCGCGGAGCAGCTTCTTTCCTGCTGGGAAAGCAGCGGATGGGATCAAGACCGC 1399
 QY 1168 GTGCGCATGCTAGCCCGAGGGGCCAGAG-----GTATTAAAGAGCGCAGAGCCTCAGTA 1221
 DB 1400 ATCCGATGCGGAGCTCCAGCGCGGAGCGGCTCTTCCAGCAGCAGCTGCGCACCTCCA 1459
 QY 1222 GGTGACAGGAGGTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1278
 DB 1460 ACAATGCCACCTCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1519
 QY 1279 CAGAGAGCTGAGCTTCAACGAGCGAACCCGCTTCCGCGCTTCCGCTGCTGCTGCTGCTGCTGCTG 1338
 DB 1520 CAAAGAGCTGAGCTTCAATGACCGCACCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCGCT 1573
 QY 1339 TCTCAGCAAAACAGTGTATGATGTGACACAGCCTTGGCAGCTGATGATGATGATGATGATGAT 1398
 DB 1574 -----AAACCCCGCACCTCTGCTGAGGATGCCCC---CCTCAGAGGAGATGAGCAGAG 1621
 QY 1399 GAAAAGGATGCCAGTGTGATGTATCAGTGGAAAGACTCACCCCAACCACTTAAAGACTGTC 1458
 DB 1622 GAGAAGAGCTACCAAGTGTGAGCTCAAGTGGAGCAGCATCATGCTGCTGCTGAGACAGTC 1681
 QY 1459 ATTGAGCTATCAGAAATTTGAAATTTTCAATTTGTCGAAACGGAAGTTTAAAGGAAACGTTA 1518
 DB 1682 ATCGCTCCATCAGGATTTCTCAAGTTCTGCTGCGCCAAAAGGAAATTTCAAGAGGACACTG 1741
 QY 1519 CGTCCATATGATGTAAGATGTTCATGAACTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1578
 DB 1742 CGACCGTACGAGCTGGAAGGAGCTGATGAGCAGTCTCAGAGGCGCACCTTGGATGAAATC 1801
 QY 1579 TGTAGAATTAAGAGCTTCAAAACAGCTGTTGATCAAAATTTCTTGGAAAGGCG---AAATC 1635
 DB 1802 GCGCGGATCAAGAGCTGCAAACTCCGCTGAGCACTTGGGTGCGGGGCGCGCGGAGC 1861
 QY 1636 ACATCAGATAGAGAGCGAGAGAAATTAACAGAGAAACATGAGACCAAGAGATGCTC 1695
 DB 1862 AGGAAGGCGCGGAGAGGCGCAAGGGGCGCTCCGACGCGGAGGTGGTGGATGAAATC 1921
 QY 1696 AGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1755
 DB 1922 AGCATGATGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981
 QY 1756 GACTGCTTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCTGCTGCTGCTGCTGCTGCTGCT 1815

Db 1982 GACCTGCTGTTGGGCTTCTATTTCGGCTGCGCTG-----GCTCTGGCACTCGGCCAGC 2035
Qy 1816 TTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1875
Db 2036 CTGGGGCGCGTGAAGTGGCGTGTTCACACCCGACATCCTCGGACTACACAGCCCT 2095
Qy 1876 GTGGATAGCAAGAATCTTTTCGGGTTCGCGACAAA 1909
Db 2096 GTGGACACGAGGACATCTCGCTCCGACAGA 2129

RESULT 13

AD331698
ID AD331698 standard; DNA; 2335 BP.

XX AC AD331698;

XX DT 29-JAN-2004 (first entry)

XX DE Human 32394 gene #SEQ ID 55.

XX KW Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;

XX KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;

XX KW cardiovascular; disorder; ischaemia; aortic bending;

XX KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;

XX KW angina; cardiomyopathy; cardiac death; gene; ds.

XX OS Homo sapiens.

XX PN WO2003065984-A2.

XX PD 14-AUG-2003.

XX PF 29-JAN-2003; 2003WO-US002571.

XX PR 01-FEB-2002; 2002US-0353224P.

XX PR 15-MAR-2002; 2002US-0364529P.

XX PR 19-APR-2002; 2002US-0373861P.

XX PR 29-APR-2002; 2002US-0376287P.

XX PR 12-JUN-2002; 2002US-0388080P.

XX PR 24-JUN-2002; 2002US-0390971P.

XX PR 03-JUL-2002; 2002US-0394130P.

XX PR 10-JUL-2002; 2002US-0394797P.

XX PR 21-AUG-2002; 2002US-0404904P.

XX PR 23-AUG-2002; 2002US-0405450P.

XX PR 04-SEP-2002; 2002US-0408070P.

XX PR 06-NOV-2002; 2002US-0424300P.

XX PR 05-DEC-2002; 2002US-0431042P.

XX PR 05-DEC-2002; 2002US-0431079P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;

XX PI Stagliano N, Perodin J, Rodrigue-Way A;

XX XX WPI; 2003-731468/69.

XX DR P-PSDB; AD331699.

XX PT Identifying a compound capable of treating a cardiovascular disorder
(e.g. atherosclerosis) comprises assaying the ability of the compound to
modulate the expression or activity of e.g. 1682, 6169 or 6193
polypeptide or nucleic acid.

XX PS Disclosure; SEQ ID NO 55; 328pp; English.

XX CC The invention relates to a method for identifying a compound capable of
treating a cardiovascular disorder. The present invention identifies the
differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 33394, 3484,
345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,

CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
CC 6585 genes in cardiovascular disease states. The methods are useful in
CC diagnosing, preventing and treating cardiovascular disorders, such as
CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
CC stenosis, arterial inflammation, vascular wall remodeling, coronary
CC microembolism, tachycardia, bradycardia, pressure overload, aortic
CC bending, coronary artery ligation, vascular heart disease, valvular
CC disease, including but not limited to, valvular degeneration caused by
CC calcification, rheumatic heart disease, endocarditis, or complications of
CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC heart failure, sinus node dysfunction, angina, heart failure.
CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC including but not limited to, pericardial effusion and pericarditis;
CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC cardiovascular developmental disorders. The methods may also be used for
CC identifying compounds that modulate cardiovascular disorders. Sequences
CC given in AD331644-AD331769 represent the genes and proteins that may be
CC regulated by a compound of the invention.

XX SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 19.2%; Score 518.4; DB 10; Length 2335;

Best Local Similarity 60.1%; Pred. No. 8.5e-142;

Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

Qy 217 TACCGCGGCTGCAGAACTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGTTC 276

Db 320 TACCGCGGCTGCAGAACTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGTTC 379

Qy 277 ATCTACCAACGCTTTCGTTTTCTCTTGTCTTGTCTTGTATTTCTGCTAGTGTTCCT 336

Db 380 GTCTACCAACGCTTTCATATTTTGTCTTGTCTTGTCTGCTGCTGCTGTGCTGCC 439

Qy 337 ACCATCCCTGAGCACAAATTCGCTTCAAGTTCCCTTTGATCTCTCGAGTTCGTGATG 396

Db 440 ACTATCCAGGAGCACCAGGAATTTGCCAAAGAGTCTCTCTCATCTTGAATTCGTGATG 499

Qy 397 ATTCTGCTCTTGGTTGGAGTTTCATCATTCGATCTGCTGCGGTTGCTGTGTCGA 456

Db 500 ATCGTGTGTTTCGGCTTGGAGTATCATCGTCCGGTCTGCTCGCGGATGCTGCTGCCG 559

Qy 457 TATAGAGGATGGCAAGAAAGACTGAGGTTTCTCGAAAGCCCTTCTGTGTTATAGATACC 516

Db 560 TACCGAGGATGGCAGGTCGCTTCGGCTTTCGCAAGAAAGCCCTTCTGTCTCATCGACTTC 619

Qy 517 ATTCTTCTTATTCGCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATTTTCC 576

Db 620 ATCGTGTTCGTGGCTCGTGGCGCTCATCGCGCGGTACCCAGGGCAACATCTTCGCC 679

Qy 577 ACCTTCGACTCAGAAGTCTCGGTTTCTTACAGATCTCTCGCATGCTGCGCATGACCGA 636

Db 680 ACCTTCGCGCTCGCAGCATGCGCTTCTGAGATCTCTGCGCATGCTGCGCATGACCGC 739

Qy 637 AGGGGAGGCACCTTGAAATTAATCTGGTTTCACTGGTTTATGCTCAGCAAGAAATTAATC 696

Db 740 CGCGGCGCACCTGGAAGCTCTGGGCTCAGTGTCTACGCGCATAGCAAGAGCTGATC 799

Qy 697 ACACCTTGGTACATAGGATTTTGGTCTTATTTTTCGTTTCGTTTCCTTCTATCTGTTG 756

Db 800 ACCGCTTGGTACATCGGTTTCTGCTCATCTTCGCTCTCTTCTGCTCTACCTGCGCC 859

Qy 757 GAAAGGATGCCAATAAAGATTTTCTACATATGATGCTCTCTGTTGGGGCACATTT 816

Db 860 GAGAAGGACGCCAACTCCGACTTCTCTCTTACCGCGACTCGCTCTGGTGGGACGATT 919

Qy 817 ACATTGACAACTATTGGCTATGGAGACAAAACCTCCCTTAACCTTGGCTGGGAAGATTGCTT 876

Db 920 ACATTGACAACTATCGGCTATGGTGAAGACCGCACACATGCTGGGCGAGGTCCTG 979

Qy 877 TCTCAGGCTTTCGACTCCTTGGCAATTTCTTTTTCGACTTCTCTGCGCGCATTTCTTGGC 936

Db 980 GCTGCTGGCTTGGCTTACTGGGCACTCTTTCTTTGCCCTGCTGCCGCACTCCTAGGC 1039
Qy 937 TCAGGTTTTCATTAAGATCAAGAACAAACACCGCAGAAAAACATTTGAGAAAAAGG 996
Db 1040 TCGGCTTTGCTTGAAGTCCAGGAGCAGCACCGGCAGAACACTTCGAGAACGCGAGG 1099
Qy 997 AACCCAGCTGCCAACCCTCACTCAGTGTGTTGGGTAGTTACGCACTGATGAGAAATCT 1056
Db 1100 ATGCCGCGACCAACCTCACTCCAGGCTGCTGGCGCTGTACTCCACCGATATGAGCGG 1159
Qy 1057 GTTTCCATTCAACTGGAAGCCACACTTGAAGGCCCTTGACACACCTGCGACG----- 1107
Db 1160 GCCTACTGACAGCACTGCTACTACTATGACAGTATCTCCATCTTCAGAGAGCTG 1219
Qy 1108 CCTACCAAGAAAGAACCAAGGGGAGCATCAAGCATCAGAAAGTA----- 1152
Db 1220 GCCCTCTGTTGAGCAGCGTCAACGCGGCCGCAATGGGGCCCTTACGCGCCCTGGAGGTG 1279
Qy 1153 ----- 1152
Db 1280 CGCGCGCGCGGTACCCGACGGAGACCCCTCCCGTTACCGCGCCGTTGCCACCTGCCAC 1339
Qy 1153 -----AGTTTAAAGGACGA 1167
Db 1340 CGCGCGCGCAGCACTCTTCTGCTGGGGAAGCAGCGGATGGGCATCAAGAGCCGC 1399
Qy 1168 GTGCGCATGGTACGCCAGGGCCGAG-----GTATTAAAGCCGACAAAGCCTCAGTA 1221
Db 1400 ATCCGCATGGCAGCTCCAGCGCGGACGGGTCTTCCAAAGCAGCAGCTGGCACCTCCA 1459
Qy 1222 GGTACAGAGGCTCCCAAGCAGCAGCATCACAGCGAGG--GCAGTCCACCACAAAGTG 1278
Db 1460 ACAATGCCACCTCCCAAGCAGCAGCAGGTGGTGAGGCCACACCCACCAAGAGTG 1519
Qy 1279 CAGAAGAGCTGGAGCTTCAACAGCAGCAGCCGCTTCCGGGCCCTCGCTGCGCCTCAAAAGT 1338
Db 1570 CAAGAGAGCTGGAGCTTCAATGACCGCAGCCGCTTCCGGGCATCTCTGAGACTC----- 1573
Qy 1339 TCTCAGCCAAACAGATGATAGTGTGACACAGCCCTTGGCACTGATGATATATGAT 1398
Db 1574 -----AAACCCGCGACCTCTGCTGAGATGCC-----CCTCAGAGGAAGTAGCAGAG 1621
Qy 1399 GAAAGAGATCCAGTGTGATGTATCAGTGAAGACCTCACCCACCACTTAAACCTGTC 1458
Db 1622 GAGAAGAGCTACCAAGTGTGAGCTCAGGTGAGCAGCATCATGCTGCTGTGAACACAGTC 1681
Qy 1459 ATTCCAGCTATCAGAAATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTA 1518
Db 1682 ATCCGCTCCATCAGGATTTCTCAAGTTCTGCTGGCCAAAGGAAATTCAGAGGACACTG 1741
Qy 1519 CGTCCATATGATTAAGAGATGTATTGAACAATATCTGTGTGTCATCTGGACATGTTG 1578
Db 1742 CGACCGTACGACGTGAAGAGAGCTATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG 1801
Qy 1579 TGTAGATTAAAGCTTCAACACAGTGTGTCATCAAAATCTTGGAAAGGGC-----AAATC 1635
Db 1802 GCGCGATCAAGAGCTCCAAACTCGGTGACCAAAATTTGGTTCGGGGCCCGGGGAC 1861
Qy 1636 ACATCAGATAAGAGAGCCGAGAGAAATAACAGCAGAACATGACACACAGACATCTC 1695
Db 1862 AGGAAGCCCGGAGAGAGGCGACAAAGGGGCCCTCCGACGCGGAGGTGGTGGATGAAATC 1921
Qy 1696 AGTATGCTCGGTGCGGTGCTCAAGGTTCAAAAACAGGTACAGTCCATAGAGTCAAGCTG 1755
Db 1922 AGCATGATGGAGCGGTGCTCAAGGTGAGAGAGAGGTGCACTCATCGACACAGAGCTG 1981
Qy 1756 GACTCGCTACTAGACATCTATCAACAGGTCTCTTCGAAAGGCTGTGCTCAGCCCTCGCT 1815
Db 1982 GACCTGCTGTGGGCTTCTATTTCGGCTGCTGCTG-----GCTGCGCACCTCGGCCAGC 2035
Qy 1816 TTGGGCTCATTCAGATCCACCTCTTTGAATGTGAACAGACATCTGATATCAAGCCCT 1875
Db 2036 CTGGGCGCGGTGCAAGTGCCTGTTTCGACCCCGACATCACCTCCGACTACACAGCCCT 2095

Qy 1876 GTGGATAGCAAGATCTTTTCGGGTTCCGCAAAA 1909
Db 2096 GTGGACCACGAGACATCTCCGTTCCGCAAGA 2129

RESULT 14

AA57140
ID AAX57140 standard; DNA; 2273 BP.

XX AAX57140;

XX 22-JUL-1999 (first entry)

XX Mouse KCNQ2 cDNA.

XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;
KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;
KW gene therapy; drug screening; ss.

XX Mus musculus.

XX Key Location/Qualifiers

XX CDS 1..2273

XX FT FT a

XX FT /product= "KCNQ2"

XX FT /note= "Partial sequence, no stop codon given"

XX PN W09921875-A1.

XX PD 06-MAY-1999.

XX PF 23-OCT-1998; 98WO-US022375.

XX PR 24-OCT-1997; 97US-0063147P.

XX PA (UTAH) UNIV UTAH RES FOUND.

XX PI Singh NA, Leppert MF, Charlier C;

XX DR WPI; 1999-312938/26.

XX DR P-PSDB; AAY08345.

XX PT Nucleic acid encoding potassium channels KCNQ2 and 3.

XX PS Claim 1; Page 153-156; 195pp; English.

XX This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available

XX SQ Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 0 U; 16 Other;

XX Query Match 19.2%; Score 516; DB 2; Length 2273;

XX Best Local Similarity 57.6%; Pred. No. 4.3e-141;

XX Matches 1030; Conservative 2; Mismatches 694; Indels 72; Gaps 4;

Qy 64 GGCCTGCTACTGTGGGACCCCGCCACGCTTGGTGGCGCGGTGGCTGAGG 123

PF 26-JUN-1998; 98WO-US013276.
XX
PR 12-AUG-1997; 97US-0055599P.
XX
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Blunar MA, Dworetzky S, Yang W, Levesque PC, Gribkoff VK;
PI Neubauer MG, Little WA;
XX WPI; 1999-190047/16.
DR P-PSDB; AAY01530.
XX
XX New potassium channels, KCNQ2 and KCNQ3 - may be involved in
PT neurotransmission and neuroprotection, used to treat, e.g. ataxia.
XX
XX PS Claim 7; Fig 10A-D; 64pp; English.
XX
XX The present sequence encodes murine KCNQ2/KvLr1. KCNQ proteins are
CC nervous system-specific potassium channels. In neurons, potassium
CC channels regulate neuronal excitability, action potential shape and
CC firing pattern, and neurotransmitter release. KCNQ modulators may be used
CC to treat disorders such as ataxia, myokymia, seizures, Alzheimer's
CC disease, Parkinson's disease, age-associated memory loss, learning
CC deficiencies, motor neuron diseases, epilepsy, and stroke
XX
SQ Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 U; 0 Other;
Query Match 18.9%; Score 510; DB 2; Length 2169;
Best Local Similarity 58.1%; Pred. No. 2.5e-139;
Matches 1043; Conservative 0; Mismatches 670; Indels 81; Gaps 5;
QY 64 GGCCTGCTACTGCTGGGCAACCGCGCCGACGCTTGGTGGCGGGGGTGGCGCTGAGG 123
DB 67 GGCTTCGTGGGGCTGGACCCCGCGCGCCGACCTCCACACGCGACGCGGCTACTCATC 126
QY 124 GAGAGCGCGCGGCAAGCAGCGGGCGCGGATGAGCTGTGGGGAAGCCGCTCTCTTAC 183
DB 127 GCGGGCTCCGAGGCCCCAGCGCGGAGCGTGTGGAGAGCCGCGGCGGCGGCG 186
QY 184 ACGAGTAGCAGAGCTGCGCGCGCAACGTCAGTACCGGCGGGTGCAGAACCTACTGTAC 243
DB 187 GGAGCGCGGAAGCCCGGAGCGAAGCGCTTCTACCGCAAGCTGCAGAAATTCCTCTAC 246
QY 244 AACCTGCTGGAGAGACCCCGCGTGGCGTTCATCTACACGCTTTCGTTTCTCCTT 303
DB 247 AACGTGCTAGAGCGCGCGCGCTGGCGCTTCACTACACGCTTTCGTTTCTCCTTTA 306
QY 304 GTCTTTGGTTGCTTGAATTTGTCAGTGTCTTCTACCATCCCTGAGCACAACAAATTTGCC 363
DB 307 GTCTTCTCCTGCTTGTGCTTCTGTTTTCACCATCAAGGAGTACGAGAGCTCT 366
QY 364 TCAAGTTGCTCTTGAATCTGAGGTTGCTGATGATGTCGCTTGTGGTGGAGTTCAATC 423
DB 367 GAGGGGGCCCTCTACATCTTGGAAATCGTACTATCGTGTATTCGCTGTGTGAGTACTTT 426
QY 424 ATTGCAATCTGCTGCGGGTGTGCTGATATAGAGATGCGAAGGAGACTGAGG 483
DB 427 GTGAGGACTCTGGGCTGCAAGCTGTGTTGCGGTATCGAGGCTGAGGGGCGAGCTCAAG 486
QY 484 TTTGCTCCAAAGCCCTCTGCTGTATAGATACCATTTGTTCTTATCGCTTCAATAGCAGTT 543
DB 487 TTTGCCAGAGACCGTTCTGTGTGATGATCATGTTGCTGATTTGCCCTCAATGCTGTG 546
QY 544 GTTTCGCAAAACCTCAGGGTAATATTTTGGCAGCTCTGCACAGAGTCTCGGTTTC 603
DB 547 CTGGCTGCTGTTTCCAGGGCAATGCTCTTTCACATCTGCGCTTCGAGGCTTCGGTTC 606
QY 604 CTACAGATCTCCGATGCTGGATGACCGAAGGGGAGGACCTTGGAAATTAATCTGGT 663
DB 607 TTGCAAAATCTTGGGATGATCCGTATGACCGAGGGGTGGACCTGGAACTCTTGGGA 666
QY 664 TCAGTGGTTTATGCTCAGCAAGAAATTAATCAAGCTTGGTATAGGATTTTGGTT 723

667 TCGGTAGTCTACGCTCACAGCAAGAGCTGGTCACTGCTGCTGTATGCTTCTCTCTGC 726
724 CTTATTTTTCGCTCTTTCCTTCTATCTGTTGGAAGGATGCCAATAAGAGTTTCT 783
727 CTCATCTCGCTCATTTCTGTTGTAATTTGGCAGAAAGGGTGAATGACCACTTTGAC 786
784 ACATATGCAAGTCTCTCTGTTGGGCAACAATTACATTTGACAACTATTGGCTATGGAGAC 843
787 ACCTACGCAATGCACTCTGTTGGGTCTGATCACCTGACGACCATTTGGTACGGGAC 846
844 AAAACTCCCTCACTTGGCTGGGAAGATGCTTTCTGCGAGGCTTTCGACTCTCTTGGCAT 903
847 AAGTACCTCTCAGACCTGGAACGGAGCTGCTGCGACGACCTTTTACCTCTCATTTGGTGC 906
904 TCTTTCTTTCGACTTCTGCGGCACTTCTGCTCAGGTTTGGCTTTCATTTAAAGTACAGAA 963
907 TCGTTCTTCTCTCTCTGCTGCAATTTGGGATTCGGGCTTTGCCCTGAAAGTCCAAGAG 966
964 CAACACCGCCAGAAACAATTTGAGAAAGAAAGGAAACCCAGCTGCCAACCTCATTCAGTGT 1023
967 CAGCATCGGCAAAAACACTTTGAGAAACGGCGAACCCTGCGCAGGCTGTGATCCAGTCT 1026
1024 GTTTGGCTAGTTTACGCACTGATGAGAAAT----- 1054
1027 GCCTGGAGATTCTATGCTACTAACCTCTCACGCAACGACCTGCACCTCCACGTGGCAGTAC 1086
1055 -----CTGTTTCCATTGCAACCTGGAGCCACACTTGAAGGCTTGCAC 1098
1087 TAGAGCGGACAGTCACTGTCCCCTGTACAGACTCATCCCACTCTGAACACAGCTGGAG 1146
1099 ACCTGACGCCCTACCAAGA-----AAGAAACAAAGGGGAA 1131
1147 CTGCTGAGGNAATCTAAGAGCAATCTGGACTCACCTCTCAGGAAGAGGCCACAGCCAGAG 1206
1132 GCATCAAGCAGTCAGAGCTTAAGTTTAAAGAGCGAG-----TGGCATGGCTAGCCCCAGG 1188
1207 CCATCAACAGTCAAGAGTCACTTTGAAAGATCGTCTCTTCCAGCCCCCGAGGCGATG 1266
1189 GGCACAGATTAAAGAGCGCAGCAAGCTCAGTAGGTGACAGGAGTCCCCCAAGCACCGAC 1248
1267 GTGCGCAAGGAAAGGGGTCTCCCAGGCCACAGCGTCCGCGGTCCCCCAGTGGGAT 1326
1249 ATCACAGCCGAGGCGAGTCCCAACAAAGTGACAGAGCTGGAGCTTCAACGACCGAACC 1308
1327 CAGAGTCTTATGACAGCCCGAGAGGTGCCCAAGAGCTGGAGCTTTGGTGAACGCGAGC 1386
1309 CGCTTCGCGCTCTGCTGCGCTCAAAAGTTCTCAGCCAAAACAGAGTATAGATGCTGAC 1368
1387 CGCACAGCCAGGCTTTCCGCATCAAGGGTGTGCTCCCGGAGAAATTCAGAAGCAAGC 1446
1369 ACAGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1428
1447 C---TCCCTGGGAGGACATCGTAGAGGACAAACAGAGCTGTAACTCGGAGTTGTGACT 1503
1429 GAAGACCTCAACCCACACCTTAAACCTGCTCAATTCGAGCTATCAGAAATATGAAATTTCA 1488
1504 GAAGATCTTACCTCCCTGSCCTCAAAGTTAGCATCAGAGCTGTGTGTGTTATGCGGTCTTG 1563
1489 GTTGCAAAACGGAAGTTTAAAGAAACGTTACGTCATATGATGATGATGATGATGATGATGATG 1548
1564 GTATCTAAGCGAAAGTTCAAAGAGAGTCTCGGCCATATGATGATGATGATGATGATGATGATG 1623
1549 CAATATTTCTGCTGCTCATCTGGACATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1608
1624 CAGTACTCGGCTGGAACACTTGGATATGTTGTTCCCGCATCAAGAGCTGCGAGTCCAGAGTG 1683
1609 GATCAAAATCTTGAAAGAGGCAAAATCAATCAGATGATGATGATGATGATGATGATGATGATG 1668
1684 GACCAGATTGTTGGGGGGGGGGCCCAACAAATAACGATGATGATGATGATGATGATGATGATG 1740
1669 GCAGAACTAGACCAACAGAGCTCTCAGTATGCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1728
1741 GCGGAAACGAGGCTGCGCGGAGACCCCGAGCATGATGATGATGATGATGATGATGATGATGATG 1800

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 10:31:37 ; Search time 1499.51 Seconds
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Title: US-09-810-796-2
Perfect score: 2694
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Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2694	100.0	2694	9 US-09-866-020-1	Sequence 1, Appli
2	2694	100.0	2694	9 US-09-810-796-2	Sequence 2, Appli
3	2694	100.0	2694	19 US-10-948-493-1	Sequence 1, Appli
4	2690.4	99.9	3071	9 US-09-810-796-1	Sequence 1, Appli
5	2689.2	99.8	3137	18 US-10-661-629-1	Sequence 1, Appli
6	2681.2	99.5	3074	9 US-09-813-148-1	Sequence 1, Appli
7	2630	97.6	2667	9 US-09-810-796-3	Sequence 3, Appli
8	2625.2	97.4	2772	9 US-09-825-147-1	Sequence 1, Appli
9	2625.2	97.4	2772	18 US-10-803-268-1	Sequence 1, Appli
10	2625.2	97.4	3111	9 US-09-825-147-3	Sequence 3, Appli
11	2625.2	97.4	3111	18 US-10-803-268-3	Sequence 3, Appli

12	518.4	19.2	2335	17	US-10-353-690-55	Sequence 55, Appli
13	518.4	19.2	2335	19	US-10-850-928-1	Sequence 1, Appli
14	516	19.2	2273	16	US-10-096-578-88	Sequence 88, Appli
15	510	18.9	2169	13	US-10-128-870-22	Sequence 22, Appli
16	510	18.9	2169	14	US-10-131-885-22	Sequence 22, Appli
17	509.8	18.9	582	15	US-10-313-542-303	Sequence 303, App
18	500.6	18.6	7411	18	US-10-335-053-6	Sequence 6, Appli
19	500.6	18.6	7420	17	US-10-295-027-281	Sequence 281, App
20	500.6	18.6	7420	18	US-10-643-795A-75	Sequence 75, Appli
21	500.6	18.6	7420	19	US-10-948-518-75	Sequence 75, Appli
22	500.6	18.6	7863	15	US-10-084-817-335	Sequence 335, App
23	478.4	17.8	5595	18	US-10-820-307-8	Sequence 8, Appli
24	465.8	17.3	2766	18	US-10-820-307-6	Sequence 6, Appli
25	465.4	17.3	896	13	US-10-128-870-1	Sequence 1, Appli
26	465.4	17.3	896	14	US-10-131-685-1	Sequence 1, Appli
27	465	17.3	548	10	US-09-826-734-269	Sequence 269, App
28	464	17.2	2814	16	US-10-096-578-90	Sequence 90, Appli
29	460.8	17.1	2565	13	US-10-128-870-26	Sequence 26, Appli
30	460.8	17.1	2565	14	US-10-131-685-26	Sequence 26, Appli
31	460.8	17.1	2914	16	US-10-096-578-6	Sequence 6, Appli
32	457.4	17.0	2755	18	US-10-820-307-4	Sequence 4, Appli
33	455.8	16.9	1848	18	US-10-744-796-5	Sequence 5, Appli
34	454.2	16.9	4512	15	US-10-084-817-334	Sequence 334, App
35	452	16.8	575	15	US-10-313-542-305	Sequence 305, App
36	432.2	16.0	1878	18	US-10-744-796-3	Sequence 3, Appli
37	432.2	16.0	4596	18	US-10-723-860-7636	Sequence 7636, Ap
38	425.4	15.8	455	17	US-10-242-535A-25396	Sequence 25396, A
39	425.4	15.8	455	17	US-10-085-783A-25396	Sequence 25396, A
40	425	15.8	3287	13	US-10-128-870-19	Sequence 19, Appli
41	425	15.8	3287	14	US-10-131-685-19	Sequence 19, Appli
42	423.4	15.7	1425	10	US-09-960-706-511	Sequence 511, App
43	423.4	15.7	1425	10	US-09-873-319-313	Sequence 313, App
44	423.4	15.7	1425	16	US-10-116-712-662	Sequence 662, App
45	423.4	15.7	1932	18	US-10-744-796-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US2002040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIORITY FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIORITY FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 100.0%; Score 2694; DB 9; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAAGGATGTGGAGTTCGGGCGGCGGAGGTGTCTGTAACCTCGGACGCCAGCGGCG 60
Db 1 ATGAAGGATGTGGAGTTCGGGCGGCGGAGGTGTCTGTAACCTCGGACGCCAGCGGCG 60
Qy 61 GACGGCTGTCTACTGTCTGGGACCCCGCGCCACGCTTGTGTGGCGCGCGGTGGCCTG 120

Db	120		1141	AGTCAGAGCTAAGTTTAAAGGAGCGAGTGCCTAGCTAGCCCCAGGGCGCAGAGTATT	1200
Qy	120		1201	AAGAGCCGCAAGCCCTCAGTAGGTGACAGGAGGTCCCCAAGCAGCCGACATCACAGCCGAG	1260
Db	180		1201	AAGAGCCGCAAGCCCTCAGTAGGTGACAGGAGGTCCCCAAGCAGCCGACATCACAGCCGAG	1260
Qy	180		1261	GSCAGTCCACCACAAAGTGCAGAAAGCTGGAGCTTCAACGACCCGAAACCCGCTTCGGGCC	1320
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Qy	240		1321	TCGCTCGGCTCAAAAGTTCTCAGCCAAAACAGGTGATAGATGCTGACACAGCCCTTGGC	1380
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Qy	300		1381	ACTGATGATGATATGATGAAAAGGATGCCAGTGTGATGATCACTGAGGACCTCACC	1440
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Qy	360		1441	CCACCACCTTAAACCTGTCATTCGAGCTATCAGATTTATGAAATTTTCATGTCGAAAACGG	1500
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Qy	960		2041	GTGCAATTAAGTCAAGCGATGGCTCAGCAGTGGCGCCACCAACACCATTTGCAACCAA	2100
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Db	1200		2221	AGCATTTCTGACGTCACCACTGCTTGTGCTTCCAAAGGAAATGTTTACGTTGACAG	2280

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RESULT 2
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: IAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1e1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2
Query Match 100.0%; Score 2694; DB 9; Length 2694;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	2641	AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACCTGAAATAA	2694

RESULT 3
US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-493-1

Query Match	100.0%;	Score 2694;	DB 19;	Length 2694;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2694;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

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 Qy 1021 TGTGTTTGGCTAGTTAGCAGCTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCCA 1080
 Db 1021 TGTGTTTGGCTAGTTAGCAGCTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCCA 1080
 Qy 1081 CACTTGAAGGCTTGCACACTGCAAGCCCTACCAAGAAAGAACAGGGGAAGCATCAAGC 1140
 Db 1081 CACTTGAAGGCTTGCACACTGCAAGCCCTACCAAGAAAGAACAGGGGAAGCATCAAGC 1140
 Qy 1141 AGTCAGAGCTAAAGTTTAAAGAGCGAGTGGCTAGCCCGGAGGGGCGAGAGTATT 1200
 Db 1141 AGTCAGAGCTAAAGTTTAAAGAGCGAGTGGCTAGCCCGGAGGGGCGAGAGTATT 1200
 Qy 1201 AAGAGCCGAAGCTCAGTAGTGTGACAGAGGTTCCCAAGCAATCAGAGCCGAG 1260
 Db 1201 AAGAGCCGAAGCTCAGTAGTGTGACAGAGGTTCCCAAGCAATCAGAGCCGAG 1260
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 Db 1261 GGCAGTCCCAAGAGTGCAGAGAGCTGAGCTTCAACGACCGAATCCGCTTCCGGCCC 1320
 Qy 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAAACAGTGTAGATGCTGACAGCCCTTGGC 1380
 Db 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAAACAGTGTAGATGCTGACAGCCCTTGGC 1380
 Qy 1381 ACTGATGATGATATGATGAAAGGATGCGCAGTGTGATGATGATGATGATGATGATGAT 1440

Db 1381 ACTGATGATGATATGATGAAAGGATGCGCAGTGTGATGATGATGATGATGATGATGAT 1440
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 Db 1441 CCACACATTAACACTGCTCATTCGAGCTATCAGAAATTTTCATGTTGCAAAACGG 1500
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 Db 1501 AAGTTTAAAGGAAACGTTACGTCATATGATGTAAAGATGTCAATTGAAACAATTTCTGCT 1560
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 Db 1561 GGTCAATCTGGACATGTTGTGTAGAAATTAAGAGCCTTCAACACGCTGTTGATCAAAATCTT 1620
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 Db 1621 GGAAAGGCGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAAACATGAG 1680
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 Db 1741 ATAGAGTCCAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1800
 Qy 1801 GCCTCAGCCCTCGCTTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
 Db 1801 GCCTCAGCCCTCGCTTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
 Qy 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGCAACAAAACAGTGGCTGC 1920
 Db 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGCAACAAAACAGTGGCTGC 1920
 Qy 1921 TTATCCAGATCAACTAGTGCCAAATCTCGAGAGGCTGCAAGTTCATTTCTGACGCAAAAT 1980
 Db 1921 TTATCCAGATCAACTAGTGCCAAATCTCGAGAGGCTGCAAGTTCATTTCTGACGCAAAAT 1980
 Qy 1981 GAGTTTCAAGTCCAGACTTCTACGCTTACGCTTACTATGCAAGTCAAGCAACACAG 2040
 Db 1981 GAGTTTCAAGTCCAGACTTCTACGCTTACGCTTACTATGCAAGTCAAGCAACACAG 2040
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 Db 2041 GTGCCAATTTAGTCAAGCGATGGCTCAGAGTGGCCACCAACCAATTTGCAAAACCAA 2100
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 Db 2101 ATAAATACGCAACCAAGCAGAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
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 Db 2281 TCAATCTCAGCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
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 Db 2341 TTGTCTGTCTGCTCCATGCTGCCAGGACTTGGGCAATCTTTGCTGTGCAAAACCTG 2400
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 Db 2461 GGCAGCCCAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAACCTGATGAAGAG 2520

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QY 2521 GTGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA 2580
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QY 2581 GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAAGGTTCAGATCATCTCAGAGCATTTCT 2640
D 2581 GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAAGGTTCAGATCATCTCAGAGCATTTCT 2640
QY 2641 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGGAATAA 2694
D 2641 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGGAATAA 2694

RESULT 4
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jeglia, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-0050100S
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-1

Query Match 99.9%; Score 2690.4; DB 9; Length 3071;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGGATGTGGAGTCGGGCGCGGCGAGGTGCTGTAACCTCGGACGCCGCGAGGGC 60
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QY 61 GACGGCTGTACTGTCTGGGACCCGCGCGGCGAGGTGCTGTAACCTCGGACGCCGCGAGGGC 120
D 70 GACGGCTGTACTGTCTGGGACCCGCGCGGCGAGGTGCTGTAACCTCGGACGCCGCGAGGGC 129
QY 121 AGGGAGAGCCGCGGCGAGGAGAGGCGGCGGAGTGGCTGCTGCGGAGAGCGGCTCTCT 180
D 130 AGGGAGAGCCGCGGCGAGGAGAGGCGGCGGAGTGGCTGCTGCGGAGAGCGGCTCTCT 189
QY 181 TACACGAGTAGCCAGAGCTGCGGCGCAACGTCAGTACCGGCGGCTGCAAGTACCTG 240
D 190 TACACGAGTAGCCAGAGCTGCGGCGCAACGTCAGTACCGGCGGCTGCAAGTACCTG 249
QY 241 TACACGAGTAGCCAGAGAGCCGCGGCGGAGTGGCTGCTGCGGAGAGCGGCTCTCT 300
D 250 TACACGAGTAGCCAGAGAGCCGCGGCGGAGTGGCTGCTGCGGAGAGCGGCTCTCT 309
QY 301 CTGTCTTTGGTGTGTTGATTTTGTCAAGTGTTCATCCATCCCTGAGCACAATAATG 360
D 310 CTGTCTTTGGTGTGTTGATTTTGTCAAGTGTTCATCCATCCCTGAGCACAATAATG 369
QY 361 GCCTCAAGTTCCTTGTGATCCCTGAGTTCGTGATGATGCTGCTTGTGTTGAGTTTC 420
D 370 GCCTCAAGTTCCTTGTGATCCCTGAGTTCGTGATGATGCTGCTTGTGTTGAGTTTC 429

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QY 421 ATCATTGCAATCTGGTCTCGGGTTCGTTGTCGATATAGAGATGGCAAGAACTG 480
D 430 ATCATTGCAATCTGGTCTCGGGTTCGTTGTCGATATAGAGATGGCAAGAACTG 489
QY 481 AGGTTTGTCTGAAAGCCCTTCTGTGTTTATAGATAACCAATTTCTTATTCGCTCAATAGCA 540
D 490 AGGTTTGTCTGAAAGCCCTTCTGTGTTTATAGATAACCAATTTCTTATTCGCTCAATAGCA 549
QY 541 GTTGTCTTCAAAAACCTCAGGGTAAATATTTTGGCAGCTCTGCACATCAGAAGTCTCCGT 600
D 550 GTTGTCTTCAAAAACCTCAGGGTAAATATTTTGGCAGCTCTGCACATCAGAAGTCTCCGT 609
QY 601 TTCTTACAGATCTCCGATGCTGCGATGACGACGAAAGGGAGGACACTTGGAAATTAAGT 660
D 610 TTCTTACAGATCTCCGATGCTGCGATGACGACGAAAGGGAGGACACTTGGAAATTAAGT 669
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D 670 GGTTCAAGTGGTTTATGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTGG 729
QY 721 GTTCTTATTTTGTCTTCTTCTCTCTGTTGGAAGGATGCCAATAAAGAGTTT 780
D 730 GTTCTTATTTTGTCTTCTTCTCTCTGTTGGAAGGATGCCAATAAAGAGTTT 789
QY 781 TCTACATATGAGATGCTCTCTGTTGGGCGCAATTAATCAATGACAACTATTTGGCTATGGA 840
D 790 TCTACATATGAGATGCTCTCTGTTGGGCGCAATTAATCAATGACAACTATTTGGCTATGGA 849
QY 841 GACAAACTCCCTAACTTGGCTGGGAAGATGCTTCTGAGGCTTGTGCACTCTCTGGC 900
D 850 GACAAACTCCCTAACTTGGCTGGGAAGATGCTTCTGAGGCTTGTGCACTCTCTGGC 909
QY 901 ATTTCTTCTTGTGCACTTCTCTCGCGCATTTCTGCTCAGGTTTGTGCAATTAAGAGTACAA 960
D 910 ATTTCTTCTTGTGCACTTCTCTCGCGCATTTCTGCTCAGGTTTGTGCAATTAAGAGTACAA 969
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QY 1381 ACTGATGATGATATGATGATAAAGGATGCGAGTGTGATGATGATGATGATGATGATGATGATGAT 1440
D 1390 ACTGATGATGATATGATGATAAAGGATGCGAGTGTGATGATGATGATGATGATGATGATGATGAT 1449
QY 1441 CCACCACTTAAACTGCTCATTTCGAGCTATCAGAAATTAATGAAATTTCAATGTTGCAAAACGG 1500
D 1450 CCACCACTTAAACTGCTCATTTCGAGCTATCAGAAATTAATGAAATTTCAATGTTGCAAAACGG 1509
QY 1501 AAGTTTAAAGGAAACGTTTACGTCATATGATGATAAAGATGTCATTAACATATTTCTGCT 1560

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; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SERBOW, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-813-148-1

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Query Match	99.5%;	Score	2681.2;	DB	9;	Length	3074;
Best Local Similarity	99.7%;	Prod.	No.	0;			
Matches	2686;	Conservative	0;	Mismatches	8;	Indels	0;
Gaps	0;						
Qy	1	ATGAAGAGATGTGGAGT	CGGGCCGGGGACAGG	TGCTGCTGA	ACTCGGCACCGCCAGG	GGC	60
Db	215	ATGAAGAGATGTGGAGT	CGGGCCGGGGACAGG	TGCTGCTGA	ACTCGGCACCGCCAGG	GGC	274
Qy	61	GACGGCCTGCTACT	GCTGGGCACCCGCGCGCC	ACGCTTGGTGGCGCGCGG	CGTGGCCCTG		120
Db	275	GACGGCCTGCTACT	GCTGGGCACCCGCGCGCC	ACGCTTGGTGGCGCGCGG	CGTGGCCCTG		334
Qy	121	AGGAGAGACCCCGGGG	CAAGCAGAGGGGCCCG	ATGACCTGTGTGGGGA	AGCGCGCTCTCT		180
Db	335	AGGAGAGACCCCGGGG	CAAGCAGAGGGGCCCG	ATGACCTGTGTGGGGA	AGCGCGCTCTCT		394
Qy	181	TACACGAGTAGCCAG	AGCTGCCGGCGCAAC	GTCAAGTACCGCGCGGT	GCAGAACTACCTG		240
Db	395	TACACGAGTAGCCAG	AGCTGCCGGCGCAAC	GTCAAGTACCGCGCGGT	GCAGAACTACCTG		454
Qy	241	TACAACGTGCTGGAG	AGACCCCGCGGCTGGG	CGTTTCACTACCA	CGCTTTCGTTTTTCTC		300
Db	455	TACAACGTGCTGGAG	AGACCCCGCGGCTGGG	CGTTTCACTACCA	CGCTTTCGTTTTCTC		514
Qy	301	CTTGCTTTTGGTTGG	TGATTAATTTGT	CAGTGTTTTCTACCAT	CTCCCTAGCACACAAAATTG		360
Db	515	CTTGCTTTTGGTTGG	TGATTAATTTGT	CAGTGTTTTCTACCAT	CTCCCTAGCACACAAAATTG		574
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Db	575	GCCTCAAGTTGCCCT	TTGATCCTCGAGTT	CGTGATGATTGCTGTT	GGTTTGGAGTTC		634
Qy	421	ATCATTCGAATCTGG	CTCGGGTTGCTGTT	TGTCGATATAGAGGA	TGGCAAGGAAGCTG		480
Db	635	ATCATTCGAATCTGG	CTCGGGTTGCTGTT	TGTCGATATAGAGGA	TGGCAAGGAAGCTG		694
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Db	695	AGTTTTGGTCGAAA	AGCCCTTCTGTGTT	TATAGATACCAT	TGTTCTTATCGCTTCAATAGCA		754
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Db	755	GTTCGTTTCTGAAAA	AACTCAGGGTAA	TATTTTTTCCACG	CTCGACCTCAGAGTCTCCGT		814
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Db	875	GGTTCAGTGGTTAT	GCTCAGACAGGA	ATTAATCA	CAGCTTGGTATCAT	AGGATTTTGTG	934

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Db	935	GTTCCTTAATTTTTCGTCCTTTCCCTTGTCTA	TCTGGTGGAAAGAGTGCCAATAAAGAGTTT	994
Qy	781	TCTACATATGCAGATGCTCTCGTGGGGCACAAT	TACATTGACAACTATTGGCTATGGA	840
Db	995	TCTACATATGCAGATGCTCTCGTGGGGCACAAT	TACATTGACAACTATTGGCTATGGA	1054
Qy	841	GACAAAACCTCCCTTAACTTGGCTGGGAAGAT	TGCTTTTCTGCAGGCTTTGCACCTCCTTGGC	900
Db	1055	GACAAAACCTCCCTTAACTTGGCTGGGAAGAT	TGCTTTTCTGCAGGCTTTGCACCTCCTTGGC	1114
Qy	901	ATTTCCTTTCTTTGGCACTTCCTGCGCGGCA	TTCTTTGGCTCAGGTTTGGATTAAAGTACAA	960
Db	1115	ATTTCCTTTCTTTGGCACTTCCTGCGCGGCA	TTCTTTGGCTCAGGTTTGGATTAAAGTACAA	1174
Qy	961	GAACACACCGCCAGAAACACTTTGAGAAAGAG	NAAGNACCCAGCTGCCACCTCATTCAG	1020
Db	1175	GAACACACCGCCAGAAACACTTTGAGAAAGAG	NAAGNACCCAGCTGCCACCTCATTCAG	1234
Qy	1021	TGTGTTGGCGGTAGTTACGCAAGCTGATGAA	AAATCTGTTTTCCATTGCAACTCTGGAAGCCA	1080
Db	1235	TGTGTTGGCGGTAGTTACGCAAGCTGATGAA	AAATCTGTTTTCCATTGCAACTCTGGAAGCCA	1294
Qy	1081	CACTTGAAGCCCTTGCAACCTCGACCCCTT	CAAGAAAGAACAAAGGGGAAGCATCAAGC	1140
Db	1295	CACTTGAAGCCCTTGCAACCTCGACCCCTT	CAAGAAAGAACAAAGGGGAAGCATCAAGC	1354
Qy	1141	AGTCAGAAAGCTAAGTTTAAAGGACGAGT	CGCGCATGGCTAGCCAGGGGCCAGAGTATT	1200
Db	1355	AGTCAGAAAGCTAAGTTTAAAGGACGAGT	CGCGCATGGCTAGCCAGGGGCCAGAGTATT	1414
Qy	1201	AAGAGCCGACAAGCCTCAGTAGGTGACAG	GAGGTCCTCCCAAGCACCGACATCACAGCCGAG	1260
Db	1415	AAGAGCCGACAAGCCTCAGTAGGTGACAG	GAGGTCCTCCCAAGCACCGACATCACAGCCGAG	1474
Qy	1261	GGCAGTCCCAACAAAGTGCAAGAGCTG	GAGGTTCAAACGACCGAAACCCGCTTCCCGSCC	1320
Db	1475	GGCAGTCCCAACAAAGTGCAAGAGCTG	GAGGTTCAAACGACCGAAACCCGCTTCCCGSCC	1534
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Db	1535	TCGCTGGCGCTCAAAAGTTCTCAGCCAAA	ACCAAGTATAGATGCTGACACAGGCCCTTGGC	1594
Qy	1381	ACTGATGATGTATGATGAAAAGGATG	CCAGTGTGTATCAGTGGAAAGACCTCAAC	1440
Db	1595	ACTGATGATGTATGATGAAAAGGATG	CCAGTGTGTATCAGTGGAAAGACCTCAAC	1654
Qy	1441	CCACCCTTAAAACTGTCAATTCGAGCT	TATCAGAAATATGAAATTTCATGTGCAAAACGG	1500
Db	1655	CCACCCTTAAAACTGTCAATTCGAGCT	TATCAGAAATATGAAATTTCATGTGCAAAACGG	1714
Qy	1501	AAGTTTAAAGAAACGTTACGTCCATAT	GATGTTAAAAAGATGTCTATTGAAACAATTTCTGCT	1560
Db	1715	AAGTTTAAAGAAACGTTACGTCCATAT	GATGTTAAAAAGATGTCTATTGAAACAATTTCTGCT	1774
Qy	1561	GGTCATCTGACATGTTGTGTAGAAAT	TAAAGCCCTTCAACACAGCTGTGATCAAAATCTTT	1620
Db	1775	GGTCATCTGACATGTTGTGTAGAAAT	TAAAGCCCTTCAACACAGCTGTGATCAAAATCTTT	1834
Qy	1621	GGAAAAGGGCAAAATCACATCAGATA	AGAGAGCCGAGAGAAAATAACACAGACAACATGAG	1680
Db	1835	GGAAAAGGGCAAAATCACATCAGATA	AGAGAGCCGAGAGAAAATAACACAGACAACATGAG	1894
Qy	1681	ACCACAGACGATCTCAGTATGCTTCG	TGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1740
Db	1895	ACCACAGACGATCTCAGTATGCTTCG	TGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1954
Qy	1741	ATAGATCCAAAGCTGACCTGCCTACT	AGACATCTATCAACAGGTCTCTCGGAAGGCTCT	1800
Db	1955	ATAGATCCAAAGCTGACCTGCCTACT	AGACATCTATCAACAGGTCTCTCGGAAGGCTCT	2014
Qy	1801	GCCTCAGCCCTCGCTTTGGCTTTCAT	TTCAGATCCCCACCTTTTGAATGTGAACAGACATCT	1860

; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 1									
; LENGTH: 2772									
; TYPE: DNA									
; ORGANISM: homo sapiens									
US-09-825-147-1									
Query Match 97.48; Score 2625.2; DB 9; Length 2772;									
Best Local Similarity 98.94; Pred. No. 0;									
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;									
QY	1	ATGAAGATGTGAGTGGGCGGCGGCGAGGTGCTGCTGAACCTGGAGCGCGCAGGGC	60						
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QY	61	GACGGCTGTACTGTGGGACCCGCGCGGCGAGCTTGGTGGCGCGCGGTGGCGCTG	120						
DB	166	GACGGCTGTACTGTGGGACCCGCGCGGCGAGCTTGGTGGCGCGCGGTGGCGCTG	225						
QY	121	AGGAGAGCCGCGGCGGCGAGCGGCGCGGATGAGCTGTGGGGAAGCGGCTCTCT	180						
DB	226	AGGAGAGCCGCGGCGGCGAGCGGCGCGGATGAGCTGTGGGGAAGCGGCTCTCT	285						
QY	181	TACAGAGTACAGAGCTGCGGCGGCGAACTCAAGTACCGGCGGCGGAGCACTACTG	240						
DB	286	TACAGAGTACAGAGCTGCGGCGGCGAACTCAAGTACCGGCGGCGGAGCACTACTG	345						
QY	241	TACAAGCTGTGGAGAGACCCGCGGCGGCTTCACTACACGCTTTCGTTTTCTC	300						
DB	346	TACAAGCTGTGGAGAGACCCGCGGCGGCTTCACTACACGCTTTCGTTTTCTC	405						
QY	301	CTTGTCTTTTGTGCTTGAATTTGTCACTGTTTTCTACATCCCTGAGCACAAAAATTG	360						
DB	406	CTTGTCTTTTGTGCTTGAATTTGTCACTGTTTTCTACATCCCTGAGCACAAAAATTG	465						
QY	361	GCCTCAAGTTGCTCTTGAATCTGAGTTCGTGATGATGTCGTTTGGTTTGGAGTTC	420						
DB	466	GCCTCAAGTTGCTCTTGAATCTGAGTTCGTGATGATGTCGTTTGGTTTGGAGTTC	525						
QY	421	ATCATTCGAATCTGCTCGGCGTGTGTTGTCGATATAGAGGATGCAAGGAGACTG	480						
DB	526	ATCATTCGAATCTGCTCGGCGTGTGTTGTCGATATAGAGGATGCAAGGAGACTG	585						
QY	481	AGGTTTGTGCGAAGCCCTTCTGTTATAGATACATTTCTTATCGCTTCAATAGCA	540						
DB	586	AGGTTTGTGCGAAGCCCTTCTGTTATAGATACATTTCTTATCGCTTCAATAGCA	645						
QY	541	GTGTTTCTGCAAAACTCAGGTAATATTTTGGCAGCTGTGCACTCAGAACTCCGT	600						
DB	646	GTGTTTCTGCAAAACTCAGGTAATATTTTGGCAGCTGTGCACTCAGAACTCCGT	705						
QY	601	TTCTTACAGATCCTCGCATGTTGGCGATGGAACGAGGAGGAGCACTTGGAAATTA	660						
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QY	661	GGTTTCAAGTGTATGCTCACAGCAGGAATTAATCACAGCTTGTACATAGATTTTG	720						
DB	766	GGTTTCAAGTGTATGCTCACAGCAGGAATTAATCACAGCTTGTACATAGATTTTG	825						
QY	721	GTTCCTTATTTTTCGTTCTTCTTCTTCTATCTGGTGGAAAGGATGCCAATAAGAGTT	780						
DB	826	GTTCCTTATTTTTCGTTCTTCTTCTTCTATCTGGTGGAAAGGATGCCAATAAGAGTT	885						
QY	781	TCTACATATGAGATGCTCTCTGGTGGGCGCAATTTACATTTGACAACTATGGCTATGA	840						
DB	886	TCTACATATGAGATGCTCTCTGGTGGGCGCAATTTACATTTGACAACTATGGCTATGA	945						
QY	841	GACAACTCCCTTACTTGGCTGGGAGATTCCTTCTGCGAGGCTTTCACCTCTGGC	900						
DB	946	GACAACTCCCTTACTTGGCTGGGAGATTCCTTCTGCGAGGCTTTCACCTCTGGC	1005						
QY	901	ATTTCTTCTTCTGCACTTCTGCGGCAATTTCTTGGCTCAGGTTTTCATTTAAAGTACAA	960						

2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTCACAAACCA 2100
Db |||||
2119 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTCACAAACCA 2178
Qy |||||
2101 ATAAATACGGCACCACAGCAGAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
Db |||||
2179 ATAAATACGGCACCACAGCAGAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2238
Qy |||||
2161 GCATCAAGCATCTGCCAGGCGCAGAACTCTGCACCTTAAACCTTGCAGGCTTACAGGAA 2220
Db |||||
2239 GCATCAAGCATCTGCCAGGCGCAGAACTCTGCACCTTAAACCTTGCAGGCTTACAGGAA 2298
Qy |||||
2221 AGCATTTCTGACGTCAACACCTGCTTGTGCTTCAAGGAAATGTTTCAGGTTGCACAG 2280
Db |||||
2299 AGCATTTCTGACGTCAACACCTGCTTGTGCTTCAAGGAAATGTTTCAGGTTGCACAG 2358
Qy |||||
2281 TCAATCTCACAAGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
Db |||||
2359 TCAATCTCACAAGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2418
Qy |||||
2341 TTGCTCTGTCGTCACATGTCGCGGAGGACTTTGGGCAATCTTCTGTCGCAAAACCTG 2400
Db |||||
2419 TTGCTCTGTCGTCACATGTCGCGGAGGACTTTGGGCAATCTTCTGTCGCAAAACCTG 2478
Qy |||||
2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
Db |||||
2479 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2538
Qy |||||
2461 GCGCCCAAGATTTTACCCCAATGGAGGGAATCAAAATGTTTATATGATGAAGAG 2520
Db |||||
2539 GCGCCCAAGATTTTACCCCAATGGAGGGAATCAAAATGTTTATATGATGAAGAG 2598
Qy |||||
2521 GTGGTCCGAGAGACAGACACACTTTTGTATGCGGACCGACGCTGCCAGGAA 2580
Db |||||
2599 GTGGTCCGAGAGACAGACACACTTTTGTATGCGGACCGACGCTGCCAGGAA 2658
Qy |||||
2581 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
Db |||||
2659 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2718
Qy |||||
2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694
Db |||||
2719 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2772

RESULT 9

US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens

US-10-803-268-1

Query Match 97.4%; Score 2625.2; DB 18; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
Qy 1 ATGAGGATGTGGAGTCCGGGCGGGGAGGGTGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 60
Db |||||
106 ATGAGGATGTGGAGTCCGGGCGGGGAGGGTGTGCTGCTGAACTCGGCAGCCGCCAGGGGC 165
Qy 61 GACGGCTGTCTACTGCTGGGCAACCGCGGGCAGCGTTGGTGGCGGGCGGGTGGCCCTG 120
Db |||||
166 GACGGCTGTCTACTGCTGGGCAACCGCGGGCAGCGTTGGTGGCGGGCGGGTGGCCCTG 225
Qy 121 AGGAGAGCCCGCGGGCAAGCAGGGGCGCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT 180
Db |||||
226 AGGAGAGCCCGCGGGCAAGCAGGGGCGCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT 285
Qy 181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAGGTACCGGCGGGTGCAGAACTACCTG 240
Db |||||
286 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAGGTACCGGCGGGTGCAGAACTACCTG 345
Qy 241 TACAACTGTGTGGAGAGACCCCGGGCTGGGGGTTTCATCTACACGCTTTCGTTTTCTC 300
Db |||||
346 TACAACTGTGTGGAGAGACCCCGGGCTGGGGGTTTCATCTACACGCTTTCGTTTTCTC 405
Qy 301 CTGCTCTTTGGTGTGCTGATTTGTCAGTGTTCATCATCTCCCTGAGCACACAAATTTG 360
Db |||||
406 CTGCTCTTTGGTGTGCTGATTTGTCAGTGTTCATCATCTCCCTGAGCACACAAATTTG 465
Qy 361 GCCTCAAGTTGCCCTTGTGATCTCGAGTTCGTGTGATGATTGTCGTTTGGTTGGAGTTC 420
Db |||||
466 GCCTCAAGTTGCCCTTGTGATCTCGAGTTCGTGTGATGATTGTCGTTTGGTTGGAGTTC 525
Qy 421 ATCATTCGAATCTGGTCTGCGGGTTCGTTGTGATATAGAGGATGCAAGAGAGACTG 480
Db |||||
526 ATCATTCGAATCTGGTCTGCGGGTTCGTTGTGATATAGAGGATGCAAGAGAGACTG 585
Qy 481 AGGTTGCTCCAAAGCCCTCTGTTTATAGATACCACTTGTTCCTTATCGCTTCAATAGCA 540
Db |||||
586 AGGTTGCTCCAAAGCCCTCTGTTTATAGATACCACTTGTTCCTTATCGCTTCAATAGCA 645
Qy 541 GTTGTCTCTGCAAAACCTCAGGGTAAATATTTTTCGACGCTCTGCACTCAGAACTCCGT 600
Db |||||
646 GTTGTCTCTGCAAAACCTCAGGGTAAATATTTTTCGACGCTCTGCACTCAGAACTCCGT 705
Qy 601 TTCTACAGATCTCCGATGCGGATGCGGATGCGAAGGGGAGGCACTTGGAAATACCTG 660
Db |||||
706 TTCTACAGATCTCCGATGCGGATGCGAAGGGGAGGCACTTGGAAATACCTG 765
Qy 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCAGCTTGGTACATAGGATTTTGG 720
Db |||||
766 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCAGCTTGGTACATAGGATTTTGG 825
Qy 721 GTTCTTATTTTTCGCTCTTTCCTTGTCTATCTGGTGGAAAGAGATGCAATAAAGAGTTT 780
Db |||||
826 GTTCTTATTTTTCGCTCTTTCCTTGTCTATCTGGTGGAAAGAGATGCAATAAAGAGTTT 885
Qy 781 TCTACATATGAGATGCTCTCTGTTGGGCAATTAATACATTGACAACTATTTGGCTATGGA 840
Db |||||
886 TCTACATATGAGATGCTCTCTGTTGGGCAATTAATACATTGACAACTATTTGGCTATGGA 945
Qy 841 GACAAATCTCCCTAACTTGGCTCGGAGATGCTTCTTCGAGGCTTTCGCTCCTCTCGC 900
Db |||||
946 GACAAATCTCCCTAACTTGGCTCGGAGATGCTTCTTCGAGGCTTTCGCTCCTCTCGC 1005
Qy 901 ATTTCTTTTTCGCTCTTTCCTGCGGCACTTCTTGGCTCAGGTTTTCGATTTAAAGTACAA 960
Db |||||
1006 ATTTCTTTTTCGCTCTTTCCTGCGGCACTTCTTGGCTCAGGTTTTCGATTTAAAGTACAA 1065
Qy 961 GAAACAACCGCCAGAAACACTTTTGAGAAAGAGAAAGGAAAGCCAGCTGCCAACTCATTCAG 1020
Db |||||
1066 GAAACAACCGCCAGAAACACTTTTGAGAAAGAGAAAGGAAAGCCAGCTGCCAACTCATTCAG 1125

Db 165 ATGAAGGATGTGGAGTCGGGCGGGGCGAGGGTGTCTGAACTCGCGCAGCGCGAGGGGC 224
QY 61 GACGGCTGTACTGTCTGGCAACCGCGGGCCACGCTTGGTGGCGGGCGGTGGCCTG 120
Db 225 GACGGCTGTACTGTCTGGCAACCGCGGGCCACGCTCGGTGGCGGGCGGTGGCCTG 284
QY 121 AGGAGAGCGCGCGGGGCAAGCAGAGGGGCGCGGATGAGCTGTCTGGGGAAGCGCTCTCT 180
Db 285 AGGAGAGCGCGCGGGCAAGCAGAGGGGCGCGGATGAGCTGTCTGGGGAAGCGCTCTCT 344
QY 181 TACACAGTAGCAGAGCTGCGCGGGCCAAAGTCAAGTACCGGGGGTGCAGAACTACCTG 240
Db 345 TACACAGTAGCAGAGCTGCGCGGGCCAAAGTCAAGTACCGGGGGTGCAGAACTACCTG 404
QY 241 TACACAGTGTCTGAGAGACCCCGCGCTGGGGGTTTCATCTACACGCTTTCGTTTTC 300
Db 405 TACACAGTGTCTGAGAGACCCCGCGCTGGGGGTTTCATCTACACGCTTTCGTTTTC 464
QY 301 CTGTGCTTTGGTGTCTGATTTTGTCAAGTGTCTTACCATCCCTGAGCACACAAATTTG 360
Db 465 CTGTGCTTTGGTGTCTGATTTTGTCAAGTGTCTTACCATCCCTGAGCACACAAATTTG 524
QY 361 GCCTCAAGTTGCTCTGATCTCGAGTTCGTGATGATTTGCTCTTGGTTTGGAGTTC 420
Db 525 GCCTCAAGTTGCTCTGATCTCGAGTTCGTGATGATTTGCTCTTGGTTTGGAGTTC 584
QY 421 ATCATTTCGAATCTGTCTGGGGTGTCTGTCTCGATATAGAGGATGCCAGGAGACCTG 480
Db 585 ATCATTTCGAATCTGTCTGGGGTGTCTGTCTCGATATAGAGGATGCCAGGAGACCTG 644
QY 481 AGGTTTGTCTCGAAAGCCCTTCTGTGTATAGATACCAATTTCTTATCGCTTCAATAGCA 540
Db 645 AGGTTTGTCTCGAAAGCCCTTCTGTGTATAGATACCAATTTCTTATCGCTTCAATAGCA 704
QY 541 GTTGTCTCTGCAAAAACCTCAGGGTAATATTTTTGCGACGTCTGCACTCAGAACTCTCGT 600
Db 705 GTTGTCTCTGCAAAAACCTCAGGGTAATATTTTTGCGACGTCTGCACTCAGAACTCTCGT 764
QY 601 TTCTTACAGATCCTCGGATGTGGCGCATGGACCGAAGGGAGGACCTTGGAAATTA 660
Db 765 TTCTTACAGATCCTCGGATGTGGCGCATGGACCGAAGGGAGGACCTTGGAAATTA 824
QY 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGATAGGATTTT 720
Db 825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGATAGGATTTT 884
QY 721 GTTCTTAATTTTGTCTTCTGTCTATCTGTGGTGAAGGATGCCAAATAAGAGTTT 780
Db 885 GTTCTTAATTTTGTCTTCTGTCTATCTGTGGTGAAGGATGCCAAATAAGAGTTT 944
QY 781 TCTATATGAGATGCTCTGTGGGCGCAATTAATTCACAACTATTGGCTATGGA 840
Db 945 TCTATATGAGATGCTCTGTGGGCGCAATTAATTCACAACTATTGGCTATGGA 1004
QY 841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCCCTGGC 900
Db 1005 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCCCTGGC 1064
QY 901 ATTTCTTTTGTGCACTTCTGCGGGCATTTCTTGGCTCAGGTTTGCATTTAAAGTACA 960
Db 1065 ATTTCTTTTGTGCACTTCTGCGGGCATTTCTTGGCTCAGGTTTGCATTTAAAGTACA 1124
QY 961 GAAACAACCGCCAGAAACATTTTCAGAAAGAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1020
Db 1125 GAAACAACCGCCAGAAACATTTTCAGAAAGAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1184
QY 1021 TGTGTTTGGCGTAGTACGAGCTCATGAGAAATCTGTGTTTCATTTGCAACCTTGGAGGCA 1080
Db 1185 TGTGTTTGGCGTAGTACGAGCTCATGAGAAATCTGTGTTTCATTTGCAACCTTGGAGGCA 1244
QY 1081 CACTTGAAGGCTTGCACCTGCGAGCCCTACCAAGAAAGAAACAAAGGGGAAGCATCAAGC 1140

Db 1245 CACTTGAAGGCTTGCACACACCTGCGAGCCCTACCAA----- 1279
QY 1141 AGTCAGAGCTAAAGTTTAAAGAGCGAGTGGCGCATGGCTAGCCCGAGGGGCCAGAGTATT 1200
Db 1280 --TCAGAAAGCTAAAGTTTAAAGAGCGAGTGGCGCATGGCTAGCCCGAGGGGCCAGAGTATT 1337
QY 1201 AAGAGCCACAAAGCCTCAGTAGTGGTACAGAGGAGTCCCCAAGCACCGACATCACAGCCGAG 1260
Db 1338 AAGAGCCACAAAGCCTCAGTAGTGGTACAGAGGAGTCCCCAAGCACCGACATCACAGCCGAG 1397
QY 1261 GGCAGTCCCAACAAGTGCAGAGAGCTGGAGCTTCAAAGCGACCGAAACCGCTTCCGGGCC 1320
Db 1398 GGCAGTCCCAACAAGTGCAGAGAGCTGGAGCTTCAAAGCGACCGAAACCGCTTCCGGGCC 1457
QY 1321 TCGCTGCGCCCTCAAAAGTTCTCAGCCAAAACAGTATAGATGTCTGACACAGCCCTTGGC 1380
Db 1458 TCGCTGCGCCCTCAAAAGTTCTCAGCCAAAACAGTATAGATGTCTGACACAGCCCTTGGC 1517
QY 1381 ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGTATGATCATCAGTGGAAAGACCTCACC 1440
Db 1518 ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGTATGATCATCAGTGGAAAGACCTCACC 1577
QY 1441 CCACCACTTAAAACTGTCTCATTTCGAGCTATCAGAAATTTATGAAATTTTCAATTTGCAAAACGG 1500
Db 1578 CCACCACTTAAAACTGTCTCATTTCGAGCTATCAGAAATTTATGAAATTTTCAATTTGCAAAACGG 1637
QY 1501 AAGTTTAAAGGAAACGTTTACGTCCTATGATGTAAAAAGATGTCTTGAACAATTTCTGCT 1560
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QY 1561 GGTCACTTGGACATGTTGTGTAGAAATTTAAAAAGCCTTCAAAACGCTTGTGATCAAAATTTCT 1620
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QY 1621 GGAAGAGGGCAAAATCACATCAGATTAAGAGAGCGAGAGAAATAAAGCAGAGAAATGAG 1680
Db 1758 GGAAGAGGGCAAAATCACATCAGATTAAGAGAGCGAGAGAAATAAAGCAGAGAAATGAG 1817
QY 1681 ACCACAGACGATCTCAGTATGCTCGTGGGTGGTCAAGGTTTGAAGAAACAGGTACAGTCC 1740
Db 1818 ACCACAGACGATCTCAGTATGCTCGTGGGTGGTCAAGGTTTGAAGAAACAGGTACAGTCC 1877
QY 1741 ATAGAGTCCAAAGCTGGACTGCTTACTAGACATCTATCAACAGGTCCTTTCGGAAGGCTCT 1800
Db 1878 ATAGAAATCCAAAGCTGGACTGCTTACTAGACATCTATCAACAGGTCCTTTCGGAAGGCTCT 1937
QY 1801 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1860
Db 1938 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1997
QY 1861 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCAACAAAACAGTGGCTGC 1920
Db 1998 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCAACAAAACAGTGGCTGC 2057
QY 1921 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTTCGAGTTCATTTCTGACGCAAAAT 1980
Db 2058 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTTCGAGTTCATTTCTGACGCAAAAT 2117
QY 1981 GAGTTCAGTGGCAGACTTTTCTAGCGCTTACGCTTACTATGCAAGTCAAGCAACAG 2040
Db 2118 GAGTTCAGTGGCAGACTTTTCTAGCGCTTACGCTTACTATGCAAGTCAAGCAACAG 2177
QY 2041 GTGCCAAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTTGCAAAACAA 2100
Db 2178 GTGCCAAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTTGCAAAACAA 2237
QY 2101 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2160
Db 2238 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2297
QY 2161 GCCATCAAGCATCTGCCAGGCCAGCAAACTCTGCAACCTTAACCTTGCAGGCTTACAGAA 2220
Db 2298 GCCATCAAGCATCTGCCAGGCCAGCAAACTCTGCAACCTTAACCTTGCAGGCTTACAGAA 2357

2221 AGCATTTCTGACGTCACCACTGCTTGTGTTGCTTCCAAAGGAAATGTTTCAAGTTGCACAG 2280
2358 AGCATTTCTGACGTCACCACTGCTTGTGTTGCTTCCAAAGGAAATGTTTCAAGTTGCACAG 2417
2281 TCAAAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
2418 TCAAAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2477
2341 TTGCTGTCTGTCCATGTTGCGGACGAGTCTGGGCAAAATCTTGTCTGTGCAAAACCTG 2400
2478 TTGCTGTCTGTCCATGTTGCGGACGAGTCTGGGCAAAATCTTGTCTGTGCAAAACCTG 2537
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2461 GGCAGCCAAAGATTTTATCCCAATGAGGGAATCCAAATGTTTATTAAGTGTGATGAGAG 2520
2598 GGCAGCCAAAGATTTTATCCCAATGAGGGAATCCAAATGTTTATTAAGTGTGATGAGAG 2657
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2581 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT 2640
2718 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT 2777
2641 AAGGAGGAGAAAGTACAGAGTCCCTCAGCTTGCCTCATGTCAAACTGMAATAA 2694
2778 AAGGAGGAGAAAGTACAGAGTCCCTCAGCTTGCCTCATGTCAAACTGMAATAA 2831

RESULT 11
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication NO. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 97.4%; Score 2625.2; DB 18; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
QY 1 ATCAAGGATGTGAGTCCGGGCGGGGAGGGTCTGCTGAACTCGGACGCCGCCAGGGGC 60
DB 165 ATGAGGATGTGAGTCCGGGCGGGGAGGGTCTGCTGAACTCGGACGCCGCCAGGGGC 224
QY 61 GACGGCTGTACTGTGTGGGACCCCGGGGCGGACCCCTTGTGGGCGGCGGGTGGCCTG 120

DB 225 GACGGCTGTACTGTGGGCAACCCGCGCGCCACGCTCGGTGGCGGGCGGTGGCGT 284
QY 121 AGGAGAGCCCGCGGGGCAAGCAGGGGCGCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT 180
DB 285 AGGAGAGCCCGCGGGGCAAGCAGGGGCGCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT 344
QY 181 TACACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGGCGGGTGCAGAACTTACCTG 240
DB 345 TACACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGGCGGGTGCAGAACTTACCTG 404
QY 241 TACAAAGTGTGGAGAGACCCCGGGCTGGGGTTCATCTACACGCTTTTGGTTTCTC 300
DB 405 TACAAAGTGTGGAGAGACCCCGGGCTGGGGTTCATCTACACGCTTTTGGTTTCTC 464
QY 301 CTTGTCTTTGGTGTCTTCAATTTGTTCAGTGTCTTCTACCATCCCTGAGCACACAAAATTG 360
DB 465 CTTGTCTTTGGTGTCTTCAATTTGTTCAGTGTCTTCTACCATCCCTGAGCACACAAAATTG 524
QY 361 GCTCAAGTTGCTCTTGTATCCTGGAGTTCGTGATGATTTGTCTTGGTTTGGAGTTC 420
DB 525 GCTCAAGTTGCTCTTGTATCCTGGAGTTCGTGATGATTTGTCTTGGTTTGGAGTTC 584
QY 421 ATCAATTCGAATCTGTCTCGGGGTTCTGTTCGATATAGGAGTGCAGGAAGACTG 480
DB 585 ATCAATTCGAATCTGTCTCGGGGTTCTGTTCGATATAGGAGTGCAGGAAGACTG 644
QY 481 AGGTTTGTCTGAAAGCCCTTCTGTATAGATACCAATTTCTTATCGCTTCAATAGCA 540
DB 645 AGGTTTGTCTGAAAGCCCTTCTGTATAGATACCAATTTCTTATCGCTTCAATAGCA 704
QY 541 GTTGTCTTCTGCAAAAACCTCAGGGTAATATTTTGGTCCAGCTCTGCACTCAGAGTCTCGT 600
DB 705 GTTGTCTTCTGCAAAAACCTCAGGGTAATATTTTGGTCCAGCTCTGCACTCAGAGTCTCGT 764
QY 601 TTCCTACAGATCTCTCGCATGTTGCGCATGGACCGGAGGGAGGCACTTGGAAAATTACTG 660
DB 765 TTCCTACAGATCTCTCGCATGTTGCGCATGGACCGGAGGGAGGCACTTGGAAAATTACTG 824
QY 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTGTGATAGAGATTTTG 720
DB 825 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTGTGATAGAGATTTTG 884
QY 721 GTTCTTATTTTTCGCTTCTTCTATCTGTTGGAAGGATGCCAATAAAGAGTTT 780
DB 885 GTTCTTATTTTTCGCTTCTTCTATCTGTTGGAAGGATGCCAATAAAGAGTTT 944
QY 781 TCTACATATGAGATGCTCTCTGTTGGGCAACAATTACATTCACAATTTTGGCTATGGA 840
DB 945 TCTACATATGAGATGCTCTCTGTTGGGCAACAATTACATTCACAATTTTGGCTATGGA 1004
QY 841 GACAAAACCTCCCTAACTTGGCTGGGGAAGATTCCTTCTGACGCTTTGCACTCCTTGGC 900
DB 1005 GACAAAACCTCCCTAACTTGGCTGGGGAAGATTCCTTCTGACGCTTTGCACTCCTTGGC 1064
QY 901 ATTCTTTCTTTGCACTTCTGCGGCACTTCTGGCTCAGGTTTTCGATTAAAAGTACAA 960
DB 1065 ATTCTTTCTTTGCACTTCTGCGGCACTTCTGCGTCAAGTTTTCGATTAAAAGTACAA 1124
QY 961 GAACAACACCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCAACCTCATTTAG 1020
DB 1125 GAACAACACCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCAACCTCATTTAG 1184
QY 1021 TGTCTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTCGCAACTGGAAGCCA 1080
DB 1185 TGTCTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTCGCAACTGGAAGCCA 1244
QY 1081 CACTTGAAGGCTTGCACACTGAGCCCTACCAAGAAAGAACCAAGGGGAGCATCAAGC 1140
DB 1245 CACTTGAAGGCTTGCACACTGAGCCCTACCAAGAAAGAACCAAGGGGAGCATCAAGC 1279
QY 1141 AGTCAGAGCTTAAGTTTAAAGGAGCGAGTGGGCAATGCTAGCCCCCAGGGCCAGGATTT 1200
DB 1280 --TCAAGAGCTAAAGTTTAAAGGAGCGAGTGGGCAATGCTAGCCCCCAGGGCCAGGATTT 1337


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; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55

Query Match      19.2%; Score 518.4; DB 17; Length 2335;
Best Local Similarity 60.1%; Pred. No. 1.8e-148;
Matches 1103; Conservative 0; Mismatches 566; Indels 165; Gaps 8;

QY 217 TACCGCGGGTGAGAACTACCTGTACAGCTGCTGAGAGACCCCGCGGCTGGGGCTTC 276
DB 320 TACCGCGGCTGAGAACTGGGTCTACAGCTGCTGAGAGCGGCGCGGCTGGGGCTTC 379
QY 277 ATCTACCAACGCTTTCTGTTTCTCTTGTCTTGTGTTGTTGTTGTTGTTGTTTCT 336
DB 380 GTCTACCAACGCTTTCTGTTTCTCTTGTCTTGTGTTGTTGTTGTTGTTGTTGTT 439
QY 337 ACCATCCCTGAGACACAAATTCGCTCAAGTTGCTCTTGTGTTGTTGTTGTTGTTG 396
DB 440 ACTATCCAGGAGACCCAGGAACTTGCCAAAGAGTGTCTCTCTATCTTGGAAATTCG 499
QY 397 ATTGTCGCTTTGTTGAGTTTCATCATTCGAAATCTGTTCTGCGGTTGCTGTTGCTGA 456
DB 500 ATCTGTTTTCGGCTTGGAGTACATCGTTCGGGTCTGTTGCGCGGATGCTGTCGCGC 559
QY 457 TATAGAGATGGCAAGGAACTGAGTTTCTCTGAAAGCCCTTCTGTTGTTATAGATACC 516
DB 560 TACCAGGATGGCAGGTTCGCTTCGCTTTCGCAAGAGCCCTTCTGTTGTTGTTGTTG 619
QY 517 ATTGTTCTTATCGCTTCAATAGAGTTGTTTCTGCAAAATCTCAGGGTAAATTTTGGC 576
DB 620 ATCTGTTTTCGGCTTCGGTTCGCTCATCGCGGGGTACCCAGGGCAACATCTTCGCC 679
QY 577 AGCTCTGCACTCAGAACTTCGTTTCTCAGATCTTCGCTTCGCTTCGCTTCGCTTCG 636
DB 680 AGCTTCGGCTTCGCGAGCATGCGCTTCCTGCGAGATCTTCGCGATGGTTCGCGATG 739
QY 637 AGGGAGGACCTTGAATTAAGTGGTTCAGTGGTTATGTTTATGTTTACAGCAAGAAAT 696
DB 740 CCGCGCGGACCTGGAAGCTGCTGGGCTCAGTGGTTCAGGTTTACGGGCTAGCAAG 799
QY 697 ACAGCTTGTGTACATAGGATTTTGGTCTTATTTTCTGTTTCTGTTTCTGTTTCTG 756
DB 800 ACCGCTGTGTACATCGGGTTCCTGTTGTTCTATCTTCGCTTCGCTTCGCTTCGCT 859
QY 757 GAAAAGGATGCCAATAAGATTTTCTACATATGAGATGCTCTCTGTTGGGGGACAAAT 816
DB 860 GAGAGGAGCCAACTCCGACTTCTCTCTACGCGGACTCGCTCTGTTGGGGGACGAT 919
QY 817 ACATTGACAACTATTGGCTATGAGACAAATCCCTTAACTTGGCTGGGAAATTTGCTT 876
DB 920 ACATTGACAACTATTGGCTATGAGACAAATCCCTTAACTTGGCTGGGAAATTTGCTT 979
QY 877 TCTGAGGCTTTGCACTCCCTTGGCAATTTCTTTTGTGCACTTCTCTGCGGCAATTTG 936
DB 980 GCTGCTGGCTTGGCTTACTGGGCAATTTCTTTTGTGCTTCTCTGCGGCAATTTG 1039
QY 937 TCAGGTTTGGCATTAAGATGAGAAACACCGCCAGAAACACTTTTGAGAAAAGAGG 996
DB 1040 TCCGGCTTTGCGCTGAAGGTTCAGAGGAGACACCGGCAAGACATTCAGAAAGCGAGG 1099
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QY 1057 GTTTCATTTGCACTTGGAAAGCCACATTTGAGGCCCTTGCACACCTGTCAGC----- 1107

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DB 1220 GCCCTCTTTGTTGAGCAGCTGCAACGGGCGCGCAATGGGGCTTACGGCCCTTGAGGCTG 1279
QY 1153 ----- 1152
DB 1280 CGGCGGGCGGTTACCGAGCGGAGCACCTCCCGTTTACCGCGCGTTGCCACCTGCCAC 1339
QY 1153 -----AGTTTAAAGAGGA 1167
DB 1340 CGGCGGGCGGAGCACCTCTCTGCTGGGGAAGACAGCGGATGGGATCAAAAGCCGC 1399
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DB 1520 CAAAAGAGCTGAGCTTCAATGACCGACCGGCTTCCGCGGATCTCTGAGAGCTC----- 1573
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RESULT 13
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 ; Sequence 1, Application US/10850928
 ; Publication No. US20050037460A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JENTSCH, Thomas J.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:10:16 ; Search time 8514.67 Seconds
(without alignments)
12043.352 Million cell updates/sec

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Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: gb_est2:
3: gb_hic:
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5: gb_est4:
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7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	681.8	25.3	732	6 CD629756	CD629756 55049343J
7	679.2	25.2	742	6 CD629754	CD629754 55049327J
8	656.2	24.4	717	6 CD629766	CD629766 55049391J
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ALIGNMENTS

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genomic survey sequence.
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VERSION AY407013.1 GI:39762984
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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VERSION	AY407014.1	GI:39762985							
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ORGANISM	Pan troglodytes								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.								
AUTHORS	1 (bases 1 to 2014) Clark,A.G., Gnanoussi,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios								
TITLE	Science 302 (5652), 1960-1963 (2003)								
JOURNAL	14671302								
PUBMED	2 (bases 1 to 2014)								
REFERENCE	Clark,A.G., Gnanoussi,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA								
AUTHORS	This sequence was made by sequencing genomic exons and ordering them based on alignment								
TITLE	Location/Qualifiers								
JOURNAL	1.2014								
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Qy	511	GATACATGTTCTTATCGCTTCAATAGCAGTTGTTCTCGAAAAAATCAGGTAATATT	570
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Qy	691	TTAATCAGACTGTGTACATAGGATTTTGGTTCTTATTTTTCGTTCTTCTCTGCTCAT	750
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Qy	751	CTGGTGGAAAAGGATGCCAATAAAGAGTTTCTACATATGAGATGCTCTCTGGTGGGCG	810
Db	721	CTGGTGGAAAAGGATGCCAATAAAGAGTTTCTACATATGAGATGCTCTCTGGTGGGCG	780
Qy	811	ACAATTACATTGAACATATTGGCTATGGAGACAAAACTCCCTTAATCTGGCTGGGAAGA	870
Db	781	ACAATTACATTGAACATATTGGCTATGGAGACAAAACTCCCTTAATCTGGCTGGGAAGA	840
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Db	841	TGCTTTCTGAGGCTTGGCACTCTCTGCAATTTCTTTCTTTGCACTTCTGCGGCAATT	900
Qy	931	CTTGCTCAGGTTTGGCAATTAAGTACAAGAACCAACCGCCGAGAAACACTTTTGAGAAA	990

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Qy	1111	ACCAAGAAACAAAGGGGAAGCATCAAGCAGTCAAGAGCTTAAGTTTAAAGGAGCGAGTG	1170
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Qy	1171	CGCATGGCTAGCCCCAGGGGCGCAGAGTATTAAAGCCGACAGCCCTCAGTAGGTGACAGG	1230
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QY 1394 ATGATGAAAGAGATGCCAGTGTGATGATATAGTGGAGACCTCACCCACCACTTAAAA 1453
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Db 961 CCAGTGGCAACATCTCGAGAGGCTGCGAGTTCATCTGACGCCAAATGAGTTGAGTGGCC 1020
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LOCUS 55049367J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD629762
ACCESSION CD629762
VERSION CD629762.1 GI:40278028
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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Matches 754; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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/clone_lib="FLP"
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QY 1135 TCAAGCAGTCAGAAGCTAAGTTTAAAGAG-CGAGTGGCGCATGGCTAGCCCCAGGGGCA 1193
DB 623 TCAAGCAGTCAGAAGCTAAGTTTAAAGAGCGGAGTGGCATGGCTAGCCCCAGGGGCA 564

QY 1194 GAGTATTAAAGCCCAAGCCTCAGTAGGTGACAGAGGTCCTCCCAAGCACCAGCATCAC 1253
DB 563 GAGTATTAAAGCCCAAGCCTCAGTAGGTGACAGAGGTCCTCCCAAGCACCAGCATCAC 504

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LOCUS 55049391J1 FLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD629766
ACCESSION CD629766
VERSION CD629766.1 GI:40278032
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
Fu.G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
JOURNAL CONTACT: Fu GK
COMMENT
Incyte Genomics, Inc.
3150 Porter Dr., Palo Alto, CA 94304, USA
Tel.: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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Best Local Similarity 98.3%; Pred. No. 1.6e-176;
Matches 705; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

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[illegible]

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VERSION CD629752.1 GI:40278018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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RESULT 12
BE158938
LOCUS BE158938
DEFINITION MRO-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE158938
VERSION BE158938.1 GI:8621659
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 658)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2-MRO-HT0404-210
200-001-c04&t3=2000-02-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 657.
Location/Qualifiers
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CD629765.1 GI:40278031
EST. Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 599)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com

Location/Qualifiers
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/note="Vector: pDrive Cloning Vector"

Query Match 22.1%; Score 594.4; DB 6; Length 599;
Best Local Similarity 99.8%; Pred. No. 8.e-159;
Matches 595; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14
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LOCUS
CD629760
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/note="Organ: head neck; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Query Match 22.3%; Score 600.2; DB 2; Length 658;
Best Local Similarity 95.5%; Pred. No. 2e-160;
Matches 639; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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951 AAAAGTACAGAAACACACCCGAGAAACATTTGAGAAAGAGAACCCAGCTGCCAA 1010
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1311 CTTCCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAACCCAGTATGCTGACAC 1370
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1371 AGCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1430
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RESULT 13
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LOCUS
DEFINITION
55049391H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION
CD629765
599 bp mRNA linear EST 12-JAN-2004

Qy	1721	TTGAAAAA 1728
Dd	28	TGAACA 21
 RESULT 15 CD629751		
LOCUS		
DEFINITION 55049303H1 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004		
ACCESSION CD629751		
VERSION CD629751.1 GI:40278017		
KEYWORDS EST.		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
REFERENCE 1 (bases 1 to 624)		
AUTHORS Fu,G.K., Wang,J.T., Yang J., Au-Young,J. and Stuve,L.L.		
TITLE Circular rapid amplification of cDNA ends for high-throughput extensions cloning of partial genes		
JOURNAL Genomics 84 (1), 205-210 (2004)		
COMMENT Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel.: 6508454102 Email: gfu@incyte.com.		
FEATURES		
source Location/Qualifiers		
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Best Local Similarity 97.8%; Pred.No. 8.7e-156; Indels 4; Gaps 2;		
Matches 614; Conservative 0; Mismatches 10;		
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Dd	61	ACTTGCGTGGGAAGATGCTTTCGCAGGCTTTGCACCTCCTGGCATTTCTTTGCA 120
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Dd	121	CTTCTCTGCCGGCATCTTGSGCTCAGGTTTTTGCAATTAAGTACAAGAACCAACCGCCAG 180
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Search completed: April 11, 2005, 21:31:56
Job time : 8526.67 secs

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RESULT 2

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US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

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Query Match	99.8%;	Score 2662.2;	DB 4;	Length 3111;	
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1801 CAGATCCACACCTTTGAAATGTGAACAGACATCTGATATCAAAAGCCCTGTGGATAGCAAA 1860
1965 CAGATCCACACCTTTGAAATGTGAACAGACATCTGATATCAAAAGCCCTGTGGATAGCAAA 2024
1861 GATCTTCGGGTTCGGACAAACACAGTGGCTGTATCCAGATCAATAGTGGCAACATC 1920
2025 GATCTTCGGGTTCGGACAAACACAGTGGCTGTATCCAGATCAATAGTGGCAACATC 2084
1921 TCGAGAGCCCTGCAATCTGAGCCCAATAGATTCAGTGGCCAGACATTTCTAGCG 1980
2085 TCGAGAGCCCTGCAATCTGAGCCCAATAGATTCAGTGGCCAGACATTTCTAGCG 2144
1981 CTTAGCCCTACTATGACAGTCAAGCAACACAGGTGCCAATTAGTCAAAAGCATGGCTCA 2040
2145 CTTAGCCCTACTATGACAGTCAAGCAACACAGGTGCCAATTAGTCAAAAGCATGGCTCA 2204
2041 CGAGTGGAGCCACCAACACCATTTGCAACCAATAATAGTGGCAACCCAGCCAGCAGCC 2100
2205 CGAGTGGAGCCACCAACACCATTTGCAACCAATAATAGTGGCAACCCAGCCAGCAGCC 2264
2101 CCAACAACTTTACAGATCCACCTCTCTCCAGCCATCAAGCATCTCCAGGCGAGAA 2160
2265 CCAACAACTTTACAGATCCACCTCTCTCCAGCCATCAAGCATCTCCAGGCGAGAA 2324
2161 ACTCTGACCCCTAACCCCTGAGGCTTACAGAAAGCATTTCTGAGTCAACACCTGCTT 2220
2325 ACTCTGACCCCTAACCCCTGAGGCTTACAGAAAGCATTTCTGAGTCAACACCTGCTT 2384
2221 GTTGGCTCCAGGAAATGTTACAGTTGCAAGTCAAAATCTCACCAGGACCGTTCTATG 2280
2385 GTTGGCTCCAGGAAATGTTACAGTTGCAAGTCAAAATCTCACCAGGACCGTTCTATG 2444
2281 AGGAAAGCTTTGACATGGAGGAGAAACTCTGTTGTCTGTGTCCTCATGTCGCGAAG 2340
2445 AGGAAAGCTTTGACATGGAGGAGAAACTCTGTTGTCTGTGTCCTCATGTCGCGAAG 2504
2341 GACTTTGGCAATCTTTGTGTGTGCAAAACCTGTAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2400
2505 GACTTTGGCAATCTTTGTGTGTGCAAAACCTGTAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2564
2401 CAACTTTGAGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2460
2565 CAACTTTGAGGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2624
2461 AGGGAATCCAAATGTTTATATCTGATGAAGAGTGGGTCCCGAAGACAGACAGACAGAC 2520
2625 AGGGAATCCAAATGTTTATATCTGATGAAGAGTGGGTCCCGAAGACAGACAGACAGAC 2684
2521 ACTTTTGTATGCGCAGCCGAGGAGTGGCTTGGATCAGATCAGATCAGATCAGATCAGAT 2580
2685 ACTTTTGTATGCGCAGCCGAGGAGTGGCTTGGATCAGATCAGATCAGATCAGATCAGAT 2744

2581 ACTGGAAGGTACGATCATCTCAGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCGCTC 2640
2745 ACTGGAAGGTACGATCATCTCAGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCGCTC 2804
2641 AGCTTGCTCATCTCAAACTGAAATAA 2667
2805 AGCTTGCTCATCTCAAACTGAAATAA 2831
RESULT 3
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1
Query Match 98.4%; Score 2625.2; DB 4; Length 3137;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;
Qy 1 ATGAAGGATGTGAGTCGCGCGGCGGAGGTCGTGTAACTCGCGAGCGCGGCGGCG 60
Db 1 ATGAAGGATGTGAGTCGCGCGGCGGAGGTCGTGTAACTCGCGAGCGCGGCGGCG 60
Qy 61 GACGGCTGTCTACTGCTGGGCAACCGCGCGGCGGAGGTCGTGTCGCGCGGCGGCGGCTG 120
Db 61 GACGGCTGTCTACTGCTGGGCAACCGCGCGGCGGAGGTCGTGTCGCGCGGCGGCGGCTG 120
Qy 121 AGGAGAGCGCGCGGCGGCAAGCAGGCGGCGGAGGTCGTGTCGCGGCGGCGGCGGCTCTCT 180
Db 121 AGGAGAGCGCGCGGCGGCAAGCAGGCGGCGGAGGTCGTGTCGCGGCGGCGGCGGCTCTCT 180
Qy 181 TACACGATGACGACAGTCGCGCGGCAAGTCGTAAGTACCGCGGCGGTCGAGAACTACCTG 240
Db 181 TACACGATGACGACAGTCGCGCGGCAAGTCGTAAGTACCGCGGCGGTCGAGAACTACCTG 240
Qy 241 TACAACTGTGAGAGACCCCGCGGCTGGCGGTTCACTACACAGCTTTTCGTTTTTCTC 300
Db 241 TACAACTGTGAGAGACCCCGCGGCTGGCGGTTCACTACACAGCTTTTCGTTTTTCTC 300
Qy 301 CTTCCTTTGGTGTGATTTTGTCAAGTGTTCACCATCCCTGAGACACAAAAATTG 360
Db 301 CTTCCTTTGGTGTGATTTTGTCAAGTGTTCACCATCCCTGAGACACAAAAATTG 360
Qy 361 GCCTCAAGTGGCTCTTGATTCCTGAGTTCGTAAGTTCGTCCTTTGGTTCGAGTTC 420
Db 361 GCCTCAAGTGGCTCTTTGATCTCGAGTTCGTAAGTTCGTCCTTTGGTTCGAGTTC 420
Qy 421 ATCAATTCGAATCTGCTGCGGTTGCTGTTGTCGATATAGAGTACGAGGAGGAGACTG 480
Db 421 ATCAATTCGAATCTGCTGCGGTTGCTGTTGTCGATATAGAGTACGAGGAGGAGACTG 480
Qy 481 AGGTTTGTGCGAAAGCCCTCTCTGTATAGATACCATTTTTCGCTTCAATAGCA 540
Db 481 AGGTTTGTGCGAAAGCCCTCTCTGTATAGATACCATTTTTCGCTTCAATAGCA 540
Qy 541 GTTGTTCGCAAAAACCTCAGGTAATATTTTCCGCGCTGCACTCAGAGGTCCTCGT 600
Db 541 GTTGTTCGCAAAAACCTCAGGTAATATTTTCCGCGCTGCACTCAGAGGTCCTCGT 600

Qy	601	TTCTTACAGATCTTCGCGCATGGTGGCGATGGAACCGAAGGGGAGGCACTTTGGAATTACTG	660
Db	601		
Qy	601	TTCTTACAGATCTTCGCGCATGGTGGCGATGGAACCGAAGGGGAGGCACTTTGGAATTACTG	660
Db	601		
Qy	661	GGTTCAAGTGGTTATATGCTTCAGACGAAGAAATTAATCACAGCTTCGTCATAGGATTTTGG	720
Db	661	GGTTCAAGTGGTTATATGCTTCAGACGAAGAAATTAATCACAGCTTCGTCATAGGATTTTGG	720
Qy	721	GTTCTTATTTTTTCGTCTTTTCCTTCTATCTCGTGGAAAAAGGATGCCAATAAAGAGTTT	780
Db	721	GTTCTTATTTTTTCGTCTTTTCCTTCTATCTCGTGGAAAAAGGATGCCAATAAAGAGTTT	780
Qy	781	TCTACATATCAGATGCTCTCTGCTGGGGCACAATTACATTGACAACTATTTGGCTATGGA	840
Db	781	TCTACATATCAGATGCTCTCTGCTGGGGCACAATTACATTGACAACTATTTGGCTATGGA	840
Qy	841	GACAAAACTCCCTTAACTTTGGCTGGGAAGATTGCTTTCTGCAGAGCTTTGCACTCCTTGGC	900
Db	841	GACAAAACTCCCTTAACTTTGGCTGGGAAGATTGCTTTCTGCAGAGCTTTGCACTCCTTGGC	900
Qy	901	ATTTCTTTCTTTTGGCACTTCTCTGCCGGCATCTCTGGCTCAGGTTTTCGATTTAAAGTACAA	960
Db	901	ATTTCTTTCTTTTGGCACTTCTCTGCCGGCATCTCTGGCTCAGGTTTTCGATTTAAAGTACAA	960
Qy	961	GAACAAACACCGCCAGAAACACTTTTGAGAAAGAGGAACCCAGCTGCCAACCTCATTCAG	1020
Db	961	GAACAAACACCGCCAGAAACACTTTTGAGAAAGAGGAACCCAGCTGCCAACCTCATTCAG	1020
Qy	1021	TGTTGTTTGGGCTAGTTACGCACTGATGAGAAATCTGTTTCCATTGCAACTCGGAAGCCA	1080
Db	1021	TGTTGTTTGGGCTAGTTACGCACTGATGAGAAATCTGTTTCCATTGCAACTCGGAAGCCA	1080
Qy	1081	CACTTGAAGGCTTGCAACACTGCAGCCCTACCAAA	1115
Db	1081	CACTTGAAGGCTTGCAACACTGCAGCCCTACCAAAAGAAAGCAAGGGGAAGCATCAAGC	1140
Qy	1116	--TCAGAAAGCTTAAGTCTTAAGGACGAGTGGCGATGCTAGCCCGGAGGAGAGTATT	1173
Db	1141	AGTCAGAAAGCTTAAGTCTTAAGGACGAGTGGCGATGCTAGCCCGGAGGAGAGTATT	1200
Qy	1174	AAGAGCCGACAAGCCCTCAGTAGGTGACAGGAGGTCCCAAGACCCGACATCACAGCCGAG	1233
Db	1201	AAGAGCCGACAAGCCCTCAGTAGGTGACAGGAGGTCCCAAGACCCGACATCACAGCCGAG	1260
Qy	1234	GGCAGTCCCAAAAGTGCAGAGAGCTGGAGCTTTCAACGACCCGCTCCGGGCC	1293
Db	1261	GGCAGTCCCAAAAGTGCAGAGAGCTGGAGCTTTCAACGACCCGCTCCGGGCC	1320
Qy	1294	TCGCTCGGCTCAAAAGTTCTTCAGCRAAAACCGAGTATAGATGCTGACACAGCCCTTGGC	1353
Db	1321	TCGCTCGGCTCAAAAGTTCTTCAGCRAAAACCGAGTATAGATGCTGACACAGCCCTTGGC	1380
Qy	1354	ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTCAGTGGGAAGACCTCACC	1413
Db	1381	ACTGATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTCAGTGGGAAGACCTCACC	1440
Qy	1414	CCACCACTTAAACTGTTCATTCGAGCTATCAGAAATTATGAAATTTGATGTCGAAACGG	1473
Db	1441	CCACCACTTAAACTGTTCATTCGAGCTATCAGAAATTATGAAATTTGATGTCGAAACGG	1500
Qy	1474	AAGTTTAAAGAAAGCTTACGTTCATATGATGCTTAAAGATGTCATTTGAACCAATATCTGCT	1533
Db	1501	AAGTTTAAAGAAACATTCAGTTCATATGATGCTTAAAGATGTCATTTGAACCAATATCTGCT	1560
Qy	1534	GGTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAAAACAGCTGTGTGATCAAAATCTTT	1593
Db	1561	GGTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAAAACAGCTGTGTGATCAAAATCTTT	1620
Qy	1594	GGAAAAAGGCAAAATCAATCAGATAGAAAGCCGAGAGAAATTAACAGCAGAACATGAG	1653
Db	1621	GGAAAAAGGCAAAATCAATCAGATAGAAAGCCGAGAGAAATTAACAGCAGAACATGAG	1680

QY	1654	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGGTCAGTCC	1713
DB	1681	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGGTCAGTCC	1740
QY	1714	ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT	1773
DB	1741	ATAGAAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT	1800
QY	1774	GCCTCAGCCCTCGCTTTTGGCTTCATTCCAGATCCCACTCTTTTGAATGTGAACAGACATCT	1833
DB	1801	GCCTCAGCCCTCGCTTTTGGCTTCATTCCAGATCCCACTCTTTTGAATGTGAACAGACATCT	1860
QY	1834	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTCGACAAAAACAGTGGCTGC	1893
DB	1861	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTCGACAAAAACAGTGGCTGC	1920
QY	1894	TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCCCTGCAGTTCTATTCTGACGCCAAAT	1953
DB	1921	TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCCCTGCAGTTCTATTCTGACGCCAAAT	1980
QY	1954	GAGTTTCAGTGCCAGACATTTCTACGCGTTAGCCCTACTATGCAcAGTCAAGCAACACAG	2013
DB	1981	GAGTTTCAGTGCCAGACATTTCTACGCGTTAGCCCTACTATGCAcAGTCAAGCAACACAG	2040
QY	2014	GTGGCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGGCCACCAACACCATTCGAAACCA	2073
DB	2041	GTGGCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGGCCACCAACACCATTCGAAACCA	2100
QY	2074	ATAAATACGGCACCCAAAGCCAGCAGCCCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2133
DB	2101	ATAAATACGGCACCCAAAGCCAGCAGCCCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2160
QY	2134	GCCATCAAGCATCTGCCAGGCCAGAAAACTCTGCAcCCTAACCTGTGAGGCTTACAGAA	2193
DB	2161	GCCATCAAGCATCTGCCAGGCCAGAAAACTCTGCAcCCTAACCTGTGAGGCTTACAGAA	2220
QY	2194	AGCATTTCTGACGTCACCACTCGCTGTTTGCCTCCAAAGGAAATGTTTCAGGTTGCAcAG	2253
DB	2221	AGCATTTCTGACGTCACCACTCGCTGTTTGCCTCCAAAGGAAATGTTTCAGGTTGCAcAG	2280
QY	2254	TCAAATCTCAcCAAGGACCGTTCTATCAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2313
DB	2281	TCAAATCTCAcCAAGGACCGTTCTATCAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340
QY	2314	TTGTCTGTCTGTCCATGTGTGCCAAGGACTTGGGCAAACTTTTGTCTGTGTGCAAAACCTG	2373
DB	2341	TTGTCTGTCTGTCTGTGCCAATGTGTGCCAAGGACTTTGGGCAAACTTTTGTCTGTGTGCAAAACCTG	2400
QY	2374	ATCAGGTTCGACCCAGGAACTGAAATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2433
DB	2401	ATCAGGTTCGACCCAGGAACTGAAATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2460
QY	2434	GGCAGCAAGATTTTTTACCACAAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG	2493
DB	2461	GGCAGCAAGATTTTTTACCACAAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG	2520
QY	2494	GTGGGTCCGNAAGACAGAGACAGACATTTTGTATGTCGCCACCGCAGCCTGCCAGGAA	2553
DB	2521	GTGGGTCCGNAAGACAGAGACAGACATTTTGTATGTCGCCACCGCAGCCTGCCAGGAA	2580
QY	2554	GCTGCCCTTTCATCAGACTCTCTAAGGACTTGGAAAGGTTCAGATCATCTCAGAGCATTTGT	2613
DB	2581	GCTGCCCTTTCATCAGACTCTCTAAGGACTTGGAAAGGTTCAGATCATCTCAGAGCATTTGT	2640
QY	2614	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATCTCAAACTGAAATAA	2667
DB	2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATCTCAAACTGAAATAA	2694

RESULT 4
US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131

; GENERAL INFORMATION:
 ; APPLICANT: STEINMEYER, Klaus
 ; APPLICANT: LERCHE, Christian
 ; APPLICANT: SCHERER, Constanze
 ; APPLICANT: SEEBOHM, Guiscard
 ; APPLICANT: BUSCH, Andreas E.
 ; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNOS, A NEW TARGET FOR DISEASES OF THE NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
 ; FILE REFERENCE: 38005-119
 ; CURRENT APPLICATION NUMBER: US/09/813,148
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: DE 100 13 732.6
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/194,041
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3074
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-148-1

Query Match	98.1%	Score 2617.2	DB 4	Length 3074
Best Local Similarity	98.7%	Pred. No. 0		
Matches 2659	Conservative 0	Mismatches 8	Indels 27	Gaps 1
Qy 1	ATGAAGATGTGGAGTGGCGGGGAGGGTGTCTGAACTCGGCAGCGCCGAGGGG	60		
Db 215	ATGAAGATGTGGAGTGGCGGGGAGGGTGTCTGAACTCGGCAGCGCCGAGGGG	274		
Qy 61	GACGGCTGTACTGTCTGGGACCGCGGGCCACCGTGTGGTGGCGCGGGTGGCGTG	120		
Db 275	GACGGCTGTACTGTCTGGGACCGCGGGCCACCGTGTGGTGGCGCGGGTGGCGTG	334		
Qy 121	AGGAGAGCGCGCGGGGCAAGCAGGGGGCCGGATGAGCCTGTGGGGAGCCGCTCTCT	180		
Db 335	AGGAGAGCGCGCGGGGCAAGCAGGGGGCCGGATGAGCCTGTGGGGAGCCGCTCTCT	394		
Qy 181	TACACGAGTACGAGAGCTGCGCGGCAACGCTCAAGTACCGCGGGGTGCAGAACTACCTG	240		
Db 395	TACACGAGTACGAGAGCTGCGCGGCAACGCTCAAGTACCGCGGGGTGCAGAACTACCTG	454		
Qy 241	TACAAAGTGTGGAGAGACCGCGGGTGGCGGTTCATCTACACGCTTTCGTTTTCCTC	300		
Db 455	TACAAAGTGTGGAGAGACCGCGGGTGGCGGTTCATCTACACGCTTTCGTTTTCCTC	514		
Qy 301	CTTGCTTTTGTGCTGATTTTGTACGTGTTTCTACATCCCTGAGCACACAAATTG	360		
Db 515	CTTGCTTTTGTGCTGATTTTGTACGTGTTTCTACATCCCTGAGCACACAAATTG	574		
Qy 361	GCCTCAAGTTCGCTTGTATCTGGAGTTCGATGATGTCGTTTGGTTTGGAGTTC	420		
Db 575	GCCTCAAGTTCGCTTGTATCTGGAGTTCGATGATGTCGTTTGGTTTGGAGTTC	634		
Qy 421	ATCATTCGAATCTGTCTGGGGTTCGTTTGTGATATAGAGATGCGAGGAGAGCTG	480		
Db 635	ATCATTCGAATCTGTCTGGGGTTCGTTTGTGATATAGAGATGCGAGGAGAGCTG	694		
Qy 481	AGGTTTGTTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGTTCAATAGCA	540		
Db 695	AGGTTTGTTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGTTCAATAGCA	754		
Qy 541	GTTGTTTCTGAAAAAATCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAAGTCCGT	600		
Db 755	GTTGTTTCTGAAAAAATCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAAGTCCGT	814		
Qy 601	TTTCCTACAGATCCTCCGATGTGCGCATGAGACCGAAGGGAGGACCTTGGAAATTAATG	660		
Db 815	TTTCCTACAGATCCTCCGATGTGCGCATGAGACCGAAGGGAGGACCTTGGAAATTAATG	874		
Qy 661	GGTTTCAGTGGTTTATGCTCACAAGCAAGGAATTAATCACAAGTTCGTACATGGAATTTTGT	720		

Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KNO2 AND KNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 88
; LENGTH: 2273
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2271)
US-09-177-650-88

Query Match 18.3%; Score 489.2; DB 3; Length 2273;
Best Local Similarity 57.0%; Pred. No. 2e-138;
Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;

Qy	64	GGCTGCTACTGCTGGGACCCGCGCCGACGCTTGGTGGCGGCGGTGGCTGAGG	123
Db	67	GGCTTCGTGGGCTGAGCCCGCGGCGCCGANTCCACGCGCGGCGGCTACTCATC	126
Qy	124	GAGACCGCGGCGGGAAGAGGGGCGCGGATGAGCTGTGGGGAAGCCCTCTCTTAC	183
Db	127	GCGGGCTCCGAGGCCCCCAAGCGCGGCANCTNTTGAACAGCCGCGGAGCGGCGG	186
Qy	184	ACGAGTAGCAGAGCTGCGGCGCAACGCTCAAGTACCGCGGCGGTGCAGAACTACCTGTAC	243
Db	187	GGAGCGGGAAGCCCCCNANCGAACGCTTCTACCGCAAGCTGCAGAACTTCTCTAC	246
Qy	244	AACGCTGCTGAGAGACCCCGCGGTGGGCTTCATCTACCGCTTTCGTTTCTCTTT	303
Db	247	AACGCTGCTGAGAGCGGCGCGGCTGCGGTTCATCTACCGCTTCGTTTCTCTCTG	306
Qy	304	GTCCTTGGTGTGATTTGTGCTGCTTCTACCATCCCTGAGCAGACACAAAATTGGCC	363
Db	307	GTCTTCTCTGCTTGTGCTTCTGCTGTTTCCACCATCAAGGAGTACGAGAAGCTCT	366
Qy	364	TCAAGTTGCTCTTGATCTGAGTTGCTGATGATGCTCTTCTTGGTTTGGAGTTTATC	423
Db	367	GAGGGGCGCTCTACATCTTGAATCTGACTATCGTGTATTCGGTGTGAGTACTTT	426
Qy	424	ATTGGAATCTGCTGCGGTTGCTGTGTGATATGAGGATGCAAGGAGTCTGAGG	483
Db	427	GTGAGGATCTGGGCTGAGGCTGCTGTGCGGTATCGAGGCTGAGGCGGAGGCTCAAG	486
Qy	484	TTTGTGCAAGCCCTTCTGCTTATAGATACATTTCTTATCGCTTCAATACAGTT	543
Db	487	TTTGCAGGAACCGTTCTGTGTATGATATATATATATATATATATATATATATAT	546
Qy	544	GTCTTGCAGAAACTCAGGTAATATTTTTCAGCTCTGCACTCAGAACTCTCGGTTTC	603
Db	547	CTGGCTGCTGGTTCCAGGGCAATGCTTTTGCACATCTGCGCTTCGGAGCTTCGGTTTC	606
Qy	604	CTACAGATCCTCGCATGTGGCATGGAACCGAGGGAGGACATTTGGAATTTCTGGGT	663
Db	607	TTGCAAACTCTGCGATGATCGTATGAGACCGGAGGGGTGGCACCTTGGAACTCTTGGGA	666
Qy	664	TCACTGCTTATGCTCACAGCAAGGAATTAATACAGCTTGTGTACATAGATTTTGGTT	723
Db	667	TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGAATGCTGCTGTGTATATGCTCTGCT	726
Qy	724	CTTATTTTTCGTTCTTCTGCTATCTGGTGGAAAGGATGCCAATAAAGAGTTTCT	783

Db	727	CTCATCTTGGCTCTCATTTCTTGGTGTACTTGGCAGAAAAGGGTGAGAATGACCACTTTGAC	786
Qy	784	ACATATGAGATGCTCTCTGGTGGGCACAATTACATTGACAACTATTGGCTATGAGAC	843
Db	787	ACCTACGAGATGCACTCTGGTGGGTCTGATCACCTGACGACCAATGGCTACCGGGAC	846
Qy	844	AAACTCCCTAACTTTGGCTGGGAAGATTGCTTCTGAGGCTTTGCACTCTCTTGGCAAT	903
Db	847	AAGTACCTCAGACCTGGAACGGAGGCTGCTGGCAGGACCTTTACCTCATTTGGTGTG	906
Qy	904	TCCTTTCTTGGCACTTCTCTCGGCACTTCTGGCTCAGGTTTGCATTTAAAGTACAGAA	963
Db	907	TCGTCTTCTTGGCTCTCTCGGCTGGCAATTTGGGATCGGCTTTGCCCTGAAAGTCCAAG	966
Qy	964	CAACACCGCCAGAAACACTTTGAGAAAGAAAGAAAGCCAGCTGCCAACCTCATTTAGTGT	1023
Db	967	CAGCATCGGCAAAAACACTTTGAGAAACCGCGGAAACCTTCGGCAGGCTGTGATCCAGTCT	1026
Qy	1024	GTCTGGGTAGTTACGCGAGCTGAT-----	1047
Db	1027	GCTGGAGATTCTATGCTACTTAACCTCTCAGCGCACCGACCTGCACCTCCACGTGGCAGTAC	1086
Qy	1048	---GAGAAATCTGTTTCCATTGCAACTGGAAGCCACACTTTGAAGGCTTTGCACACTGC	1104
Db	1087	TACGAGCGNACAGTCACTGCTCCCATGTACAGCTCAAAACTCAAACTATGGGGCTCC	1146
Qy	1105	AGCCTTACC-----AATCAGAACTAAGTTTA	1132
Db	1147	AGACTCATCCACTCTGAAACAGCTGGAGCTGTGAGGAATCTCAGAGCAATCTGGA	1206
Qy	1133	AGAGAGGAGTGGCGATGGCTAGCCCGAGGGGCGAGAGTATTAAGAGCCGCAAGACCTCAG	1192
Db	1207	CTACCTTCAGGAAGGAGCCACAGCCAGAGCCATCAAGAGCCCGGAGGATGGCTGCC	1266
Qy	1193	TAGTGTACAGAGGTCCTCCCAAGCACCGACATCAGC-----	1229
Db	1267	AAGGAAAGGGGTCTCCCGAGGCGCAGACGCTCCGCGGTCCCGCAGTGGGATCAGAGT	1326
Qy	1230	--CGAGGGGAGTCCCAAAAGTGCAGAGAGCTTGAAGCTTCAACGACCGAAACCGGCTTC	1287
Db	1327	CTGTATGACAGCCCGAGCAAGGTGCCAGAGCTTGGTGTGAGCCGCGCACA	1386
Qy	1288	CGGCGCTCGCTGGCGCTCAAAAGTTCTCAGCCAAACACAGTATAGTGTGACACAGCC	1347
Db	1387	CGCCAGGCTTTCCGCACTCAAGGGTGTGCTATCCCGGAGAAATTCAGAAAGCAAGGCTC	1446
Qy	1348	CTTGGCACTGATGATGTATATGATAAGAAAGGATGCCAGTGTGATGTATCAGTGGAAAGAC	1407
Db	1447	CCTGGGAGGACATCTGTAGAGGACACAGAGCTGTAACTGCGAGTTTGTGACTGAAGAT	1506
Qy	1408	CTCACCCCCACACTTAAACCTGTCTATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCA	1467
Db	1507	CTTACCCCTCGGCTCAAAAGTYAGCATCAGAGCCGTGTGTGTATGCGGTTCTTGTATCT	1566
Qy	1468	AAACGGAAGTTTAAAGGAAACGTTACGTCATATGATGTAAAGATGTCAATGAAACAATAT	1527
Db	1567	AAGCGAAGTTTCAAGAGAGGCTCTCGGCCATATGATGTGAGGACGCTCATCGAACAGTAC	1626
Qy	1528	TCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAACACGCTGTGTATCAA	1587
Db	1627	TCGGCTGAGACCTTGGATATGTTGTCCCGCATCAAGAGCTTCAGAGCCGAGAGTGGACCG	1686
Qy	1588	ATTCTTGGAAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATTAACAGCAGAA	1647
Db	1687	ATTGTGGGGCGGCGCCNACAAATTAAGGATPAAGG---TCGCAACAAAGGCCAGCGGAA	1743
Qy	1648	CATGAGACCAAGACAGATCTCAGTATGCTCGGTGGGTGTCAGGTTGAAAAACAGGTA	1707
Db	1744	ACGAGAGTGGCCCGAAGACCCAGCATGATGGGAGCGCTTGGGAAAGGTGGGAAACAGGTC	1803
Qy	1708	CAGTCCATAGATCCAGCTGAGCTGCTACTAGACATCTATCAACAG	1755

Db 1804 TTGTCCATGGAAAGAGCTCGACTTCTTGGTGAGCATCTATACAG 1851

RESULT 9

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US-09-105-058C-22
; Sequence 22, Application US/09105058C
; Patent No. 6403360
;
; GENERAL INFORMATION:
;
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
;
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;
; FILE REFERENCE: 3053-4052
;
; CURRENT APPLICATION NUMBER: US/09/105,058C
;
; CURRENT FILING DATE: 1998-06-26
;
; PRIOR APPLICATION NUMBER: US 60/055,599
;
; PRIOR FILING DATE: 1997-08-12
;
; NUMBER OF SEQ ID NOS: 28
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 22
;
; LENGTH: 2169
;
; TYPE: DNA
;
; ORGANISM: mouse
;
US-09-105-058C-22

```

Query Match	17.8%;	Score 475.6;	DB 3;	Length 2169;
Best Local Similarity	57.0%;	Pred. No. 2.9e-134;		
Matches 1022; Conservative	0;	Mismatches 664;	Indels 108;	Gaps 4

64	QY	GGCCTGCTACTGCTGGGCACCCGCGCGGCACGCTTGGTGGCGCGCGCGTGGCCTGAGG	123
67	Db	GGCTTCGTTGGGCTGGAGCCCGCGCGCGCCGACCTCCACACGCAACGCGCGCTACTCATC	126
124	QY	GAGAGCGCGCGGGCAAGCAGCGGGGCGCCGAGTGGCTGTGGGAAGCGGCTCTCTTAC	183
127	Db	GCGGGCTCCGAGGCCCAAGCGCGGCGAGCGTTTGTAGCAAGCCGCGACCGCGCGCGG	186
184	QY	ACGAGTAGCCAGAGCTGCGGGCGCAACGCTCAAGTACCGGGCGGTGCGAACTACTCTGAC	243
187	Db	GGAGCGCGGAAGCCCGCAAGCGCAACGCCCTTCTACCGAAGCTGCAGAAATTTCCCTCTAC	246
244	QY	AACGCTCTGGAGAGACCCGCGGCTGGGGCTTCATCTACACGCTTTCGTTTTCTCCCTT	303
247	Db	AACGCTGTAAGCGCGCCCGCGGCTGGGCGTTCATCTACCACGCTACGTTCTCTTTTA	306
304	QY	GTCTTTGGTGTCTGATTTTGTTCAGTGTTTTCTACCATCCTCGAGCACACAAATTTGGCC	363
307	Db	GTCTTCTCTGCTTGTGCTTCTGTGTTTTCCACCATCAAGNGTACGAGAGAGCTCT	366
364	QY	TCAAGTTGCTCTTGATCTCTGAGGTTCTGTGATGATGTCTGCTTTGGTTTGGAGTTTCATC	423
367	Db	GAGGGGGCCCTACATCTTGGAAATCGTACTATCGTGGTATTCGGTGTGTAGTAGTACTTT	426
424	QY	ATTTCGAACTGCTGTCCGGGTGCTGTGTGATATAGAGGATGGCAAGGAAGACTGAGG	483
427	Db	GTGAGGATCTGGGCTGCAGGCTGCTGTTTGCCEGTATCGAGGCTGGAGGGCAGGCTCAAG	486
484	QY	TTTGTCTGAAAGCCCTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCAGTT	543
487	Db	TTTGCCAGGAAGCCGTTCTGTGTGATGATATCATGGTGTGATTCGCTCCATTCGTGTG	546
544	QY	GTTTCTGCAAAACTCAGGGTAATATTTTCCACGCTTCGCTACAGAAAGTCTCCGTTTC	603
547	Db	CTGGCTGCTGGTTCCAGGGCAATGCTCTTTGCCACATCTGCGCTTCGAGCTTTCGCGTTC	606
604	QY	CTACAGATCCTCCGCAATGGTGGGCATGAGACGAAGGGGAGGCACTTGGAAATTTACTGGGT	663
607	Db	TTGCAAACTCTCGGATGATCCGTATGGACCGAGGGGTGGCACCTGGAAAGCTCTTGGGA	666

Db 1741 GCGGAAACGGAGCTGCCGAGACCCAGCATGATGGACGGCTTGGGAAGGTGGAGAAA 1800
QY 1702 CAGGTACAGTCCATAGAGTCCAGAGCTGGAGCTGCTACTAGACATCTATCAACAG 1755
Db 1801 CAGGTCTGCTCATGTAAGAGAGCTGAGCTTCTTGGTGAGCACTATACACAG 1854

RESULT 10
US-09-105-058C-1
; Sequence 1, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
; OTHER INFORMATION: y=c or t; r=a or g; m=a or c; k=g or t; s=g or c;
; OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-09-105-058C-1

Query Match 17.5%; Score 465.4; DB 3; Length 896;
Best Local Similarity 53.7%; Pred. No. 2e-131;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;
QY 190 ACCGAGAGTCCGCGGACGCTCAAGTACCGCGGGTGCAGAACTACTGTACAACTG 249
Db 13 RGSMSRSCMSYSAAGAGMGAACGCCWMTACCSCMSMTSCARMTTTSMTCTACACGS 72
QY 250 CTGGAGAGACCCGCGGCTGGCGGTTCATCTACCAGCTTTCGTTTTCTCCTCTCTTT 309
Db 73 CTRGAGMGRCCSGGGCTGGCGGYTSMYTTACCAGCGSTWSGTGTCTCTBHTDGYVTS 132
QY 310 GGTGTGCTGATTGTGTCAGTGTTCCTACATCCCTGAGCACACAAAATGGCCTCAAGT 369
Db 133 KSSTGCTYBTKCTGCTGTS-YKWCACMWTCAAGGAGTAYGAGAMRKYTCBRRGRS 191
QY 370 TGCTCTTGCATCTGAGTCTGATGATGCTGCTTTGTTGTTGGAGTTCATCAATCGA 429
Db 192 KSCCTYYWNTVYTGARAYMKTKYATIKYISRTVITGGHYBGAGTWYKYKTGWR 251
QY 430 ATCTGTCTGCGGGTGTCTGTTGTCATATAGAGGATGCCAAGAGACTGAGTTGCT 489
Db 252 ATCTGGGCGCGMTGYTSYTCGCGRTACMRWGGCTGGMGGGSGMGRCTSAAGTTGCC 311
QY 490 CGAAGCCCTTCTGTTATAGATACATGTTCTTATCGCTCAATACAGTGTCTTCT 549
Db 312 MGAARCCVCTSTGYRTGTWBTGAYATCWTKGTCTSATYGCCTCYRKTSCDGTGTSKGY 371
QY 550 GCAAAACTCAGGTAATATTTTGGACGCTGCACTCAGAACTCCGCTTTCTCTACAG 609
Db 372 GYBGHWMCCAGGCAAYGYTYKGYACVTCY---CTBCGAGCYTGGSTCTYTCRAC 428
QY 610 ATCCTCGCATGTGGCGCATGAGCCGAGGGGAGGCACTTGGAATATCTCGAGTTCAGTG 569

Db 429 ATVTTCGSGATGWTSCGBATGACCGGMRGHHGGCACTCGGAAGCTBYTGGMTCDGV 488
QY 670 GTTTATGCTCAGCAAGGAATTAATACAGCTTGTATACATAGGATTTTGGTCTCTATT 729
Db 489 RTCTRYGCGYCACAGCAARGACTSRTSACKGCTGTATCATYGGYTTCTBWSHCTCATC 548
QY 730 TTTTCGCTCTTCTCTGCTTATCTGTGGAAGAGGATGCCAATAAAGAGTTTCTCATAT 789
Db 549 CTYKCYTCCTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
QY 790 GCAGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
Db 609 GCRGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
QY 850 CCCTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
Db 669 CCYMARACSTGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
QY 910 TTTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
Db 729 TTYGCTKCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
QY 970 CGCAGAAACACTTTGAGAAAG 1029
Db 789 MGRKARAAACACTTTGAGAAAG 848
QY 1030 CGTAGTTAGCAGCTGA 1046
Db 849 AGRTWTYATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

RESULT 11
US-09-495-050A-305
; Sequence 305, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P;
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 305
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006F6
; NAME/KEY: unsure
; LOCATION: 486, 510, 552, 573
; OTHER INFORMATION: a, t, c, g, or other
US-09-495-050A-305

Query Match 16.9%; Score 452; DB 4; Length 575;
Best Local Similarity 95.0%; Pred. No. 1.8e-127;
Matches 509; Conservative 0; Mismatches 22; Indels 5; Gaps 4;
QY 1594 GGAAAGGGGCAATACATCATAGATAAGAGAGCGAGAGAAATAACGAGAGACATGAG 1653
Db 1 GGAAAGGGGCAATACATCATAGATAAGAGAGCGAGAGAAATAACGAGAGACATGAG 60
QY 1654 ACCAGAGAGATCTCAGTATGCTCGTGGTGTCTCAGGTTGAAAGAGAGAGAGAGAGAG 1713
Db 61 ACCAGAGAGATCTCAGTATGCTCGTGGTGTCTCAGGTTGAAAGAGAGAGAGAGAGAG 120
QY 1714 ATAGAGTCCAGAGTGGAGTGGCTGCTACTAGACATCTCAACAGGTCCTTCGAAAGGCTCT 1773

Db	121	ATAGAAATCCAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	180
Qy	1774	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACACCTTTTGGATGTGAACAGACATCT	1833
Db	181	GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGGATGTGAACAGACATCT	240
Qy	1834	GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGCACAAACAGTGGCTGC	1893
Db	241	GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGCACAAACAGTGGCTGC	300
Qy	1894	TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCTGCGAGTTCACTTCGACGCCAAAT	1953
Db	301	TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCTGCGAGTTCACTTCGACGCCAAAT	359
Qy	1954	GAGTTTCAGTGCACAGACTTTCTACGCGCTTAGCGCTTACTATGACAGTCAAGCAACACAG	2013
Db	360	GAGTTTCAGTGCACAGACTTTCTACGCGCTTAGCGCTTACTATGACAGTCAAGCAACACAG	417
Qy	2014	GTGCCAAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCGCCACCAACCATTTGCCAAACCA	2073
Db	418	GTGCCAA-TAGTCAAGCGATGGCTCAGCAGTGGCAGCGCCACCAACCATTTGC-AAACCA	475
Qy	2074	ATAAATACGGCACCCAGCCAGCAGCGCCCAACAACTTACAGATCCCAACCTCTCT	2129
Db	476	ATTAATACGGNACCCAGCCAGCGAGGCCCAANTTACAGTCTCTCTCAGCTCT	531
RESULT 12			
US-09-105-058C-26			
; Sequence 26, Application US/09105058C			
; Patent No. 6403360			
; GENERAL INFORMATION:			
; APPLICANT: Blonar, Michael A.			
; APPLICANT: Dworetzky, Steven			
; APPLICANT: Gribkoff, Valentin K.			
; APPLICANT: Levesque, Paul C.			
; APPLICANT: Little, Wayne A.			
; APPLICANT: Neubauer, Michael G.			
; APPLICANT: Yang, Wen-Pin			
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME			
; FILE REFERENCE: 3053-4052			
; CURRENT APPLICATION NUMBER: US/09/105,058C			
; CURRENT FILING DATE: 1998-06-26			
; PRIOR FILING DATE: 1997-08-12			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 26			
; LENGTH: 2565			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-105-058C-26			

Query Match	16.0%	Score	427.2	DB 3	Length	2565
Best Local Similarity	56.7%	Pred.	No. 2.1e-119			
Matches	923	Conservative	0	Mismatches	118	Gaps
				Indels	57	Gaps
Qy	13	GAGTCGGCGCGGGCAGGGTGCTGCTCAACTCGGCAGCGCGCAGGGGCGAGCGGCTGCTGTA	72			
Db	43	CGGCGCGCGCGCGGACGAGGAGCGGAAAGTGGGGCTGCGCCCGCGGACGTGGAGCAA	102			
Qy	73	CTGCTGGGCAACCCGCGCGGCAACGCTTGTGTGGCGGCGGTGGCCCTGAGGGAGAGCGCG	132			
Db	103	GTCACCTTGGCGCTTCGGGGCGGAGCGCAAAAGACGGGACCCCTGCTGCTGGAGGGCGG	162			
Qy	133	CGGGGCAAGCAGGGGGCGCGATCAGACCTGCTGGGGAAAGCGGCTCTCTTACACGAGTAGC	192			
Db	163	GGCCGCGACGAGGGGAGCGGAGGACCCCGCAGGSCATCGGGCTCTGGGCCAAGACCCCG	222			
Qy	193	CAGAGCTGCC-----GGCGCAA	CGTCAAGTAGTCGGCGGGGTGCAGAACTACCTGTATC	243		
Db	223	CTGAGCGCGCCAGTCAAGAGAAACACGCCAAGTAGTCGGGGCATCCAAACTTTGATCTAC	282			

QY	244	AACGTGCTGGAGAGACCCCGCGGTGGCGTTCTATCTATCACGCTTTTCGTTTTCCTCT	303
DB	283	GACGCCCTGGAGAGACCCCGCGGTGGCGTGTCTTTTACCACGCGTTGGTGTTCCTGATT	342
QY	304	GTCCTTTGGTGTGCTTGATTTTGTCTAGTGTCTTTCTATCCATCCCTGAGCACACAAATTTGGCC	363
DB	343	GTCCTGGGTCCTTGATTCTGGCTGTCTGACCAATTTCAAGGAGTATGAGACTGTCTCG	402
QY	364	TCAAGTTGCCCTCTTGATCTCGGAGTTCGTGATGATTTGTCTTTTGGTTTGGAGTTTCATC	423
DB	403	GGAGACTGGCTCTTGTTACTGGAGACATTTGCTATTTTTCATCTTTGAGCCGAGTTTGCT	462
QY	424	ATTGCAATCTGGTCTCGCGGTTGCTGTTGCGATATAGAGATGGCAAGAGACTGAGG	483
DB	463	TTGAGGATCTGGGTCGTGGATGTTGTGCGGATACAAAGGCTGGCGGGCCGACCTGAAG	522
QY	484	TTTCTCGAAAGCCCTTCGTGTGTTATAGATACCAATGCTCTTATCGCTTCAATAGCAGTT	543
DB	523	TTTGCCAGGAAGCCCTCTGTGATGTTGGACATCTTTGTGCTGATGTGCTCTGTGCCAGTG	582
QY	544	GTTTCTGCAAAAACCTCAGGGTAAATTTTTTGGCCACGTCTGCACCTCAGAACTCTCCGTTTC	603
DB	583	GTTGCTGFGGAACCAAGCAATGTTCTGCGCACCT---CCCTGCGAAGCCTGCGCTTC	639
QY	604	CTACAGATCTCTCCGATGTTGCGCATGGAACGAAGGGGAGGCACTTTGGAAATTACTGGGT	663
DB	640	CTGCAGATCTCTCGCATGCTCGGATGGACCGGAGAGTGGCACCTGGAAGCTTCTGGGC	699
QY	664	TCAGTGTGTTATGCTCACACGAGGAATTAATCACAGCTTGTATACATAGATTTTGGTT	723
DB	700	TCAGCCATCTGTGCCACAGCAAGAATACTATCACGGCCTGGTACATCGGTTTCCCTGACA	759
QY	724	CTTATTTTTTTCGTTCTTCTTGTCTATCTCGTGGAAAGGATGCC-----	768
DB	760	CTCATCTTCTTCATTCTTGTCTACTCGTTGAGAAAGCGTCCAGAGGTGGATGCA	819
QY	769	-----AATAAAGAGTTTCTATATATGACAGATGCTCTCTCGTGGGGCACA	813
DB	820	CAAGGAGAGGATGAAAGAGGAGTTTGAGACCTATGCAGATGCCCTGTGCTGGGCGCTG	879
QY	814	ATTACATTGACAACTATTGGCTATGGAGCAAAACTCCCCTAATCTTGGCTGGGAGATTG	873
DB	880	ATCACCTGGCCACCATTTGGCTATGGAGACAAGACACCCAAAACGTGGGAAGCCGCTCG	939
QY	874	CTTTCTCGAGCTTTTGCACTCTCTTGGCATTTCTTTCTTTCACCTTCTCTGCGCGCATCTTT	933
DB	940	ATTGCCCGCACCTTTCCTTAATTTGGGCTCTCTTTTTCGCCCTTCAGCGGGGATCTCTG	999
QY	934	GGCTCAGGTTTTTGCAATTAAGAATCAAGAACAAACCGCCAGAAACACTTTGAGAAAAGA	993
DB	1000	GGGTCCGGGCTGGCCCTCAAGGTGCAGGACCAACCCGTGAGAAAGCACTTTGAGAAAAGG	1059
QY	994	AGGAACCCAGCTGCCAACCTCATTTAGTGTGTTGGGTAGTTTACGCAGCTGATGAGAAA	1053
DB	1060	AGGAAGCCAGCTGCTGAGCTCATTTACGGCTGCTCGGAGGTATTATGCTACCAACCCCAAC	1119
QY	1054	TCTGTTTCCAATG-----CAACTGGAAGCCAACACTTGAAGGCTTTGCACACCTCG	1104
DB	1120	AGGATTCACCTGGTGGGCACATGGAGATTTTATGAATTCAGTCGTCTTTTCTTTCTTCTTC	1179
QY	1105	AGCCCTACCAATCAGAAGCTAAGTTTTTAAGGAGCGAGTGCAGCTAGGCTAGCCCCAGGGGC	1164
DB	1180	AGGAAGAAACAGCTGGAGGCAGCATCCAGCCAAAAGCTGGGTCTCTTGGATCGGTTTCG	1239
QY	1165	CAGAGTATTAAAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCCGACATC	1224
DB	1240	CTTTCTAATCCTCGTGGTAGCAATACTATAAGGAAAGCTATTATACCCCTCTGATGTAGAT	1299
QY	1225	ACAGCCGAGGGCAGTCCCAACCAAGTGCAGAGCTGGAGGCTTCAACGACCCGAAACCCGC	1284
DB	1300	GCCATAGAAAGATGCTCTCTAAAGAACCAAGACCTTGTGGCTTTAAACATAAAGAGCGT	1359
QY	1285	TTCCGGCCCTCGTGTGGCCTCAAAAGTTCTCAGCCAAAAACAGCTGATAGATGCTGACACA	1344

Qy	996	GAACCCAGCTGCCAACCTCATTCA GTGTGTTTGGCGTAGTTACGCAGCTGA----	TGAGAA	1052
Db	1311	GAAGCCAGCTCGGGAATCATCCAGGCTGCTGGAGATATTATGCTACCAACCCCACAG	1370	
Qy	1053	ATCTGTTTTCCATTTCACACTTGGA-----AGGCCACACTTCAAGGCCCTTGACACCTTCGAG	1106	
Db	1371	GTTTGGATCTGGTGGCAACCTGGAGATCTTATGAATCAGTTGTCTCTTCCATTCCTTCAG	1430	
Qy	1107	CCCTPACCAATCAGAAGCTAAGTTTTTAAGGAGCGAGTGGCGATGGCTAGCCCCAGGGGCCA	1166	
Db	1431	GAAGAAGAACCTGGAAGCAGCAGCCAGCCAAAAGCTGGGTCTCTTGGATCGGGTTCGCCT	1490	
Qy	1167	GAGTATTAAAGGCCGACAAGCCCTCAGTAGTGCACGAGGCTCCCCAAGCACCCGACATCAC	1226	
Db	1491	TTCTAATCTCTGGTGTAGCAATACCTAAGGAAGCTATTTTACCCTCTGAACTGATGATGC	1550	
Qy	1227	AGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAAAGCACCGAACCCGCTT	1286	
Db	1551	CATAGAAGAAAGCCCTTCCAAAGAGCCAAAGCCCTGTGGCTTAAACAATAAAGAGCGTTT	1610	
Qy	1287	CCGSCCTCGCTCGCCCTCAAAAGTTCTCAGCCAAACCAAGTATAGATGCTGCACAGC	1346	
Db	1611	CCGACCGCTTCCGCATGAAGCCTAGCTTCTTGGCAGAGWTCTGAAGATGCTGGGAC	1570	
Qy	1347	CTTTGGCACTGATGATGATATGATGATGA AAAAGAGTGCAGTGTGATGATCACTGGAA GA	1406	
Db	1671	AGGCGACCCCATGGCAGAA-----GACAGGGGCTATGGGAATGACWTCCTCATGTGAGA	1724	
Qy	1407	CCTCACCCACCACCTTAAAACTGTCATTTCAGCTATCAGAAATATGAAATTTTCATGTTCG	1466	
Db	1725	CATGATCCCTRCCTWAAGGTGCCATCCGAGCTGTCAGAAATTTCTCAGHTCCGTCATYA	1784	
Qy	1467	AAAA CGGAAGTTAAGGAAA CGTTACGTCCATATGATGTAAAAAGATGTCTATTGAA CAATA	1526	
Db	1785	TAAAAAAAAGTTCAAGGAGACGTTGAGGCCCTTATGATGTGAAAAAGTGTGATTGAGCAGTA	1844	
Qy	1527	TTCTGCTGGTCACTCGACATGTTGTGTAGAATTTAAAGCCCTTCAACACGCTGTTGATCA	1586	
Db	1845	TTCGGCCGGA CACTTGACATGCTTTCCAGGATAAAGTACCTTACAGACAAGATYAGATAT	1904	
Qy	1587	AATTC T 1592		
Db	1905	GATTTT 1910		

RESULT 15

US-09-105-058C-19
; Sequence 19, Application US/09105058C

; Patent No. 6403360

GENERAL INFORMATION:
 APPLICANT: Blonar, Michael A.
 APPLICANT: Dworetzky, Steven
 APPLICANT: Gribkoff, Valentin K
 APPLICANT: Levesque, Paul C.
 APPLICANT: Little, Wayne A.
 APPLICANT: Neubauer, Michael G.

APPLICANT: Yang, Wen-Pin
TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

FILE REFERENCE: 3053-4052

; CURRENT APPLICATION NUMBER: US/0

; CURRENT FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 60/055,599
 ; PRIOR FILING DATE: 1997-09-12

; PRIOR FILING DATE: 1997-
 : NUMBER OF SEQ ID NOS: 28

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; NUMBER OF SEQ ID NOS: 28
: SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 19

; LENGTH: 3287

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; TYPE: DNA

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; ORGANISM: Homo sapiens

US-09-105-058C-19

Query Match 15.9%; Score 425; DB 3; Length 3287;

Best Local Similarity 64.7%; Pred. No. 1.2e-118; Matches 632; Conservative 0; Mismatches 345; Indels 0; Gaps 0;	
QY	64 GGCCTGCTATCTGCTGGGCAACCCGCGGGCCACGCTTTGTGTGGCGCGCGGTGGCCCTGAGG 123
Db	127 GGCCTGCTGGGCTGGACCCCGCGCGCCGACTCCACCCGGACGCGGGCGCTGCTGATC 186
QY	124 GAGAGCCGCGGGCAAGCAGGGGGCCGGATGAGCCTGTGTGGGAAGCGCTCTCTTAC 183
Db	187 GC CGGCTCCAGAGCCCCCAAGCGCGGAGCATCTCAGCAAACTCCGCGGGCGCGCG 246
QY	184 ACGAGTAGCCAGAGCTGCGCGGCCCAACGTCACAGTACCGGGGTGACAGAACTACCTGTATC 243
Db	247 GGC CGGGGAAGCCCCCAAGCGCAAGCCTTCTACGCGAAGCTGCAGAAATTTCTCTAC 306
QY	244 AAGCTGTGTGAGAGACCCCGCGGCTGGGCTTCATCTACACGCTTTGTTTTTCTCTT 303
Db	307 AACGTGTGTGAGGGCGCGCGCTGGGCTTCATCTACACGCCCTACGTTGTTCCTCCTG 366
QY	304 GTCTTTTGTTGCTTGATTTTGTACAGTGTCTTCTACCATCCCTGAGCACACAAATTTGGCC 363
Db	367 GTTTTCTTCGCTCGTGCTGTCTGTGTTTTTCCACCATCAGAGAGTATGAGAAGACTCG 426
QY	364 TCAAGTTGCCCTCTGATCTCTGGAGTTCGTGATGATGTGCTCTTTGGTTGGAGTTCAATC 423
Db	427 GAGGGGCCCTCTACATCTCTGAAATCGTACTATCGTGTGTGTGCGGTGGAGTACTTTC 486
QY	424 ATTCGAATCTGTTCTGGGCTGCTGTGTGTCGATATAGAGGATGGCAAGAACACTGAGG 483
Db	487 GTGCGGATCTGGGGCGAGGCTCTGCTGCCGCTACCGTGGCTGGAGGGGGCGGCTCAAG 546
QY	484 TTTGCTCGAAAGCCCTTCTGTTTATAGATPACATTTGTTCTTATCGCTTCAATPAGAGTT 543
Db	547 TTTGCCCGGAAAACGTTCTCTGTGATTGACATCATGCTGTCTATCGCTCCATTTGCGGTG 606
QY	544 GTTCTTGCAAAACTCAGGTTATATTTTGGCCACTCTGCACCTCAGAGTCTCCGTTTC 603
Db	607 CTGGCGCCCGGCTCCAGGGCAACGCTTTTGGCACATCTGCGCTCCGGAGCTTCGCGCTTC 656
QY	604 CTACAGATCCTCGCATGTGTGCGCATGGACCGAAGGGGAGGCACTTGGAAAATTACTGGGT 663
Db	667 CTGCAGATCTCGGATGATCCGATGGACCGCGGGGAGGCACCTGGAAGCTGCTGGGC 726
QY	664 TCAGTGTTTATGCTCACAGCAGGAATTAATCACAGCTTGGTACATAGGATTTTGGTT 723
Db	727 TCTGTGCTATGCCCAACAGCAGGAGCTGGTCACTGCTGTGTACATCGGCTTCTCTTGT 786
QY	724 CTTATTTTTTCTGTTTCTTGTCTATCTGTGTGGAAAAGGATGCCCAATTAAGAGTTTCT 783
Db	787 CTATCTCGGCTCGTTCCTGTTGTACTTGGCAGAGAGGGGAGAACGCCACTTTGAC 846
QY	784 ACATATGCAATGCTCTCTGGTGGGCACAATTAATTCAGAACTATTTGCTATGAGAC 843
Db	847 ACCTACCGGATGCACTCTGTGGGGCTGATCACGCTGACCAACATGGTATCGGACGGGAC 906
QY	844 AAAACTCCCCTAACTTGGCTGGGAAGATTGCTTTCTGAGGCTTTGCACCTCTTGGCATT 903
Db	907 AAGTACCCCGAGCTGTGAACGCGAGGCTCCTTGGCGCAACTTTCACCTCATCGGTGTC 966
QY	904 TCTTTCTTTGCACTTCTGTCGGGCACTCTTGGCTCAGGTTTGGCATTTAAAGTACAGAA 963
Db	967 TCTTCTCTCGGCTGCTGTCAGGCATCTTGGGGTCTGGGTTTGGCCCTGAAGTTCCAGGAG 1026
QY	964 CAACACCGCAGAAAACATTTTGAAGAAAAGAGAAACCCAGCTCCCAACCTCATTCAGTGT 1023
Db	1027 CAGCACAGGCAGAGCACTTTTGAAGAGAGCGGAAACCCCGCAGCAGGCTGATCCAGTCG 1086
QY	1024 GTTTGGCGTAGTTACGC 1040
Db	1087 GCCTGGAGATTTTACGC 1103

Search completed: April 11, 2005, 21:46:39

Job time : 441.362 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:10:31 ; Search time 13197.7 Seconds
(without alignments)
9791.866 Million cell updates/sec

Title: US-09-810-796-3

Perfect score: 2667

Sequence: 1 atgaaggatgtggagtcggg.....ctcatgtcaactgaaataa 2667

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pt.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2662.2	99.8	2772	6	AR565635 Sequence
2	2662.2	99.8	2772	6	AX268474 Sequence
3	2662.2	99.8	3111	6	AR565636 Sequence
4	2662.2	99.8	3111	6	AX268476 Sequence
5	2630	98.6	2694	6	AX322509 Sequence
6	2625.2	98.4	3137	6	AR430568 Sequence
7	2625.2	98.4	3137	6	AX056817 Sequence
8	2617.2	98.1	3074	6	AF202977 Homo sapi
9	2617.2	98.1	3074	6	AR393778 Sequence
10	2617.2	98.1	3074	6	AX253254 Sequence
11	2617.2	98.1	3074	6	AX456864 Sequence
12	2617.2	98.1	3074	9	AF249278 Homo sapi
13	2521	94.5	3718	6	BD275572 Novel Hum
14	2507.6	94.0	2832	9	AF263835 Homo sapi
15	2155	80.8	3108	10	AF263836 Mus muscu
16	1548.8	58.1	1552	6	CQ720576 Sequence
17	1115.8	41.8	1508	9	BC050689 Homo sapi
18	963.4	36.1	1691	9	AF272519 Homo sapi
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22	843.4	31.6	200585	2	AC146636	Otolemur
23	843.4	31.6	202246	2	AC146646	Otolemur
24	841.8	31.6	148254	2	AC151566	Dasyypus n
c 25	767.6	28.8	161759	10	AC115920	Mus muscu
c 26	764.4	28.7	212732	10	AC095904	Rattus no
27	492	18.4	2335	6	AX032994	Sequence
28	492	18.4	2335	6	AX456863	Sequence
29	492	18.4	2335	9	AF105202	Homo sapi
30	489.2	18.3	2273	6	AR216936	Sequence
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32	485.2	18.2	2827	10	AB000497	Mus muscu
33	475.6	17.8	2169	6	AR213255	Sequence
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ALIGNMENTS

RESULT 1
AR565635
LOCUS AR565635 2772 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6767736.
ACCESSION AR565635
VERSION AR565635.1 GI:53981668
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2772)
AUTHORS Hu, Y., Kieke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G.,
Zambrowicz, B., and Sands, A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;
FEATURES Location/Qualifiers
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/organism="unknown"
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Db	166	GACGGCTGTCTACTGCTGGGCACCCGGCGGCCACGCTTGTGGCGGCGGGTGGCCTG 225		
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Qy	181	TACACGAGTACGAGCTGCCGGCAAGCTCAAGTACCGCGGGTGCAGAACTACCTG 240		
Db	286	TACACGAGTACGAGCTGCCGGCAAGCTCAAGTACCGCGGGTGCAGAACTACCTG 345		
Qy	241	TACAACGTGTGGAGAGAGACCCCGGGCTGGCGGCTTCATCTACCAACGCTTTCGTTTCTC 300		


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QY 2581 ACTGGAAGTCAAGATCATCTCAGAGCATTTCTAAGGACGAGGAAGTACAGATGCCCTC 2640
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Db 2746 AGCTTGCCCTCATGTCAAACTGAAATAA 2772

RESULT 2
AX268474
LOCUS AX268474 2772 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Hu,Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source 1..2772
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN
Query Match 99.8%; Score 2662.2; DB 6; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 106 ATGAAGGATGTGGAGTCGGGCGCGGCGAGGTGCTGAACTCGGACGCCCGCAGGGGC 165
QY 61 GACGCGCTGCTACTCTGGGACCCCGCGGCCACGCTTGTGGCGCGCGGTGGCCTG 120
Db 166 GACGCGCTGCTACTCTGGGACCCCGCGGCCACGCTTGTGGCGCGCGGTGGCCTG 225
QY 121 AGGAGAGCGCGCGGCGGCAAGCAGGCGGCGCGGATGAGCTCTCTGGGAAAGCGCTCT 180
Db 226 AGGAGAGCGCGCGGCGGCAAGCAGGCGGCGCGGATGAGCTCTCTGGGAAAGCGCTCT 285
QY 191 TACAGAGTACGAGCTGCGCGGCGCAACGTCAGAGTACCGGCGGCGGAGCACTACCTG 240
Db 286 TACAGAGTACGAGCTGCGCGGCGCAACGTCAGAGTACCGGCGGCGGAGCACTACCTG 345
QY 241 TACAAGTGTGGAGAGACCCCGCGCTGGGGTTTCATCTACCGCTTTTGTGTTTTCTC 300
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QY 301 CTGTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
Db 406 CTGTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 465
QY 361 GCCTCAAGTGTGCTCTTGATCTGAGTTCGATGATGATGATGATGATGATGATGATGATG 420
Db 466 GCCTCAAGTGTGCTCTTGATCTGAGTTCGATGATGATGATGATGATGATGATGATGATG 525
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QY 721 GTTCTTATTTTTCGTCTTTCTGTTCTATCTGTTGGAAAGGATGCCAATAAAGAGTTT 780
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QY 1441 ATCAGATTAAGAAATTTTCATGTTGCAAAAACGGAAGTTTAAAGAAACGTTAGTCCATAT 1500
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Qy	721	GTTCTTATTTTTTTCGCTCTTTCTCTATCTCGTGGAAAAGGATGCCAATAAAGAGTTT	780
Db	885	GTTCTTATTTTTTTCGCTCTTTCTCTATCTCGTGGAAAAGGATGCCAATAAAGAGTTT	944
Qy	781	TCTACATATGAGATGCTCTCTGTGGGGGCAAAATACATATGACAACTATTTGGCTATGGA	840
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Qy	841	GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACCTTTGGC	900
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Qy	901	ATTTCTTTCTTTTGCACTTCTCTGCCGCAATCTCTGGCTCAGGTTTTTGATTAAGAATCAAA	960
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Db	1185	TGTGTTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTTCCATTGGCAACTGGAAGCCA	1244
Qy	1081	CACTTGAAGGCTTTGCACACCTGCAGGCCCTACCAATCAGAAGCTTAAGTTTTAAGGAGCGA	1140
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Qy	1141	GTGCGCATGCTAGCCCCAGGGGCCAGATTAATGAAGCCGACAAAGCCTCAGTAGGTGAC	1200
Db	1305	GTGCGCATGCTAGCCCCAGGGGCCAGATTAATGAAGCCGACAAAGCCTCAGTAGGTGAC	1364
Qy	1201	AGGAGGTCCCCAGACCGACATCAGCCGAGGGGAGTCCCACCAAGTGCAGAGAGC	1260
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Qy	1381	TGCCAGTGTGATGATCAGTGGGAAGACCTCACCCCACTTAAACCTGTCATTCGAGCT	1440
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Db	1785	AAGAGCCGAGAAAAATAACAGCAGAAACATGAGACACAGACCATCTCAGTATGCTCGGT	1844
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Db	1845		CGGATGGCTCAAGGTTCGAAAAACAGGTACAGTCCATAGAATCCAAGCTGGACTGCCTCACTA	1904
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Qy	2341	GACTTGGGCAAAATCTTTTGTCTGTGC AAAACCTGATCAGGTCGACCGAGGAACTGAAATATA	2400	
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Qy	2581	ACTTGAAGGTCACGATCATCTCAGACGATTTGTAAAGCAGGAGAAAGTACAGATGCCCTC	2640	
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RESULT 4
AX268476
LOCUS
DEFINITI
ACCESSION

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QY 601 TTCTTACAGATCCTCGCATGTGCGCATGACCGAAGGGGAGCCTTGGAAATTAAGT 660
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VERSION AR393778.1 GI:40120748
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ORGANISM Unknown.
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AUTHORS Steinmeyer,K., Ierche,C., Scherer,C., Seebom,G. and Busch,A.E.
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AX253254	DEFINITION	Sequence 1 from Patent WO01/70811.	
AX253254	ACCESSION		
AX253254.1	VERSION	GI:16073802	
AX253254.1	KEYWORDS		
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AX253254.1	ORGANISM		
AX253254.1	REFERENCE		
AX253254.1	AUTHORS		
AX253254.1	TITLE		
AX253254.1	JOURNAL		

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RESULT 12
AF249278 3074 bp mRNA linear PRI 02-AUG-2000
LOCUS Homo sapiens voltage-gated potassium channel (KCNQ5) mRNA, complete cds.
ACCESSION AF249278
VERSION AF249278.1 GI:9651966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lerche, C., Scherer, C.R., Seebom, G., Derst, C., Wei, A.D., Busch, A.E.
TITLE Molecular cloning and functional expression of KCNQ5, a potassium channel subunit that may contribute to neuronal M-current diversity
J. Biol. Chem. 275 (29), 22395-22400 (2000)
PUBMED 10787416
REFERENCE
AUTHORS Lerche, C., Scherer, C.R., Seebom, G., Derst, C., Wei, A.D., Busch, A.E.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany
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ORIGIN									
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QY	61	GACGCGCTCTACTGCTGGGACACCGCGCGCCACGCTTGGTGGCGGGCGGTGGCGCTG	120						
DB	275	GACGCGCTCTACTGCTGGGACACCGCGCGCCACGCTTGGTGGCGGGCGGTGGCGCTG	334						
QY	121	AGGGAGAGCGCGCGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAAGCCGCTCTCT	180						
DB	335	AGGGAGAGCGCGCGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAAGCCGCTCTCT	394						
QY	181	TACACGAGTAGCAGAGCTGCGGCGCAACGTCAGTACCGCGGGGTGCAGAACTACTG	240						
DB	395	TACACGAGTAGCAGAGCTGCGGCGCAACGTCAGTACCGCGGGGTGCAGAACTACTG	454						
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DB	455	TACACGAGTAGCAGAGCGCGCGCTGGGGTTCATCTACCGCTTTCGTTTTC	514						
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Db	2195	GAGTTCAAGTCCAGACTTTTACGGCTTTAGCCCTTACTATGCACAGTCAAGCAACACAG	2254
QY	2014	GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGGAGCCACCAACCAATTGCAACCAA	2073
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QY	2134	GCCATCAAGCATCTGCCAGGCCAGAACTCTGCAACCCCTAACCCCTGCAGGCTTACAGGAA	2193
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Db	2615	ATCAGGTGCAACGAGAACTGAATATACAACTTTGAGGAGTGAAGTGGCTCCAGA	2674
QY	2434	GSCAGCAAGATTTTACCCCAATGGAGGAAATCCAAATGTTTATTAACATGATCAAG	2493
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QY	2494	GTGGGTCCCGAAGACAGACAGACACTTTTGTATGCCGACCCGACCTGCCAGGGAA	2553
Db	2735	GTGGGTCCCGAAGACAGACAGACACTTTTGTATGCCGACCCGACCTGCCAGGGAA	2794
QY	2554	GCTGCTTTGCATCAGACTCTCTAAGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT	2613
Db	2795	GCTGCTTTGCATCAGACTCTCTAAGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT	2854
QY	2614	AGGCGAGGAGAACTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA	2667
Db	2855	AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA	2908

RESULT 13
BD275572
LOCUS BD275572 3718 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Human Voltage-Gated Potassium Channel.
ACCESSION BD275572
VERSION BD275572.1 GI:33085340
KEYWORDS JP 2002543768-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1	(bases 1 to 3718)
AUTHORS	Metzker, M. L., Li, W., Petrukhin, K. and Caskey, T. C.	
TITLE	Novel Human Voltage-Gated Potassium Channel	
JOURNAL	Patent: JP 2002543768-A 2 24-DEC-2002;	
COMMENT	Merck and Co Inc	
OS	Homo Sapiens	
PN	JP 2002543768-A/2	
PD	24-DEC-2002	
PF	10-APR-2000 JP 2000611548	
PR	14-APR-1999 US 60/129274	
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QY	334	TCTACCATCCCTGAGCACACAAAATGGCTTCAAGTTGCCTCTTGATCCTGGAGTTCGTG 393
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Db	1938	GGCTGTCAGTTCAATCTTGACGCCAAATGAGTTTCAGTGCACCAGACTTTTCTACGCGCTTAGC	1997
Qy	1987	CTTACTATGCACTAGTCAAGCAACACAGGTGCGCAATTTAGTCAAAAGCATGGCTCAGCAGTG	2046
Db	1998	CTTACTATGCACTAGTCAAGCAACACAGGTGCGCAATTTAGTCAAAAGCATGGCTCAGCAGTG	2057
Qy	2047	GCAGCCACCAACACCATTTGCAAAACCAAAATAATACGCGACCCCAAGCGAGCAGCGCCCAACA	2106
Db	2058	GCAGCCACCAACACCATTTGCAAAACCAAAATAATACGCGACCCCAAGCGAGCAGCGCCCAACA	2117
Qy	2107	ACTTTACAGATCCCACTCTCTCCAGGCCATCAAGCATCTGCGCCAGGCGCAGAAACTCTG	2166
Db	2118	ACTTTACAGATCCCACTCTCTCCAGGCCATCAAGCATCTGCGCCAGGCGCAGAAACTCTG	2177
Qy	2167	CACCTTAACCTCTGAGCGTTACAGGAAGCAATTTCTGACGTCAACCTGCTTGTGGC	2226
Db	2178	CACCTTAACCTCTGAGCGTTACAGGAAGCAATTTCTGACGTCAACCTGCTTGTGGC	2237
Qy	2227	TCCAAGGAAAAATGTTTCAGGTTCACAGCTCAAAATCTCACCAAGGACCGTTCTATGAGGAAA	2286
Db	2238	TCCAAGGAAAAATGTTTCAGGTTCACAGCTCAAAATCTCACCAAGGACCGTTCTATGAGGAAA	2297
Qy	2287	AGCTTTGCACATGGGAGGAGAAACTCTGTTGTTCTGTCTGTGCCATGTGCGCAAGGACTTG	2346
Db	2298	AGCTTTGCACATGGGAGGAGAAACTCTGTTGTTCTGTCTGTGCCATGTGCGCAAGGACTTG	2357
Qy	2347	GGCAAAATCTTTGTTCTGTGCAAAACCTGATCAGGTTCGACCGAGGAACCTGAATATACAAT	2406
Db	2358	GGCAAAATCTTTGTTCTGTGCAAAACCTGATCAGGTTCGACCGAGGAACCTGAATATACAAT	2417
Qy	2407	TCAGGAGTTCAGTCAAGTGGCTCCAGAGGCGACCAAGATTTTACCCCAATGGAGGGAA	2466
Db	2418	TCAGGAGTTCAGTCAAGTGGCTCCAGAGGCGACCAAGATTTTACCCCAATGGAGGGAA	2477
Qy	2467	TCCAAATGTTTATAACTGATGAAGAGGTGGGTCCGAGAGACAGAGACAGACACTTTT	2526
Db	2478	TCCAAATGTTTATAACTGATGAAGAGGTGGGTCCGAGAGACAGAGACAGACACTTTT	2537
Qy	2527	GATGCGGACCGGACCTGCGAGGAGTGCCTTTTCATCAGACTCTCTAAGGACTGGA	2586
Db	2538	GATGCGGACCGGACCTGCGAGGAGTGCCTTTTCATCAGACTCTCTAAGGACTGGA	2597
Qy	2587	AGGTTCAGATCATCTCAGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTG	2646
Db	2598	AGGTTCAGATCATCTCAGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTG	2657
Qy	2647	CCTCATGTCAAACTGAAATAA	2667
Db	2658	CCTCATGTCAAACTGAAATAA	2678
RESULT 14			
LOCUS	AF263835	2832 bp	linear
DEFINITION	Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA,		PRI 01-JUN-2000
ACCESSION	AF263835		
VERSION	AF263835.1		
KEYWORDS	GI:8132996		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 2832)		
JOURNAL	Kntazeva,M. and Han,M.		
REFERENCE	A new gene of the voltage-gated potassium channel KCNQ family,		
	KCNQ5 is a candidate gene for retinal disorders		
	Unpublished		
	2 (bases 1 to 2832)		

AUTHORS Kniazeva, M. and Han, M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2000) MDCB, University of Colorado at Boulder,
Porter Biosciences Bldg., Boulder, CO 80309, USA
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 94.0%; Score 2507.6; DB 9; Length 2832;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 2550; Conservative 0; Mismatches 9; Indels 27; Gaps 1;
Qy 109 GCGGTGCGCTGAGGAGAGCGCGCGGCGCAAGCAGGCGGCGCGGATGAGCTGTGCGG 168
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Qy 169 AAGCGCTCTTACACAGTAGCAGAGCTGCGCGGCGCAAGCTCAAGTACGCGGGGTG 228
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Qy 229 CAGAACTACCTGTACACAGTGTGAGAGAGCCCGCGGCTGGCGTTCATCTACACGCT 288
Db 121 CAGAACTACCTGTACACAGTGTGAGAGAGCCCGCGGCTGGCGTTCATCTACACGCT 180
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Qy 469 CAAGGAGACTGAGTGTTCGTCGAAAGCCCTTCTGTGTATAGATACCATTTGTTTATC 528
Db 361 CAAGGAGACTGAGTGTTCGTCGAAAGCCCTTGTGTGTATAGATACCATTTGTTTATC 420
Qy 529 GCTTCAATAGCAGTTGTTCTGCAAAAACCTCAGGTAATATTTTTGGCACGCTGCACTC 588
Db 1501 GATCAAAATTTCTTGAAAAAGGGCAAAATCACATCAGATTAAGAGCCGAGAGAAAAAACA 1560

Db 421 GCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGTAATATTTTTGGCACGCTGCACTC 480
Qy 589 AGAAGTCTCCGTTTCCCTACAGATCTCCGCGATGGTCCGATGAGCCGAGGGGAGGCACT 648
Db 481 AGAAGTCTCCGTTTCCCTACAGATCTCCGCGATGGTCCGATGAGCCGAGGGGAGGCACT 540
Qy 649 TGGAAATTTACTTGGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTAC 708
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Qy 709 ATAGGATTTTGGTTCCTTATTTTTCGTTCTCTGTTCTCTGTTCTGTTGGAAGGATGCC 768
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Db 1141 ATCACAGCGAGGCGAGTCCCAACAAAGTGACAGAGCTGGAGCTTCAACAGACCGAAC 1200
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Qy 1582 GATCAAAATTTCTGGAAGGGCAAAATCACATCAGATTAAGAGCCGAGAGAAAAAACA 1641
Db 1501 GATCAAAATTTCTGGAAGGGCAAAATCACATCAGATTAAGAGCCGAGAGAAAAAACA 1560

Qy	1642	GCAGAA	CATGAGAC	CCACAGACGATCTCAGTATGCTCGGTCCGGTGGTCAAGGTTGAAAAA	1701
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Qy	1702	CAGGTACAGTCCATAGAGTCCAAAGCTGGACTGCTCTACTAGACATCTATCAACAGGTCCCTT	1761		
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Qy	1762	CGGAAAGGCTCTGCCTCAGCCCTCGCTTTTGGCTTTCATTTCCAGATCCCACTTTTGAATGT	1821		
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Qy	1882	AAACAGTGGCTGCTTATCCAGATCAACTAGTGCACCACTTCTACGAGAGGCTTCGACAGTTCATTT	1941		
Db	1801	AAACAGTGGCTGCTTATCCAGATCAACTAGTGCACCACTTCTACGAGAGGCTTCGACAGTTCATTT	1860		
Qy	1942	CTGACGCCAAATGAGTTTCAGTGCCCAAGCTTTCTTACGCGCTTACGCCCTACTATGACACAGT	2001		
Db	1861	CTGACGCCAAATGAGTTTCAGTGCCCAAGCTTTCTTACGCGCTTACGCCCTACTATGACACAGT	1920		
Qy	2002	CACAGCACAGAGTGCCTTCTAGTCAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACC	2061		
Db	1921	CACAGCACAGAGTGCCTTCTAGTCAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACC	1980		
Qy	2062	ATTGCAAAACAAATAAATACGGCACCCAAAGCCAGCAGCCCCCAACACTTTTACAGATCCCA	2121		
Db	1981	ATTGCAAAACAAATAAATACGGCACCCAAAGCCAGCAGCCCCCAACACTTTTACAGATCCCA	2040		
Qy	2122	CCTCCTCTCCGAGCCATCAAGCATCTCGCCAGGCCAGAAACTCTGACACCTTACCCCTGCA	2181		
Db	2041	CCTCCTCTCCGAGCCATCAAGCATCTCGCCAGGCCAGAAACTCTGACACCTTACCCCTGCA	2100		
Qy	2182	GGCTTACAGAAAGACATTTCTGACGTCAACCACTGCCCTTGTGCGCTCCAAAGGAAAAATGTT	2241		
Db	2101	GGCTTACAGAAAGACATTTCTGACGTCAACCACTGCCCTTGTGCGCTCCAAAGGAAAAATGTT	2160		
Qy	2242	CAGGTTGCACAGTCAAAATCTCAACCAAGACGGTCTATGAGGAAAAAGCTTTGACATGGGA	2301		
Db	2161	CAGGTTGCACAGTCAAAATCTCAACCAAGACGGTCTATGAGGAAAAAGCTTTGACATGGGA	2220		
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Qy	2482	ACTGATGAAGAGGTGGGTCCCGAAGAGACAGACAGACATTTTGTATGCCGACCGCAG	2541		
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Qy	2542	CCTGCCAGGGAAGCTGCGTTTGGCATCAGACTCTCTAAGGACTGGAAAGGTCAACGATCATCT	2601		
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Db	2521	CAGAGCATTTTGAAGGACAGGAGAAAGTACAGATGCCCTCAGCTTGGCTCATGTCAAACTG	2580		
Qy	2662	AAATAA	2667		
Db	2581	AAATAA	2586		

RESULT 15	AF263836	3108 bp	mRNA	linear	ROD 01-JUN-2000
LOCUS	Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,				
DEFINITION	partial cds.				
ACCESSION	AF263836				
VERSION	AF263836.1	GI:8132998			
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 3108)				
TITLE	Kniazeva,M. and Han,M.				
COMMENT	A new gene of the voltage-gated potassium channel KCNQ family. KCNQ5, is a candidate gene for retinal disorders				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3108)				
AUTHORS	Kniazeva,M. and Han,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder, Porter Biosciences Bldg., Boulder, CO 80309, USA				
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QY	177	CTCTTTACACAGTAGTACGAGAGCTGCCGGCGCAACGTCACAGTACCGCGGGTGCAGAACTA 236			

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Qy 1770 CTCTGCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTGATGTGAACAGAC 1829
Db 1741 CTCTGCTCAGCCCTCCTCTGGCATCTTTCAGATCCCGCTTTTGAATGTGAACAGAC 1800
Qy 1830 ATCTGACTATCAAGCCCTGAGATAGCAAGATCTTTTCGGGTTCCGACAAAACAGTGG 1889
Db 1801 CTCTGACTATCAAGTCTCTGGATAGCAAGACCTGTCTGGCTCAGCACAAAACAGCGG 1860
Qy 1890 CTGCTTATCCAGATCAACTAGTGCACATCTCGAGAGCTCGAGTTCATTCTGACGCC 1949
Db 1861 CTGTTTAAAGAGGTGAGCTGAGTGCACATCTCAAGAGGCTGAGTTCATCTTAAACACC 1920
Qy 1950 AAATGAGTTCAGTCCAGACTTCTAGCGCTTAGCCCTACTATGACAGTCAAGCAAC 2009
Db 1921 AAATGAGTTCAGTCTCAGACTTCTATGCGCTTAGCCCTACTATGACAGCCCAAGCTAC 1980
Qy 2010 ACAGTGCCTAATTAGTCAAGCGATGCTCAGCAGTGCAGCCACCAACCATTTGCAAA 2069
Db 1981 CCAGGTACCATGAGTCAAAATGACGCTCTCGTGTAGTCCACCAATTAATCAATTGCAAA 2040
Qy 2070 CCAATAAATAACGGCACCCCAAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCT 2129
Db 2041 CCAATAAAGCGCGCACCCCAAGCAGCAGCCCAACAACTTTACAGATCCCTCTCTCT 2100
Qy 2130 CCAAGCATCAAGCATCTGCCAGGCGAGAACTCTGCAACCTAAACCTGAGGCTTACA 2189
Db 2101 CTGCGCCATCAAGCATCTGTCAGGCGCAGAACCTCTGCTCTCAAAACCCCAAGCTTACA 2160
Qy 2190 GGAAGCATTTCTCAGCTCACCCTGCTTGTGCTTCCGCTCAAGGAAATGTTGAGTTGC 2249
Db 2161 AGAGATATTTCTGATGTACCATCTGCTTGTGCTTCCAGGAAAGTGTTCAGTTGC 2220
Qy 2250 ACAGTCAAAATCTCAAGGACCGTTCATGAGGAAAGCTTTGACATGGAGGAGAAAC 2309
Db 2221 ACAGTCAAACTGACCAAGGACCGTTCCTCGAGGAAAGTTTCGACATGGAGGAGAAAC 2280
Qy 2310 TCTGTTGTCGTCTGTCCTGAGGAGGACTTGGGCAATCTTTGCTGTGCAAAA 2369
Db 2281 TCTGTTGTCGTCTGTCCTGAGGAGGATTTGGGCAATCTCTGCTGTCTGTACAAA 2340

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 08:07:42 ; Search time 1365.59 Seconds
(without alignments)
11561.287 Million cell updates/sec

Title: US-09-810-796-3
Perfect score: 2667
Sequence: 1 atgaagatgtggatcgagg.....ctcatgtcaactgaataa 2667

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2667	100.0	2667	4	AAS14653 Human CDN
2	2662.2	99.8	2772	5	AAS14653 Human ion
3	2662.2	99.8	3111	5	AAS14653 Human ion
4	2630	98.6	2694	4	AAS14652 Human CDN
5	2630	98.6	2694	6	AAS14652 Human pot
6	2626.4	98.5	3071	4	AAS14651 Human CDN
7	2625.2	98.4	3137	4	AAS14651 Human CDN
8	2617.2	98.1	3074	4	AAS14651 Human CDN
9	2615.6	98.1	3074	10	AAS14651 Human pot
10	2521	94.5	3718	3	AAS14651 Human KCN
11	963.4	36.1	125910	3	AAS14651 Human KCN
12	509.8	19.1	582	8	AAS14651 Human KCN
13	492	18.4	2335	3	AAS14651 Human KCN
14	492	18.4	2335	10	AAS14651 Human KCN
15	489.2	18.3	2273	2	AAS14651 Human KCN
16	475.6	17.8	2169	2	AAS14651 Human KCN
17	472.2	17.7	7407	10	AAS14651 Human KCN
18	472.2	17.7	7407	10	AAS14651 Human KCN
19	472.2	17.7	7407	10	AAS14651 Human KCN
20	472.2	17.7	7407	10	AAS14651 Human KCN

21	472.2	17.7	7411	10	ADD29557 Human tum
22	472.2	17.7	7420	11	ADN38963 Cancer/an
23	472.2	17.7	7420	11	ADP65810 Human mRN
24	472.2	17.7	7420	11	ADP65731 Human pot
25	472.2	17.7	7420	12	ADL06495 Human tum
26	472.2	17.7	7863	10	ADJ56529 Human CDN
27	470.6	17.6	7407	10	ADB78685 Human pot
28	465	17.4	548	6	ABA90234 Human ORF
29	452.2	17.0	7413	5	AAS74832 DNA encod
30	452	16.9	575	8	ACA04857 cDNA enco
31	447	16.8	2565	2	AAS81548 Human bra
32	447	16.8	3195	5	AAS74831 DNA encod
33	445.2	16.7	5595	13	ADS17851 Rattus no
34	436.6	16.4	3029	2	AAS81547 Human bra
35	427.4	16.0	1848	12	ADH51119 Potassium
36	427.4	16.0	1848	12	ADM77995 KCNQ2-15b
37	427.2	16.0	2565	2	AAS26596 Nucleotid
38	427.2	16.0	2914	2	AAS57059 Human KCN
39	427.2	16.0	2926	10	ADB78690 Human pot
40	427.2	16.0	2926	10	ADB78682 Human pot
41	427.2	16.0	2926	10	ADB78691 Human pot
42	426.8	16.0	2814	2	AAS57141 Mouse KCN
43	425.6	16.0	2926	10	ADB78689 Human pot
44	425.4	16.0	2766	13	ADS17849 Rattus no
45	425	15.9	3287	2	AAS26587 Nucleotid

ALIGNMENTS

RESULT 1
AAS14653
ID AAS14653 standard; cDNA; 2667 BP.
AC AAS14653;
XX
DT 18-DEC-2001 (first entry)
XX Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.
XX Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..2967
FT /*tag= a
FT /product= "hKCNQ5-2"
XX
XX WO200170759-A1.
XX
XX 27-SEP-2001.
XX
XX 20-MAR-2001; 2001WO-US009328.
XX
XX 21-MAR-2000; 2000US-0190954P.
XX (ICAG-) ICAGEN INC.
XX Jegla TJ;
XX
XX WPI; 2001-611467/70.
XX P-PSDB; AAU09021.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximately a- subunits.
XX
XX Claim 5; Page 63-64; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states. is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2
XX
SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;
Query Match 100.0%; Score 2667; DB 4; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGATGTGGAGTGGGGCGGGGCGAGGTGCTGCTGAACCTGGCAGCGCGCAGGGGC 60
DB 1 ATGAAGATGTGGAGTGGGGCGGGGCGAGGTGCTGCTGAACCTGGCAGCGCGCAGGGGC 60
QY 61 GACGCGCTGCTACTGCTGGGCAACCGCGCGCCACGCTTGGTGGCGGGCGGTGGGCTG 120
DB 61 GACGCGCTGCTACTGCTGGGCAACCGCGCGCCACGCTTGGTGGCGGGCGGTGGGCTG 120
QY 121 AGGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAGCCGCTCTCT 180
DB 121 AGGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAGCCGCTCTCT 180
QY 181 TACAGAGTGGCAGCTGCGCGGCAACGCTCAAGTACCGGCGGTGCAGAACTACCTG 240
DB 181 TACAGAGTGGCAGCTGCGCGGCAACGCTCAAGTACCGGCGGTGCAGAACTACCTG 240
QY 241 TACAACTGCTGGAGAGACCCCGCGGCTGGGCGTTTCACTACCAAGCTTTCGTTTTCTC 300
DB 241 TACAACTGCTGGAGAGACCCCGCGGCTGGGCGTTTCACTACCAAGCTTTCGTTTTCTC 300
QY 301 CTGTGCTTTGGTGTGATTTGTGAGTTTGTGAGTTTGTGATTTGTGATTTGTGAGTTT 360
DB 301 CTGTGCTTTGGTGTGATTTGTGAGTTTGTGAGTTTGTGATTTGTGAGTTTGTGAGTTT 360
QY 361 GCTCAAGTGGCTCTGATCTGAGTTTGTGAGTTTGTGATTTGTGATTTGTGAGTTT 420
DB 361 GCTCAAGTGGCTCTGATCTGAGTTTGTGAGTTTGTGATTTGTGATTTGTGAGTTT 420
QY 421 ATCAATTCGAATCTGCTGCGGGTTGCTGTTGATATAGAGGATGCAAGGAGACTG 480
DB 421 ATCAATTCGAATCTGCTGCGGGTTGCTGTTGATATAGAGGATGCAAGGAGACTG 480
QY 481 AGTTTGTCTGGAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATCGCTCAATAGCA 540
DB 481 AGTTTGTCTGGAAGCCCTTCTGTGTTATAGATACATTTGTTCTTATCGCTCAATAGCA 540
QY 541 GTTGTCTTCTGCAAAACTCAGGGTAATATTTTGGCAGCTCTGCACTCAGAACTCCGT 600
DB 541 GTTGTCTTCTGCAAAACTCAGGGTAATATTTTGGCAGCTCTGCACTCAGAACTCCGT 600
QY 601 TTCCTACAGATCTCTCGCATGGTGGCCATGGACCGGAGGGGAGGCACTTGGAAATCTG 660
DB 601 TTCCTACAGATCTCTCGCATGGTGGCCATGGACCGGAGGGGAGGCACTTGGAAATCTG 660

QY 661 GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCAAGCTTGTGTACATAGGATTTTG 720
DB 661 GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCAAGCTTGTGTACATAGGATTTTG 720
QY 721 GTTCTTATTTTTCGCTCTTTCTGCTCTATCTGTGTGAAAAAGGATGCCAATAAAGAGTTT 780
DB 721 GTTCTTATTTTTCGCTCTTTCTGCTCTATCTGTGTGAAAAAGGATGCCAATAAAGAGTTT 780
QY 781 TCTACATATGCAAGTGTCTCTGTGGGGGCAATTAATCAATGCAACTATTGGCTATGCA 840
DB 781 TCTACATATGCAAGTGTCTCTGTGGGGGCAATTAATCAATGCAACTATTGGCTATGCA 840
QY 841 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTCTGAGGCTTGTGCACTCTCTGGC 900
DB 841 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTCTGAGGCTTGTGCACTCTCTGGC 900
QY 901 ATTTCTTTTTCGCACTTCTCTGCGGCAATTTGCTCAGTGTTCATTTAAAGTACAA 960
DB 901 ATTTCTTTTTCGCACTTCTCTGCGGCAATTTGCTCAGTGTTCATTTAAAGTACAA 960
QY 961 GAACAAACCGCGCAAGAACACTTTGAGAAAGAGAACCCAGCTGCCAACCTCTATCAG 1020
DB 961 GAACAAACCGCGCAAGAACACTTTGAGAAAGAGAACCCAGCTGCCAACCTCTATCAG 1020
QY 1021 TGTGTTTGGCGTAGTTTACGCACTGATGAGAAATCTGTTTCCATTGCAACCTTGGAGCCA 1080
DB 1021 TGTGTTTGGCGTAGTTTACGCACTGATGAGAAATCTGTTTCCATTGCAACCTTGGAGCCA 1080
QY 1081 CACTTGAAGGCTTGCACACCTTGCAGCCCTACCAATCAGAAGCTAAGTTTAAAGAGCGA 1140
DB 1081 CACTTGAAGGCTTGCACACCTTGCAGCCCTACCAATCAGAAGCTAAGTTTAAAGAGCGA 1140
QY 1141 GTGCGCATGGCTAGCCCGGAGGCGCAGAGTATTAGAGCCGCAAGCCCTCAGTAGGTGAC 1200
DB 1141 GTGCGCATGGCTAGCCCGGAGGCGCAGAGTATTAGAGCCGCAAGCCCTCAGTAGGTGAC 1200
QY 1201 AGAGAGTCCCCAAGACACCGACATCAAGCCGAGGCGAGTCCCACCAAGTGCAGAGAGC 1260
DB 1201 AGAGAGTCCCCAAGACACCGACATCAAGCCGAGGCGAGTCCCACCAAGTGCAGAGAGC 1260
QY 1261 TGAGGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGGGCTCAAAAGTTCTCAGGCCA 1320
DB 1261 TGAGGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGGGCTCAAAAGTTCTCAGGCCA 1320
QY 1321 AAACCACTGATAGATCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGAT 1380
DB 1321 AAACCACTGATAGATCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGAT 1380
QY 1381 TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 ATCAGAAATTAAGAAATTTGATGTTGCAAAACCGAAGTTTAAAGAAACGTTTACGTCATAT 1500
DB 1441 ATCAGAAATTAAGAAATTTGATGTTGCAAAACCGAAGTTTAAAGAAACGTTTACGTCATAT 1500
QY 1501 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 GATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 AAAAGCCCTTCAACACGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 AAAAGCCCTTCAACACGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 AAGAGCCGAGGAGAAATAACAGCAGAACATGAGACCAAGCAGATCTCAGTAGTCTCGGT 1680
DB 1621 AAGAGCCGAGGAGAAATAACAGCAGAACATGAGACCAAGCAGATCTCAGTAGTCTCGGT 1680
QY 1681 CGGTGTGTCAAGGTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGACTGCTCTACTA 1740
DB 1681 CGGTGTGTCAAGGTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGACTGCTCTACTA 1740

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QY 1741 GACATCTATCAACAGGTCTTCGGAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTC 1800
Db |||||
QY 1741 GACATCTATCAACAGGTCTTCGGAAGGCTCTGCTCAGCCCTGCTTGGCTTCATTC 1800
Db |||||
QY 1801 CAGATCCCACTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGATAGCAA 1860
Db |||||
QY 1801 CAGATCCCACTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGATAGCAA 1860
Db |||||
QY 1861 GATCTTTGGGTTTCGCAACAAACAGTGGCTCTTATCCAGATCAACTAGTCCCAACATC 1920
Db |||||
QY 1861 GATCTTTGGGTTTCGCAACAAACAGTGGCTCTTATCCAGATCAACTAGTCCCAACATC 1920
Db |||||
QY 1921 TCGAGAGGCTCAGTTTCTGAGCCAAATGAGTTTCAGTCCCAAGACTTTTACGCG 1980
Db |||||
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Db |||||
QY 1981 CTTAGCCCTACTATGACAGTCAAGCAACACAGAGTGGCAATTAGTCAAGCGATGGCTCA 2040
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QY 1981 CTTAGCCCTACTATGACAGTCAAGCAACACAGAGTGGCAATTAGTCAAGCGATGGCTCA 2040
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Db |||||
QY 2041 GCAGTGGCAGCCCAACCAACATTGCAACCAAAATAATACGGCACCCCAAGCCAGCGC 2100
Db |||||
QY 2101 CCAACAACCTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2160
Db |||||
QY 2101 CCAACAACCTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2160
Db |||||
QY 2161 ACTCTGCACCTTAACCTGCGAGCTTACAGGAAGCAATTTGAGTCAACCTGCTT 2220
Db |||||
QY 2161 ACTCTGCACCTTAACCTGCGAGCTTACAGGAAGCAATTTGAGTCAACCTGCTT 2220
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QY 2221 GTTGCTTCAAGGAAATGTTGAGGTTGCACAGTCAAACTCTCACAAGGACGCTTCTATG 2280
Db |||||
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Db |||||
QY 2281 AGGAAAGCTTTGACATGGAGGAGAACTCTGTTGCTGTCTGCTGCCATGGTCCGAAG 2340
Db |||||
QY 2341 GACTTGGCAATCTTTGCTGTGCAAACTGATCAGTCAACCGAGGAACCTGAATATA 2400
Db |||||
QY 2341 GACTTGGCAATCTTTGCTGTGCAAACTGATCAGTCAACCGAGGAACCTGAATATA 2400
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QY 2401 CAACCTTTAGGAGTGAGTCAAGTGGCTCCAGAGCAGCCAAAGATTTTACCCCAATGG 2460
Db |||||
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QY 2461 AGGGAATCCAAATTTGTTTATACTGATGAAGAGTGGGTCCGGAAGACAGACAGAC 2520
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QY 2521 ACTTTTGTGCGCAGCCGAGCTGCGAGGAGCTGCTTTGCAATCAGACTCTCTAAGG 2580
Db |||||
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QY 2581 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAGGCGAGGAGAAAGTACAGATGCCCTC 2640
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Db |||||
QY 2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db |||||
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Db |||||
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RESULT 2

AAH43633

ID AAH43633 standard; cdNA; 2772 BP.

XX AC AAH43633;

XX XX

DT 21-JAN-2002 (first entry)

XX

```
DE Human ion-channel forming protein ORF.
XX Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX Homo sapiens.
XX WO200175108-A1.
XX 11-OCT-2001.
XX 03-APR-2001; 2001WO-US010875.
XX 03-APR-2000; 2000US-0194255P.
XX (LEXI-) LEXICON GENETICS INC.
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI; 2001-656987/75.
XX P-PSDB; AAB47678.
XX New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.
XX Claim 1; Page 34-35; 41pp; English.
XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The oligonucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.
CC The polypeptides are further used in generating antibodies
XX SQ Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;
Query Match 99.8%; Score 2662.2; DB 5; Length 2772;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

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QY 1 ATGAAGGATGTGGAGTCCGGCCGGGGCAGGGTGTGCTGAACCTCGCAGCCCGCCAGGGGC 60
Db 106 ATGAAGGATGTGGAGTCCGGCCGGGGCAGGGTGTGCTGAACCTCGCAGCCCGCCAGGGGC 165
QY 61 GACGGCTCTACTGCTGGGCACCGCGCGCCAGCTTGGTGGCGCGGGTGGCCTG 120
Db 166 GACGGCTCTACTGCTGGGCACCGCGCGCCAGCTTGGTGGCGCGGGTGGCCTG 225
QY 121 AGGGAGAGCCCGCGGGGCAAGCAGGGGGCCCGGATGAGCCCTGTGGGAAAGCCGCTCTCT 180
Db 226 AGGGAGAGCCCGCGGGGCAAGCAGGGGGCCCGGATGAGCCCTGTGGGAAAGCCGCTCTCT 285
QY 181 TACACGAGTACCGAGCTGCCGCGCAACGTCAAGTACCGCGGGTGCAGAACTACCTG 240
Db 286 TACACGAGTACCGAGCTGCCGCGCAACGTCAAGTACCGCGGGTGCAGAACTACCTG 345
QY 241 TACAACTGCTGGAGAGACCCCGGGCTGGGGGCTTCACTACCAAGCTTTCGTTTCTC 300
Db 346 TACAACTGCTGGAGAGACCCCGGGCTGGGGGCTTCACTACCAAGCTTTCGTTTCTC 405
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QY	301	CTTGCTTTGGTTCGTTGATTTTGTGAGTGTCTTACGATCCTCGAGCACAAAATTG	Db	1486	TGCCAGTGTGATGTATCAGTGGAGACCTCACCCACCACCTTAAACCTGTCAATCGAGCT	1545
Db	406	CTTGCTTTGGTTCGTTGATTTTGTGAGTGTCTTACGATCCTCGAGCACAAAATTG	QY	1441	ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAGATTTTAAGGAAACGTTAGCTCCATAT	1500
QY	361	GCCTCAAGTTGCTTCCTGATGCTCGAGTTCGTGATGATTTGCTTTTGGTTTGGAGTTC	Db	1546	ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAGATTTTAAGGAAACATTAAGTCCATAT	1605
Db	466	GCCTCAAGTTGCTTCCTGATGCTCGAGTTCGTGATGATTTGCTTTTGGTTTGGAGTTC	QY	1501	GATGTAAAAGATGTCAATGAACAAATATCTGCTGCTCATCTGGACATGTGTGTGTAGAATT	1560
QY	421	ATCATTCGAATCTGGTCTCGGGTGTGTTGTGCGATATAGAGATGGCAAGAGACTG	Db	1606	GATGTAAAAGATGTCAATGAACAAATATCTGCTGCTCATCTGGACATGTGTGTGTAGAATT	1665
Db	526	ATCATTCGAATCTGGTCTCGGGTGTGTTGTGCGATATAGAGATGGCAAGAGACTG	QY	1561	AAAAGCCTTTCAAACACGTTTGAATCAAATTTCTTGGAAGAGGCAAAATCACATCAGATAAG	1620
QY	481	AGTTTGTCTCAAAAGCCCTCTGTTTATAGATACCAATTTCTTATCGCTTCAATAGCA	Db	1666	AAAAGCCTTTCAAACACGTTTGAATCAAATTTCTTGGAAGAGGCAAAATCACATCAGATAAG	1725
Db	586	AGTTTGTCTCAAAAGCCCTCTGTTTATAGATACCAATTTCTTATCGCTTCAATAGCA	QY	1621	AGAGCCGAGAGAAAATAACACAGACAGATGAGACACAGACGATCTCAGTATGCTCGGT	1680
QY	541	GTTGTTTCTGCAAAACTCAGGTAATATTTTCCACGCTCTGCATCTCAGAAGTCTCCGT	Db	1726	AGAGCCGAGAGAAAATAACACAGACAGATGAGACACAGACGATCTCAGTATGCTCGGT	1785
Db	646	GTTGTTTCTGCAAAACTCAGGTAATATTTTCCACGCTCTGCATCTCAGAAGTCTCCGT	QY	1681	CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGGTGAGCTGCCTACTA	1740
QY	601	TTCTACAGATCTCTCGCATGGTGGCATGGACCGAAGGGAGGCACTTGGAATTAATCTG	Db	1786	CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAGGTGAGCTGCCTACTA	1845
Db	706	TTCTACAGATCTCTCGCATGGTGGCATGGACCGAAGGGAGGCACTTGGAATTAATCTG	QY	1741	GACATCTATCAACAGGTCTCTCGGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTC	1800
QY	661	GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTGT	Db	1846	GACATCTATCAACAGGTCTCTCGGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTC	1905
Db	766	GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTGT	QY	1801	CAGATCCCACTTTTGAATGTGAACAGACATCTGATCAATCAAGCCCTGTGGATAGCAAA	1860
QY	721	GTTCTTATTTTTCGTTCTCTCTGCTATCTGCTGGAAAGGATGCAATTAAGAGTTT	Db	1906	CAGATCCCACTTTTGAATGTGAACAGACATCTGATCAATCAAGCCCTGTGGATAGCAAA	1965
Db	826	GTTCTTATTTTTCGTTCTCTCTGCTATCTGCTGGAAAGGATGCAATTAAGAGTTT	QY	1861	GATCTTTCCGGTTCGCAACAAAACAGTGGCTGTATTCCAGATCAACTAGTGCCAAATCTC	1920
QY	781	TCTACATATGAGATGCTCTCTGCTGGGCAATTAATCAATTAAGAGTTT	Db	1966	GATCTTTCCGGTTCGCAACAAAACAGTGGCTGTATTCCAGATCAACTAGTGCCAAATCTC	2025
Db	886	TCTACATATGAGATGCTCTCTGCTGGGCAATTAATCAATTAAGAGTTT	QY	1921	TCGAGAGGCTGAGTTCATTTCTGACGCCAAATAGTTCAGTGCCAGACTTTTCTACGGG	1980
QY	841	GACAAACTCCCTTAACCTGCTGGAGATGCTTCTGCGAGCTTTGCACTCCTTGGC	Db	2026	TCGAGAGGCTGAGTTCATTTCTGACGCCAAATAGTTCAGTGCCAGACTTTTCTACGGG	2085
Db	946	GACAAACTCCCTTAACCTGCTGGAGATGCTTCTGCGAGCTTTGCACTCCTTGGC	QY	1981	CTTTAGCCCTACTATGACAGTCAAGCAACACAGTGCCTTATAGTCAAAAGCGATGCTCA	2040
QY	901	ATTTCTTTTTCGACTTCTGCTGGGCAATTTCTGCTCAGTTCAGTTCATTAAGTACAA	Db	2086	CTTTAGCCCTACTATGACAGTCAAGCAACACAGTGCCTTATAGTCAAAAGCGATGCTCA	2145
Db	1006	ATTTCTTTTTCGACTTCTGCTGGGCAATTTCTGCTCAGTTCAGTTCATTAAGTACAA	QY	2041	GCAGTGGCAGCCCAACACCAATTGCAAAACCAAAATAAGTACGGCAACCAAGCCAGAGCC	2100
QY	961	GAAACACCCGAGAAACATTTGAGAAAGAGAGAACCCAGTCCCAACCTCATTCAG	Db	2146	GCAGTGGCAGCCCAACACCAATTGCAAAACCAAAATAAGTACGGCAACCAAGCCAGAGCC	2205
Db	1066	GAAACACCCGAGAAACATTTGAGAAAGAGAGAACCCAGTCCCAACCTCATTCAG	QY	2101	CCAAACATTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA	2160
QY	1021	TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCA	Db	2206	CCAAACATTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA	2265
Db	1126	TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCA	QY	2161	ACTCTGACCCCTTAACCTGCGAGGCTTACAGGAAAGCATTTCTGACGCTCACACCTGCTTT	2220
QY	1081	CACTTTGAAGGCTTGCACACCTGACGCCCTACCAATCAGAAAGCTAAGTTTAAAGAGCGA	Db	2266	ACTCTGACCCCTTAACCTGCGAGGCTTACAGGAAAGCATTTCTGACGCTCACACCTGCTTT	2325
Db	1186	CACTTTGAAGGCTTGCACACCTGACGCCCTACCAATCAGAAAGCTAAGTTTAAAGAGCGA	QY	2221	GTTGCTCTCAAGGAAATGTTGAGGTTGACAGTCAAAATCTCACCAGGACCGTTCTATG	2280
QY	1141	GTCGCGATGGCTAGCCCGAGGGCCAGAGTATTAAGCCGACAGCCCTCAGTAGGTGAC	Db	2326	GTTGCTCTCAAGGAAATGTTGAGGTTGACAGTCAAAATCTCACCAGGACCGTTCTATG	2385
Db	1246	GTCGCGATGGCTAGCCCGAGGGCCAGAGTATTAAGCCGACAGCCCTCAGTAGGTGAC	QY	2281	AGGAAAGCTTTGACATGGGAGGAGAACTCTGTTGCTCTGCTGCTGCTGCTGCTGCTGCTG	2340
QY	1201	AGGAGTCCCAAGCACACGACATCAAGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGAGC	Db	2386	AGGAAAGCTTTGACATGGGAGGAGAACTCTGTTGCTCTGCTGCTGCTGCTGCTGCTGCTG	2445
Db	1306	AGGAGTCCCAAGCACACGACATCAAGCCGAGGGCAGTCCCAACCAAGTGCAGAAAGAGC	QY	2341	GACTTGGGCAAAATCTTTGTTGTTGTCGCAAAACCTGATCAGGTCGACCGAGGAACCTGAATATA	2400
QY	1261	TGAGCTTCAACAGCCGAACCCGCTTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGGCA	Db	2446	GACTTGGGCAAAATCTTTGTTGTTGTCGCAAAACCTGATCAGGTCGACCGAGGAACCTGAATATA	2505
Db	1366	TGAGCTTCAACAGCCGAACCCGCTTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGGCA	QY	2401	CAACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGACCCAGATTTTATCCCAATGG	2460
QY	1321	AAACAGTATAGATGCTGACACAGCCCTTGGCCTGATGATGATGATGATGATGATGATGATG	Db	2506	CAACTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGACCCAGATTTTATCCCAATGG	2565
Db	1426	AAACAGTATAGATGCTGACACAGCCCTTGGCCTGATGATGATGATGATGATGATGATGATG	QY	2461	AGGAAATCCAAATGTTTATTAACCTGATGAAGAGTGGGTCCCGAAGAGACAGACAGAC	2520
QY	1381	TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG				

Db 2566 AGGGAATCAAAATGTTTATTAATGATGAAGAGGTGGTCCCGAAGACAGACAGACAGAC 2625
QY 2521 ACTTTTGTATGCGCAGCGCAGCTCCAGGGAAGCTGCTTTGTCATCAGACTCTCTAAGG 2580
Db 2626 ACTTTTGTATGCGCAGCGCAGCTCCAGGGAAGCTGCTTTGTCATCAGACTCTCTAAGG 2685
QY 2581 ACTGGAAGGTACAGATCATCTCAGAGCAATTTGTAAGGCGAGGAGAAAGTACAGATCCCTC 2640
Db 2686 ACTGGAAGGTACAGATCATCTCAGAGCAATTTGTAAGGCGAGGAGAAAGTACAGATCCCTC 2745
QY 2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db 2746 AGCTTGCCTCATGTCAAACTGAAATAA 2772

RESULT 3

AAH43634
ID AAH43634 standard; cDNA; 3111 BP.
XX AC
XX AAH43634;

XX 21-JAN-2002 (first entry)

XX Human ion-channel forming protein coding sequence.

XX Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 59..2831
FT CDS /*tag= a
FT /product= "Human ion-channel forming protein"

XX WO200175108-A1.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010875.

XX 03-APR-2000; 2000US-0194255P.

XX (LEXI-) LEXICON GENETICS INC.

XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;

XX WPI; 2001-656987/75.

XX P-PSDB; AAB47678.

XX New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.

XX Disclosure; Page 37-38; 41pp; English.

XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The oligonucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.

CC The polypeptides are further used in generating antibodies
XX
SQ Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;
Query Match 99.8%; Score 2662.2; DB 5; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAAGGATGTGGAGTGGGGCGGCGGAGGTGCTGCTGAACTCGGACGCGCCAGGGGCG 60
Db 165 ATGAAGGATGTGGAGTGGGGCGGCGGAGGTGCTGCTGAACTCGGACGCGCCAGGGGCG 224
QY 61 GACGCGCTGCTACTGCTGGGCAACCCGCGCGCCACGCTTGTGTGGCGGCGGCTGCTCT 120
Db 225 GACGCGCTGCTACTGCTGGGCAACCCGCGCGCCACGCTGCTGCTGGGCGGCTGCTCT 284
QY 121 AGGAGAGCCCGCGGCGGCAAGCAGGGGCGCGGATAGCCTGCTGGGGAAGCGCTCTCT 180
Db 285 AGGAGAGCCCGCGGCGGCAAGCAGGGGCGCGGATAGCCTGCTGGGGAAGCGCTCTCT 344
QY 181 TACACGAGTAGCCAGAGCTGCCGCGCAACGTCAAGTACCGCGCGGTGCAGAACTACCTG 240
Db 345 TACACGAGTAGCCAGAGCTGCCGCGCAACGTCAAGTACCGCGCGGTGCAGAACTACCTG 404
QY 241 TACAACGTGCTGAGAGACCCCGCGGCTGGGCGTTTCATCTACCAAGCTTTGTTTTTCTC 300
Db 405 TACAACGTGCTGAGAGACCCCGCGGCTGGGCGTTTCATCTACCAAGCTTTGTTTTTCTC 464
QY 301 CTTGCTTTGGTGTGTTGATTTTGTCAAGTGTGTTTCTACCATCCCTGAGACACAAAAATTG 360
Db 465 CTTGCTTTGGTGTGTTGATTTTGTCAAGTGTGTTTCTACCATCCCTGAGACACAAAAATTG 524
QY 361 GCCTCAAGTGCCTCTTGATCCTCGAGTTTCGATGATTGTCGCTCTTTGGTTTGGAGTTC 420
Db 525 GCCTCAAGTGCCTCTTGATCCTCGAGTTTCGATGATTGTCGCTCTTTGGTTTGGAGTTC 584
QY 421 ATCATTCGAATCTGGTCTCGGGGTTGCTGTTGTCGATATAGAGGATGCAAGGAAGACTG 480
Db 585 ATCATTCGAATCTGGTCTCGGGGTTGCTGTTGTCGATATAGAGGATGCAAGGAAGACTG 644
QY 481 AGGTTTGTCTGAAAGCCCTCTCTGTTATAGATACCATGTTCTTATCGCTTCAATAGCA 540
Db 645 AGGTTTGTCTGAAAGCCCTCTCTGTTATAGATACCATGTTCTTATCGCTTCAATAGCA 704
QY 541 GTTGTCTCTGCAAAAACCTCAGGGTAATAATTTTGCACGCTGCACTCAGAAAGTCTCCGT 600
Db 705 GTTGTCTCTGCAAAAACCTCAGGGTAATAATTTTGCACGCTGCACTCAGAAAGTCTCCGT 764
QY 601 TTCTTACAGATCTCTCCGATGGTGGCATGGACCGAAGGGGAGGCACCTTGGAAAATTACTG 660
Db 765 TTCTTACAGATCTCTCCGATGGTGGCATGGACCGAAGGGGAGGCACCTTGGAAAATTACTG 824
QY 661 GTTTCAGTGGTTTATGCTCAGCAAGGAATTAATCAGAGCTTGGTACATAGGATTTTGG 720
Db 825 GGTTCAGTGGTTTATGCTCAGCAAGGAATTAATCAGAGCTTGGTACATAGGATTTTGG 884
QY 721 GTTCTTATTTTTCGTCCTTTCTCTGCTGTTGTAAGGATGCAATAAGAGATT 780
Db 885 GTTCTTATTTTTCGTCCTTTCTCTGCTGTTGTAAGGATGCAATAAGAGATT 944
QY 781 TCTACATATGAGATGCTCTCTGTTGGGGCAATTAATACATTGACAACATTTGGCTATGGA 840
Db 945 TCTACATATGAGATGCTCTCTGTTGGGGCAATTAATACATTGACAACATTTGGCTATGGA 1004
QY 841 GACAAAACCTCCCTAACTTGTGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCTTGGC 900
Db 1005 GACAAAACCTCCCTAACTTGTGCTGGGAAGATTGCTTTCTGCAAGGCTTTTGCACCTCTTGGC 1064
QY 901 ATTTCTTTCTTTGTCATTTCTGCTGGGATTTCTTGGCTCAGGTTTGTGCAATTAAGTACAA 960
Db 1065 ATTTCTTTCTTTGTCATTTCTGCTGGGATTTCTTGGCTCAGGTTTGTGCAATTAAGTACAA 1124
QY 961 GAACAACACCCGCGGAGAAACACTTTTGAGAAAAGAGGAACCCAGCTGCGCAACCTCATTCAG 1020

[illegible]

	(ICAG-) ICAGEN INC.	
	Jegla TJ;	
	WPI; 2001-6111467/70.	
	P-PSDB; AAU09020.	
XX	Polypeptides and polynucleotides of potassium channel KCNQ5 for	
PA	identifying a compound modulating ion flux in eukaryotic cell or cell	
XX	membrane expressing the protein, comprises KCNQ approximately-a- subunits.	
XX	Claim 5; Page 62-63; 78pp; English.	
CC	The invention relates to an isolated polypeptide comprising an alpha-	
CC	subunit of a KCNQ potassium channel, with a hknq5 sequence having 65%	
CC	sequence identity to amino acids 343-640 of hknq5-1 amino acid sequence	
CC	and forms a KCNQ potassium channel having the characteristic of voltage-	
CC	gating with at least an additional KCNQ alpha-subunit. Also included in	
CC	the scope of the invention are the nucleic acids encoding hknq5	
CC	(including splice variants encoding hknq5-1 and hknq5-2), expression	
CC	vectors encoding them, antibodies against them, the use of 3-dimensional	
CC	computer modelling to identify molecules that bind to a KCNQ containing	
CC	potassium channel and modulate ion flux through the channel. The KCNQ	
CC	polypeptide is useful for identifying a compound that increases or	
CC	decreases ion flux through a potassium channel expressed in a eukaryotic	
CC	host cell or cell membrane. The compound (and the KCNQ nucleic acid when	
CC	used in gene therapy) is useful as a pharmaceutical agent for treating	
CC	diseases involving abnormal ion flux, such as disorders of the central	
CC	nervous system, such as epilepsy, migraines, hearing and vision problems,	
CC	psychotic disorders, seizures, learning and memory disorders, stroke and	
CC	pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a	
CC	human tissue and the use of a nucleotide sequence of KCNQ5 to search	
CC	computer databases to find variants of the sequence which are associated	
CC	with disease states, is useful for screening mutations of KCNQ5. The	
CC	present sequence is a splice variant of hknq5 encoding hknq5-1	
XX	Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;	
SQ	Query Match 98.6%; Score 2630; DB 4; Length 2694;	
	Best Local Similarity 99.0%; Pred. No. 0;	
	Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;	
QY	1 ATGAAGGATGTGGAGTCGGCGCGGGCAGGGTCTGCTGAACTCGGCACGCCAGCGGGGC 60	
DB	1 ATGAAGGATGTGGAGTCGGCGCGGGCAGGGTCTGCTGAACTCGGCACGCCAGCGGGGC 60	
QY	61 GACGGCTCTACTGCTGGGCAACC CGCGGGCACGCTTGTTGGCGGGCGGGTGGCGCTG 120	
DB	61 GACGGCTCTACTGCTGGGCAACC CGCGGGCACGCTTGTTGGCGGGCGGGTGGCGCTG 120	
QY	121 AGGGAGAGCCCGCGGGCAAGCAGGGGGCCGGATGAGCTGCTGGGGAAGCGCTCTCT 180	
DB	121 AGGGAGAGCCCGCGGGCAAGCAGGGGGCCGGATGAGCTGCTGGGGAAGCGCTCTCT 180	
QY	181 TACACGAGTAGCAGAGCTGCGCGGCACAACGTAAGTACCGCGGGTGCAGAACTACCTG 240	
DB	181 TACACGAGTAGCAGAGCTGCGCGGCACAACGTAAGTACCGCGGGTGCAGAACTACCTG 240	
QY	241 TACAAGCTGCTGAGAGACCCCGCGCTGGGGTTCATCTACACGCTTTTCGTTTTCTC 300	
DB	241 TACAAGCTGCTGAGAGACCCCGCGCTGGGGTTCATCTACACGCTTTTCGTTTTCTC 300	
QY	301 CTTCGCTTTGGTTGCTGATTGTCAGNGTTTTCTACCATCCCTGAGCACACAAAATTG 360	
DB	301 CTTCGCTTTGGTTGCTGATTGTCAGNGTTTTCTACCATCCCTGAGCACACAAAATTG 360	
QY	361 GCCTCAAGTTGCTCTTGATCTCGAGTTCGCGATGTTGCTTTGGTTTGGAGTTC 420	
DB	361 GCCTCAAGTTGCTCTTGATCTCGAGTTCGCGATGTTGCTTTGGTTTGGAGTTC 420	
QY	421 ATCATTGGAATCTGGTCTCGGGTTGCTGTTTCGTATGAGGATGCGAAGGAGCTG 480	
DB	421 ATCATTGGAATCTGGTCTCGGGTTGCTGTTTCGTATGAGGATGCGAAGGAGCTG 480	
QY	481 AGSTTTTCTCGAAAAAGCCCTTCTCTGTTATAGATAACCAITTTCTTATCGCTTCAATAGCA 540	
DB	481 AGSTTTTCTCGAAAAAGCCCTTCTCTGTTATAGATAACCAITTTCTTATCGCTTCAATAGCA 540	
QY	541 GTTGTCTTCTCGAAAAAACTCAGGGTAATAATTTTGGCCACGCTCTGCATCAGAAAGTCTCCGT 600	
DB	541 GTTGTCTTCTCGAAAAAACTCAGGGTAATAATTTTGGCCACGCTCTGCATCAGAAAGTCTCCGT 600	
QY	601 TTCTTACAGATCTCTCCGATGGTCCGATGGACCGAAGGGAGGACATTTGGAAATTTACTG 660	
DB	601 TTCTTACAGATCTCTCCGATGGTCCGATGGACCGAAGGGAGGACATTTGGAAATTTACTG 660	
QY	661 GGTTTCAAGTGTGTTTATGCTCACACAAGGAATTAATCACAGCTTTGGTACATAGGATTTTGG 720	
DB	661 GGTTTCAAGTGTGTTTATGCTCACACAAGGAATTAATCACAGCTTTGGTACATAGGATTTTGG 720	
QY	721 GTTCTTATTTTTCGTCTTCTTGTCTATCTGTGTGAAAAAGGATGCCAATAAAGAGTTT 780	
DB	721 GTTCTTATTTTTCGTCTTCTTGTCTATCTGTGTGAAAAAGGATGCCAATAAAGAGTTT 780	
QY	781 TCTTACATATGCAGATCTCTCTGGTGGGCAACAATTTACATTCGACACTATTGCCTATGCA 840	
DB	781 TCTTACATATGCAGATCTCTCTGGTGGGCAACAATTTACATTCGACACTATTGCCTATGCA 840	
QY	841 GACAAAACTCCCCTAACCTTGGCTGGGAAGAATGCTTTCTGCAGGCTTTGCACCTCTCTGGC 900	
DB	841 GACAAAACTCCCCTAACCTTGGCTGGGAAGAATGCTTTCTGCAGGCTTTGCACCTCTCTGGC 900	
QY	901 ATTTCTTTCTTTGCATCTCTCTCGGCATTTCTTGGCTCAGGTTTTCATTTAAAGTACAA 960	
DB	901 ATTTCTTTCTTTGCATCTCTCTCGGCATTTCTTGGCTCAGGTTTTCATTTAAAGTACAA 960	
QY	961 GACACACCGCCGACAGAAACACTTTGAGAAAAGNAGAACCCAGCTGCCAACCTCATTTAG 102	
DB	961 GACACACCGCCGACAGAAACACTTTGAGAAAAGNAGAACCCAGCTGCCAACCTCATTTAG 102	
QY	1021 TGTGTTTGGCTAGTTTACGCGCTGATGAGAAATCTGTTTTCATTTCACACCTTGGGAAGCCA 108	
DB	1021 TGTGTTTGGCTAGTTTACGCGCTGATGAGAAATCTGTTTTCATTTCACACCTTGGGAAGCCA 108	
QY	1081 CACTTGAAGSCCTTGCACACCTTGCACCCCTTCAAGAAAAGAACGGGGAAGCATCAACG 114	
DB	1081 CACTTGAAGSCCTTGCACACCTTGCACCCCTTCAAGAAAAGAACGGGGAAGCATCAACG 114	
QY	1116 --TCAGAGCTTAAGTTTAAAGGCGAGTGGCGATGGCTAGCCCAAGGGGCGCAGAGTATT 117	
DB	1141 AGTCAGAGCTTAAGTTTAAAGGCGAGTGGCGATGGCTAGCCCAAGGGGCGCAGAGTATT 120	
QY	1174 AACAGCCGACCAAGCTTCAGTAGTGACAGAGGTCCCAAAGCACCGACATCACAGCCGAG 123	
DB	1201 AACAGCCGACCAAGCTTCAGTAGTGACAGAGGTCCCAAAGCACCGACATCACAGCCGAG 126	
QY	1234 GGC	

QY	1534	GGTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAAAACACAGTGTGATCAAAATCTTT	1593
Db	1561	GGTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAAAACACAGTGTGATCAAAATCTTT	1620
QY	1594	GGAAAGGGCAATCAGATCAGATAGAGAGCGGAGAGAAATACAGCAGAACATGAG	1653
Db	1621	GGAAAGGGCAATCAGATCAGATAGAGAGCGGAGAGAAATACAGCAGAACATGAG	1680
QY	1654	ACCACAGACATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAACACAGGTACAGTCC	1713
Db	1681	ACCACAGACATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAACACAGGTACAGTCC	1740
QY	1714	ATAGAGTCCAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGAAAGGCTCT	1773
Db	1741	ATAGAGTCCAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGAAAGGCTCT	1800
QY	1774	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT	1833
Db	1801	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT	1860
QY	1834	GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCAAAACAGTGGCTGC	1893
Db	1861	GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCAAAACAGTGGCTGC	1920
QY	1894	TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTCGAGTTCAATCTGAGCCAAAT	1953
Db	1921	TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTCGAGTTCAATCTGAGCCAAAT	1980
QY	1954	GAGTTCAGTCCAGACATTTCTAGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2013
Db	1981	GAGTTCAGTCCAGACATTTCTAGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2040
QY	2014	GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACATTTGCAAAACAA	2073
Db	2041	GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACATTTGCAAAACAA	2100
QY	2074	ATAAATACGGCCCAACAGCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA	2133
Db	2101	ATAAATACGGCCCAACAGCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA	2160
QY	2134	GCATCAAGCATCTCCAGGCGCAAAACTCTGACCCCTTAACCTTCGAGGCTTACAGGAA	2193
Db	2161	GCATCAAGCATCTCCAGGCGCAAAACTCTGACCCCTTAACCTTCGAGGCTTACAGGAA	2220
QY	2194	AGCATTTCTGAGTCAACCTGCTTGTGCTTCAAGGAAATGTTTCAGGTTGCAAG	2253
Db	2221	AGCATTTCTGAGTCAACCTGCTTGTGCTTCAAGGAAATGTTTCAGGTTGCAAG	2280
QY	2254	TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2313
Db	2281	TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340
QY	2314	TTGTCTGTCTGCTCCATGTCGCGAGGACTTTGGGCAAACTTTGTCTGTGCAAAACCTG	2373
Db	2341	TTGTCTGTCTGCTCCATGTCGCGAGGACTTTGGGCAAACTTTGTCTGTGCAAAACCTG	2400
QY	2374	ATCAGTTCAGCAGGAACTGAATATACACTTTTCAGGAGTGAAGTGGCTCCAGA	2433
Db	2401	ATCAGTTCAGCAGGAACTGAATATACACTTTTCAGGAGTGAAGTGGCTCCAGA	2460
QY	2434	GGCAGCCAGATTTTACCCCAAAATGGAGGGAATCCAAATGTTTAACTGATGAAGAG	2493
Db	2461	GGCAGCCAGATTTTACCCCAAAATGGAGGGAATCCAAATGTTTAACTGATGAAGAG	2520
QY	2494	GTGGGTCCGAGAGACAGACAGACATTTTGTATGCGCACCGCAGCTGCCAGGAA	2553
Db	2521	GTGGGTCCGAGAGACAGACAGACATTTTGTATGCGCACCGCAGCTGCCAGGAA	2580
QY	2554	GCTGCCCTTTCATCAGACTCTTTCAGGACTGGAAGTCAAGTCAATCTCAGAGCAATTTGT	2613
Db	2581	GCTGCCCTTTCATCAGACTCTTTCAGGACTGGAAGTCAAGTCAATCTCAGAGCAATTTGT	2640

QY	2614	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA	2667
Db	2641	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA	2694
RESULT 5			
AD27192			
ID	AAD27192 standard; cDNA; 2694 BP.		
XX			
AC	AAD27192;		
XX			
DT	09-APR-2002 (first entry)		
XX	Human potassium channel polypeptide, KCNQ5 cDNA.		
DE			
XX	Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;		
KW	dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;		
KW	multiple sclerosis; MS; Parkinson's disease; ataxia; depression;		
KW	anxiety disorder; bipolar disorder; sleep disorder; eating disorder;		
KW	addiction; myokymia; Alzheimer's disease; age-associated memory loss;		
KW	learning deficiency; cognitive disorder; motor disease; neuron disease;		
KW	neurophysiological disorder; neuropsychological disorder; asthma;		
KW	neuron cell death; brain tumour; gene therapy; antisense therapy;		
KW	synaptic transmission; electrical excitability; ss.		
XX			
OS	Homo sapiens.		
XX			
PH	Location/Qualifiers		
FT	1..2694		
FT	/*tag= a		
FT	/product= "Human KCNQ5 protein"		
XX	WO200192526-A1.		
XX			
PD	06-DEC-2001.		
XX			
PF	24-MAY-2001; 2001WO-US017314.		
XX			
PR	26-MAY-2000; 2000US-0207389P.		
XX			
PA	(BRIM) BRISTOL-MYERS SQUIBB CO.		
XX			
PI	Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;		
PI	Gribkoff VK;		
XX	WPI: 2002-122069/16.		
DR	P-PSDB; AAE16599.		
XX	Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding		
PT	it, for diagnosing, treating and identifying modulators useful in		
PT	treating neurological, neurophysiological and neuropsychological		
XX	diseases.		
PS	Claim 3; Fig 1; 128pp; English.		
XX			
CC	The invention relates to potassium channel polypeptides referred to as		
CC	KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5		
CC	polypeptides are useful for identifying compounds that modulate their		
CC	biological activity. The compounds identified and KCNQ5 polynucleotides		
CC	are useful for treating acute and chronic pain, migraine, acute stroke,		
CC	dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),		
CC	multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,		
CC	depression, bipolar disorders, sleep disorders, eating disorders,		
CC	addiction, myokymia, Alzheimer's disease, age-associated memory loss, The		
CC	learning deficiencies, cognitive disorders and motor neuron diseases. The		
CC	nucleic acid molecules of the invention are further useful for treating		
CC	neurophysiological, neuropsychological disorders, asthma, neuron cell		
CC	death and brain tumours. They are also used in gene therapy and antisense		
CC	therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical		
CC	excitability in the brain and are useful for generating antibodies. They		
CC	are also useful to affinity purify biological effectors from biological		
CC	materials e.g. disease tissues or cells. The present sequence is human		
CC	KCNQ5 cDNA		

XX Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;
Query Match 98.6%; Score 2630; DB 6; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
1 ATGAAGGATGTGGAGTCGGGCGGGCGGCGGAGGTCGCTGAACTCGCGAGCCCGCAGGGGC 60
1 ATGAAGGATGTGGAGTCGGGCGGGCGGCGGAGGTCGCTGAACTCGCGAGCCCGCAGGGGC 60
61 GACGGCTGCTACTGCTGGGCAACCGCGCGGCAACGCTTGGTGGCGGCGGCGGTCGCTG 120
61 GACGGCTGCTACTGCTGGGCAACCGCGCGGCAACGCTTGGTGGCGGCGGCGGTCGCTG 120
121 AGGGAGAGCGCGGGGCAAGCAGGGGCGCGGATGAGCTGCTGGGAAAGCGCTCTCT 180
121 AGGGAGAGCGCGGGGCAAGCAGGGGCGCGGATGAGCTGCTGGGAAAGCGCTCTCT 180
181 TACAGAGTAGCAGAGCTGCGGGCGCAACGTCAGAGTACCGGGGGTGCAGAACTACCTG 240
181 TACAGAGTAGCAGAGCTGCGGGCGCAACGTCAGAGTACCGGGGGTGCAGAACTACCTG 240
241 TACAGAGTAGCAGAGCTGCGGGCGCGGCTGGGGGTCATCTACAGCTTTTGGTTTCTC 300
241 TACAGAGTAGCAGAGCTGCGGGCGCGGCTGGGGGTCATCTACAGCTTTTGGTTTCTC 300
301 CTGTGCTTTGGTGTGATTTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGT 360
301 CTGTGCTTTGGTGTGATTTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGTGTGTCAGT 360
361 GCCTCAAGTTGCTCTTGCATCTGGAGTTGTCGATGATGTCGCTTTGGTTTGGAGTTC 420
361 GCCTCAAGTTGCTCTTGCATCTGGAGTTGTCGATGATGTCGCTTTGGTTTGGAGTTC 420
421 ATCATTCGAATCTGCTGCGGGTGTGCTGTCGATGATGTCGATGATGTCGATGATGTCG 480
421 ATCATTCGAATCTGCTGCGGGTGTGCTGTCGATGATGTCGATGATGTCGATGATGTCG 480
481 AGGTTGCTCGAAGCCCTTCTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 540
481 AGGTTGCTCGAAGCCCTTCTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 540
541 GTTGTCTTCTGCAAACTCAGGGTAAATTTTGGCAAGTCGCTGCACTCAGAGTCTCGGT 600
541 GTTGTCTTCTGCAAACTCAGGGTAAATTTTGGCAAGTCGCTGCACTCAGAGTCTCGGT 600
601 TTCCTACAGATCCTCCGATGTCGATGCAAGCGGAGGCACTTGGAAATTAATCTG 660
601 TTCCTACAGATCCTCCGATGTCGATGCAAGCGGAGGCACTTGGAAATTAATCTG 660
661 GCTTCAGTGTGTTATGCTCAGAGCAAGGAATTAATCAGAGTGTGATAGGATTTTGT 720
661 GCTTCAGTGTGTTATGCTCAGAGCAAGGAATTAATCAGAGTGTGATAGGATTTTGT 720
721 GTTCTTATTTTTCGCTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721 GTTCTTATTTTTCGCTTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781 TCTACATATGAGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
781 TCTACATATGAGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
841 GACAAACTCCCTAACTTGGCTGGGAAGATTTCTTCTGAGGCTTTGCACTCTCTGGC 900
841 GACAAACTCCCTAACTTGGCTGGGAAGATTTCTTCTGAGGCTTTGCACTCTCTGGC 900
901 ATTTCTTTCTTCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
901 ATTTCTTTCTTCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
961 GAACAACTCCGCGAAGACATTTTGGAAAGAAAGCAAGCCAGCTGCGCAACCTCATTCAG 1020

Db 961 GAACAACTCCGCGAAGACATTTTGGAAAGAAAGCAAGCCAGCTGCGCAACCTCATTCAG 1020
QY 1021 TGTGTTTGGCTGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Db 1021 TGTGTTTGGCTGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
QY 1081 CACTTTGAAGGCTTGCACACCTGCGAGCCCTACCA----- 1115
Db 1081 CACTTTGAAGGCTTGCACACCTGCGAGCCCTACCAAGAAAGAAAGGGAAGCATCAAGC 1140
QY 1116 ---TCAAGAGCTAAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCGAGATATT 1173
Db 1141 AGTCAGAAAGCTAAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCGAGATATT 1200
QY 1174 AAGAGCCGACAAAGCCTCAGTAGTGCAGAGGAGTCCCAAGCAGCAGCATCACAGCCGAG 1233
Db 1201 AAGAGCCGACAAAGCCTCAGTAGTGCAGAGGAGTCCCAAGCAGCAGCATCACAGCCGAG 1260
QY 1234 GGCAGTCCCAACCAAGTGCAGAAAGTGGAGCTTCAAACGACCGAAACCCGCTTCCGGGCC 1293
Db 1261 GGCAGTCCCAACCAAGTGCAGAAAGTGGAGCTTCAAACGACCGAAACCCGCTTCCGGGCC 1320
QY 1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACAGTAGATAGTGTGACACAGCCCTTGGC 1353
Db 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACAGTAGATAGTGTGACACAGCCCTTGGC 1380
QY 1354 ACTGATGATGATATGATGAAAAGGATGCGAGTGTGATGATCAGTGGAGAGCTCAC 1413
Db 1381 ACTGATGATGATATGATGAAAAGGATGCGAGTGTGATGATCAGTGGAGAGCTCAC 1440
QY 1414 CCACCCTTAAACCTGTCAATCGAGCTATCAGAAATTTGAAATTTTCAATTTGCAAAACGG 1473
Db 1441 CCACCCTTAAACCTGTCAATCGAGCTATCAGAAATTTGAAATTTTCAATTTGCAAAACGG 1500
QY 1474 AAGTTTAAAGAAAGCTTACGTTACGTTCCATATGATGATAAGATGTCATTTGAACAATTTCTGCT 1533
Db 1501 AAGTTTAAAGAAAGCTTACGTTACGTTCCATATGATGATAAGATGTCATTTGAACAATTTCTGCT 1560
QY 1534 GGTCACTCGAGATGTTGTTGTAGAAATTAAGAGCTTCAACACAGCTGTTGATCAAAATCTTT 1593
Db 1561 GGTCACTCGAGATGTTGTTGTAGAAATTAAGAGCTTCAACACAGCTGTTGATCAAAATCTTT 1620
QY 1594 GGAAGAGGCGCAAACTCACATCAGATAAGAGCGGAGAGAAATAACAGCAGAAACATGAG 1653
Db 1621 GGAAGAGGCGCAAACTCACATCAGATAAGAGCGGAGAGAAATAACAGCAGAAACATGAG 1680
QY 1654 ACCACAGACGATCTCAGTATGCTCGGTCGGTGTCAAGGTTGAAAAACAGGTACAGTCC 1713
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTCGGTGTCAAGGTTGAAAAACAGGTACAGTCC 1740
QY 1714 ATAGAGTCCAAAGCTGGAGTCTACTAGACATCTATCAACAGGTCCTTTCGGAAGGCTCT 1773
Db 1741 ATAGAGTCCAAAGCTGGAGTCTACTAGACATCTATCAACAGGTCCTTTCGGAAGGCTCT 1800
QY 1774 GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCCACTTTTGAATTTGAACAGACATCT 1833
Db 1801 GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCCACTTTTGAATTTGAACAGACATCT 1860
QY 1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGTC 1893
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGTC 1920
QY 1894 TTATCCAGATCAACTAGTGGCAAACTCTCGAGAGGCTGTCAGTTCATTCTGACGCGCAAT 1953
Db 1921 TTATCCAGATCAACTAGTGGCAAACTCTCGAGAGGCTGTCAGTTCATTCTGACGCGCAAT 1980
QY 1954 GAGTTAGTCCCGAGACTTCTACCGCTTAGCCCTACTATGCAAGTCAAGCAACAG 2013
Db 1981 GAGTTAGTCCCGAGACTTCTACCGCTTAGCCCTACTATGCAAGTCAAGCAACAG 2040
QY 2014 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACCATTTGCAAAACCA 2073
Db 2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACCATTTGCAAAACCA 2100

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Db 550 GTTGTCTTGCAGAACTCAGGGTAATATTTTGGCCAGTCTGCATCAGAAAGTCTCCGT 609
Qy 601 TTCTTACAGATCTCCGATGTCGCGATGCGCATGGAGCCGAGGGAGGACATTTGGAAATTAATCTG 660
Db 610 TTCTTACAGATCTCCGATGTCGCGATGCGCATGGAGCCGAGGGAGGACATTTGGAAATTAATCTG 669
Qy 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGGATTTTGG 720
Db 670 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGGATTTTGG 729
Qy 721 GTTCTTATTTTTCGTTCTTCTGTCATCTGGTGGAAAGGATGCGCAATTAAGAGTTT 780
Db 730 GTTCTTATTTTTCGTTCTTCTGTCATCTGGTGGAAAGGATGCGCAATTAAGAGTTT 789
Qy 781 TCTACATATGAGATGCTCTCTGGTGGGCAATTAATCACATTCACAACTATTTGGCTATGGA 840
Db 790 TCTACATATGAGATGCTCTCTGGTGGGCAATTAATCACATTCACAACTATTTGGCTATGGA 849
Qy 841 GACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 900
Db 850 GACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC 909
Qy 901 ATTTCTTTTGGCATCTTCTCGCGCATTTCTTGGCTCAGTTTGGCTAGTTTGGCAATTAAGTACAA 960
Db 910 ATTTCTTTTGGCATCTTCTCGCGCATTTCTTGGCTCAGTTTGGCTAGTTTGGCAATTAAGTACAA 969
Qy 961 GAAACACCCGCGAGAAACATTTGAGAAAGAGGAAACCCAGCTGCGCAACTCATTTAG 1020
Db 970 GAAACACCCGCGAGAAACATTTGAGAAAGAGGAAACCCAGCTGCGCAACTCATTTAG 1029
Qy 1021 TGTGTTTGGCGTAGTTACGACCTGATGAGAAATCTGTTTCCATTTGCAACCTTGGAGGCA 1080
Db 1030 TGTGTTTGGCGTAGTTACGACCTGATGAGAAATCTGTTTCCATTTGCAACCTTGGAGGCA 1089
Qy 1081 CACTTGAAGGCTTGGACACCTGACGCTTACCA----- 1115
Db 1090 CACTTGAAGGCTTGGACACCTGACGCTTACCAAGAAAGAAACAAAGGGAGGAGCATCAAGC 1149
Qy 1116 --TCAGAAAGTAAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCCGAGGGGCGAGAGTATT 1173
Db 1150 AGTCAGAAAGCTAAGTTTTTAAGAGCGAGTGCGCATGGCTAGCCCGAGGGGCGAGAGTATT 1209
Qy 1174 AAGAGCCGACAAAGCTCAGTAGTGACAGGAGGTCCTCCAAAGCACCGACATCACAGCCGAG 1233
Db 1210 AAGAGCCGACAAAGCTCAGTAGTGACAGGAGGTCCTCCAAAGCACCGACATCACAGCCGAG 1269
Qy 1234 GGCAGTCCCAACAAAGTGACAGAGCTGGAGCTTCAAGCACCGAAACCGCTTCCGGGCC 1293
Db 1270 GGCAGTCCCAACAAAGTGACAGAGCTGGAGCTTCAAGCACCGAAACCGCTTCCGGGCC 1329
Qy 1294 TCGCTGCGCCTCAAAGTCTCAGCCCAAAACCCAGTGATAGTGTGACACAGCCCTTGGC 1353
Db 1330 TCGCTGCGCCTCAAAGTCTCAGCCCAAAACCCAGTGATAGTGTGACACAGCCCTTGGC 1389
Qy 1354 ACTGATGATGTATGATGAAAGAGATGCCAGTGTGATGTATCAGTGGAGACCTCACC 1413
Db 1390 ACTGATGATGTATGATGAAAGAGATGCCAGTGTGATGTATCAGTGGAGACCTCACC 1449
Qy 1414 CCACCACTTAAACTGTCAATTCGAGCTATCAGAAATTAAGAAATTTATGTTGCAAAACGG 1473
Db 1450 CCACCACTTAAACTGTCAATTCGAGCTATCAGAAATTAAGAAATTTATGTTGCAAAACGG 1509
Qy 1474 AAGTTTAAAGGAACCTTACCTCATATGATGTAAGAGTGTGATGAAACATTTCTGCT 1533
Db 1510 AAGTTTAAAGGAACCTTACCTCATATGATGTAAGAGTGTGATGAAACATTTCTGCT 1569
Qy 1534 GGTCTATCTGGACATGTTGTGTAAGATTAAGAGCTTCAAAACAGCTGTTGATCAAAATCTT 1593
Db 1570 GGTCTATCTGGACATGTTGTGTAAGATTAAGAGCTTCAAAACAGCTGTTGATCAAAATCTT 1629
Qy 1594 GGAAAGGGCAATCACAATCAGATTAAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1653

Db 1630 GGAAAGGGCAATCACAATCAGATTAAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1689
Qy 1654 ACCACAGACGATCTCAGTATCTCGTTCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
Db 1690 ACCACAGACGATCTCAGTATCTCGTTCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1749
Qy 1714 ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTTGGAAGGCTCT 1773
Db 1750 ATAGAATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTTGGAAGGCTCT 1809
Qy 1774 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1833
Db 1810 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1869
Qy 1834 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTTCGGGTTCCGCAAAAACAGTGGCTGC 1893
Db 1870 GACTATCAAAAGCCCTGTGATAGCAAAAGATCTTTTCGGGTTCCGCAAAAACAGTGGCTGC 1929
Qy 1894 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTTGCAGTTTCATTTCTGACGCAAT 1953
Db 1930 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTTGCAGTTTCATTTCTGACGCAAT 1989
Qy 1954 GAGTTCAAGTCCGAGACTTTCTAGCGCTTACCTACTATGCAAGTCAAGCAACAG 2013
Db 1990 GAGTTCAAGTCCGAGACTTTCTAGCGCTTACCTACTATGCAAGTCAAGCAACAG 2049
Qy 2014 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2073
Db 2050 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2109
Qy 2074 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2133
Db 2110 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2169
Qy 2134 GGCATCAAGATCTGCCCCAGGCCAGAAACTCTGCAACCTTAACCTTGAAGGCTTACAGAA 2193
Db 2170 GCCATCAAGATCTGCCCCAGGCCAGAAACTCTGCAACCTTAACCTTGAAGGCTTACAGAA 2229
Qy 2194 AGCATTTCTGACGTCACCACTGCTTTCCTTCAAGGAAATGTTTCAAGTTCACAG 2253
Db 2230 AGCATTTCTGACGTCACCACTGCTTTCCTTCAAGGAAATGTTTCAAGTTCACAG 2289
Qy 2254 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTTGAATGGGAGGAGAACTCTCTG 2313
Db 2290 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTTGAATGGGAGGAGAACTCTCTG 2349
Qy 2314 TTGTCTGTCTGTCCTGTCGAGGACTTTGGCAAACTCTTTGTCTGTGCAAAACCTG 2373
Db 2350 TTGTCTGTCTGTCCTGTCGAGGACTTTGGCAAACTCTTTGTCTGTGCAAAACCTG 2409
Qy 2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTTCAGGAGTGAAGTGGCTCCAGA 2433
Db 2410 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTTCAGGAGTGAAGTGGCTCCAGA 2469
Qy 2434 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATTAACATGATGAAG 2493
Db 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATTAACATGATGAAG 2529
Qy 2494 GTGGGTCCGAGAGACAGAGACACTTTTGTGATGCGGACCGCAGCTGCGCAGGAA 2553
Db 2530 GTGGGTCCGAGAGACAGAGACACTTTTGTGATGCGGACCGCAGCTGCGCAGGAA 2589
Qy 2554 GCTGCTTTGATCAGACTCTTCAAGGACTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2613
Db 2590 GCTGCTTTGATCAGACTCTTCAAGGACTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2649
Qy 2614 AAGCAGGAGAAAGTACAGATGCGCTCAGCTTGGCTCATGTCAAACTGAAATAA 2667
Db 2650 AAGCAGGAGAAAGTACAGATGCGCTCAGCTTGGCTCATGTCAAACATGAAATAA 2703

ID	AAC85414	standard; cDNA; 3137 BP.
XX	AAC85414;	
AC	20-APR-2001	(first entry)
XX	Human KCNQ5	potassium channel subunit coding sequence.
XX	Human; KCNQ5;	heteromeric channel; chromosome 6; Parkinson's disease;
KW	central nervous system;	CNS; Alzheimer's disease; anxiety; ataxia;
KW	CNS damage; trauma;	stroke; neurodegenerative illness; schizophrenia;
KW	compulsive behaviour;	dementia; depression; Huntington's disease; mania;
KW	memory impairment;	memory dysfunction; spinal cord damage; phobia;
KW	Pick's disease;	psychosis; stroke; tremor; seizure; convulsion; epilepsy;
ds.		
XX	Homo sapiens.	
OS	Key	Location/Qualifiers
XX	CD5	1..2694
PH	/*tag=	a
FT	/product=	"KCNQ5 subunit"
FT		
XX	WO200077035-A2.	
PN	21-DEC-2000.	
XX	29-MAY-2000;	2000WO-DK000289.
XX	11-JUN-1999;	99DK-00000828.
PR	(NEUR-) NEUROSEARCH AS.	
PA	Jentech TJ;	
XX	WPI: 2001-080678/09.	
DR	P-PSDB; AAB47046.	
XX	Novel genes encoding KCNQ5	potassium channel subunits, useful for
XX	treating Alzheimer's disease,	anxiety, ataxia, stroke, dementia, disease.
PT	depression, Huntington's	disease, schizophrenia and Parkinson's
PT	disease.	
XX	Claim 2; Page 44-48;	50pp; English.
PS		
XX	This sequence encodes the	human KCNQ5 protein. The KCNQ5 protein forms
CC	heteromeric channels with	other KCNQ channel subunits, in particular
CC	KCNQ3 and KCNQ4. The	KCNQ5 gene has been localised to the long arm of
CC	chromosome 6 (6p14). Chemicals	which have the ability to bind to KCNQ5
CC	are useful for diagnosis,	treatment, prevention or alleviation of
CC	diseases related to diseases	or adverse conditions of the central nervous
CC	system (CNS), including	affective disorders, Alzheimer's disease,
CC	anxiety, ataxia, CNS	damage caused by trauma, stroke or neurodegenerative
CC	illness, cognitive deficits,	compulsive behavior, dementia, depression,
CC	Huntington's disease,	mania, memory impairment, memory disorders, memory
CC	dysfunction, motion	disorders, motor disorders, neurodegenerative
CC	diseases, Parkinson's	disease and Parkinson-like motor disorders,
CC	phobias, Pick's disease,	psychosis, schizophrenia, spinal cord damage,
CC	stroke, tremor,	seizures, convulsions and epilepsy
XX		
SQ	Sequence 3137 BP; 865 A;	749 C; 745 G; 778 T; 0 U; 0 Other;
	Query Match	98.4%; Score 2625.2; DB 4; Length 3137;
	Best Local Similarity	98.9%; Pred. No. 0;
	Matches 2664; Conservative	0; Mismatches 3; Indels 27; Gaps 1;
QY	1	ATGAAGAGTGTGAGTGGCGCGGGCAGGGTCTGCTGAACTCGGCAGCCCGCAGGGGC 60
DB	1	ATGAAGAGTGTGAGTGGCGCGGGCAGGGTCTGCTGAACTCGGCAGCCCGCAGGGGC 60
QY	61	GACGGCTGTACTGTGGGCACCCGCGGGCCACCGTCTGGTGGCGCGCGCGGTGCGCTG 120
DB	61	GACGGCTGTACTGTGGGCACCCGCGGGCCACCGTCTGGTGGCGCGCGGTGCGCTG 120

Db 1201 AAGAGCCGCAAGACCTCAGTAGTGACAGAGGTCCCAAGCACCGACATCACAGCCGAG 1260
Qy 1234 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGAGCTTCAACGACCGAACCGCTTCCGGGCC 1293
Db 1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGAGAGCTTCAACGACCGAACCGCTTCCGGGCC 1320
Qy 1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACAGTGTATAGTGTGACACAGCCCTTGGC 1353
Db 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACAGTGTATAGTGTGACACAGCCCTTGGC 1380
Qy 1354 ACTGATGATATATATGATGAAGAGAGTCCAGTGTGATGTATCAGTGTGAGAGACCTCACC 1413
Db 1381 ACTGATGATATATATGATGAAGAGAGTCCAGTGTGATGTATCAGTGTGAGAGACCTCACC 1440
Qy 1414 CCACCACTTAAACCTGCTATCGAGCTATCAGAAATTATGAAATTTATGTTTCAAAACGG 1473
Db 1441 CCACCACTTAAACCTGCTATCGAGCTATCAGAAATTATGAAATTTATGTTTCAAAACGG 1500
Qy 1474 AAGTTTAAAGAAACGTTACGTCATATGATGTAAAGATGTCAATTGAACAATATTTCTGCT 1533
Db 1501 AAGTTTAAAGAAACATTAAGTCCATATGATGTAAAGATGTCAATTGAACAATATTTCTGCT 1560
Qy 1534 GGTCTATCGGACATGTTGTGTAGAAATTAAGCCCTTCAACACGTTGTGATCAAAATTTCT 1593
Db 1561 GGTCTATCGGACATGTTGTGTAGAAATTAAGCCCTTCAACACGTTGTGATCAAAATTTCT 1620
Qy 1594 GGAAGAGGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1653
Db 1621 GGAAGAGGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1680
Qy 1654 ACCACAGAGCATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713
Db 1681 ACCACAGAGCATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy 1714 ATAGAGTCAAGCTGGACCTCTAGACATCTATCAAGGTCTCTCGGAAAGGCTCT 1773
Db 1741 ATAGAATCAAGCTGGACCTCTAGACATCTATCAAGGTCTCTCGGAAAGGCTCT 1800
Qy 1774 GCTCAGCCCTCGCTTGGCTTCATTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1833
Db 1801 GCTCAGCCCTCGCTTGGCTTCATTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1860
Qy 1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCAACAAACAGTGGCTGC 1893
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCAACAAACAGTGGCTGC 1920
Qy 1894 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCCTGAGTTCAATTCAGCGCAAT 1953
Db 1921 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCCTGAGTTCAATTCAGCGCAAT 1980
Qy 1954 GAGTTTCAGTCCAGACTTTCTACGCGCTTACGCGCTTACGACAGTCAAGCAACACAG 2013
Db 1981 GAGTTTCAGTCCAGACTTTCTACGCGCTTACGCGCTTACGACAGTCAAGCAACACAG 2040
Qy 2014 GTGCCAATTTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCAATTCGCAACCAA 2073
Db 2041 GTGCCAATTTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCAATTCGCAACCAA 2100
Qy 2074 ATAAATAGGCAACCAAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2133
Db 2101 ATAAATAGGCAACCAAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
Qy 2134 GGCATCAGCATCTGCCAGGCCAGAACTCTGACCCCTTACCCCTGAGGCTTACAGAA 2193
Db 2161 GGCATCAGCATCTGCCAGGCCAGAACTCTGACCCCTTACCCCTGAGGCTTACAGAA 2220
Qy 2194 AGCATTTCTGAGCTCACCACCTGCTTGTGCTCCAGAGAAATGTTTCAGGTTGCACAG 2253
Db 2221 AGCATTTCTGAGCTCACCACCTGCTTGTGCTCCAGAGAAATGTTTCAGGTTGCACAG 2280
Qy 2254 TCAATCTCACCAAGGACGTTCTATAGGAAAGCTTTGATCGGAGGAGAACTCTG 2313

Db 2281 TCAATCTCACCAAGGACCGTTCTATAGGAAAGCTTTGATCGGAGGAGAACTCTG 2340
Qy 2314 TTGCTGCTGCTGCCATGTCGCGAGGACTTTGGSCAAATCTTTCTGTGTGCAAAACCTG 2373
Db 2341 TTGCTGCTGCTGCCATGTCGCGAGGACTTTGGSCAAATCTTTCTGTGTGCAAAACCTG 2400
Qy 2374 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGTCCAGA 2433
Db 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGTCCAGA 2460
Qy 2434 GGCACCAAGATTTTACCCCAATGAGGGAATCCAAATTTTATTAAGTCAAGTGAAG 2493
Db 2461 GGCACCAAGATTTTACCCCAATGAGGGAATCCAAATTTTATTAAGTCAAGTGAAG 2520
Qy 2494 GTGGTCCCGAGAGACAGACAGACTTTTGATGCGCACCCAGCCTGCCAGGAA 2553
Db 2521 GTGGTCCCGAGAGACAGACAGACTTTTGATGCGCACCCAGCCTGCCAGGAA 2580
Qy 2554 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2613
Db 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCTCAGAGCAATTTGT 2640
Qy 2614 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA 2667
Db 2641 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA 2694

RESULT 8

AAH49499

ID AAH49499 standard; DNA; 3074 BP.

XX AC AAH49499;

XX DT 11-DEC-2001 (first entry)

XX DE Human KCNQ5 DNA.

XX KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
XX KW anticonvulsant; excitability modulator; membrane potential; neuron;
XX KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
XX KW screening; central nervous system disease; cardiovascular disease; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 110..2908

XX FT /tag= a

XX FT /product= "KCNQ5"

XX PN DE10013732-A1.

XX PD 27-SEP-2001.

XX PF 21-MAR-2000; 2000DE-01013732.

XX PR 21-MAR-2000; 2000DE-01013732.

XX PA (AVET) AVENTIS PHARMA DEUT GMBH.

XX PI Steinmeyer K, Lerche C, Scherer C, Seeborn G, Busch AE;

XX DR WPI; 2001-571700/65.

XX DR P-PSDB; AAB86979.

XX PT New DNA sequence encoding potassium channel KCNQ5, useful in screening
XX PT for specific modulators, potential agents for treating central nervous
XX PT system and cardiovascular diseases.

XX PS Claim 2a; Page 9-10; 20pp; German.

XX CC This invention describes a novel DNA sequence (I) encoding: (i) a
XX CC polypeptide (ii) with potassium channel KCNQ5 activity; (iii) a
XX CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of

CC	the invention have neurological, cardiovascular and anticonvulsant
CC	activity and act as modulators of the voltage-dependent KCNQ5 potassium
CC	channel, a key regulator of membrane potential and modulator of
CC	excitability of electrically activated cells such as neurons and
CC	cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
CC	are used to screen for compounds that modulate the activity of KCNQ5,
CC	potentially useful for treating central nervous system (e.g. epilepsy)
CC	and cardiovascular diseases. This sequence encodes the human potassium
CC	channel KCNQ5 protein described in the invention
XX	
Sequence	3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;
Query Match	98.1%; Score 2617.2; DB 4; Length 3074;
Best Local Similarity	98.7%; Pred. No. 0;
Matches 2659; Conservative	0; Mismatches 8; Indels 27; Gaps 1;
QY	1 ATGAAGGATGTGAGTCGGGCGGGGACGGGTCTCTCTGAACTCGGCACCGCCGACGGGC 60
DB	215 ATGAAGGATGTGAGTCGGGCGGGGACGGGTCTCTCTGAACTCGGCACCGCCGACGGGC 274
QY	61 GACGGCTGTACTGTGTGGACACCGCGGGCCACGCTTGTGTGGCGGCGGTGGCCCTG 120
DB	275 GACGGCTGTACTGTGTGGGCAACCGCGCGGCCACGCTTGTGTGGCGGCGGTGGCCCTG 334
QY	121 AGGAGAGCCCGCGGGGCAAGCAGGGGGCCGGATGAGCCTGTGTGGGAAGCGGTCTCT 180
DB	335 AGGAGAGCCCGCGGGGCAAGCAGGGGGCCGGATGAGCCTGTGTGGGAAGCGGTCTCT 394
QY	181 TACACGAGTAGCAGAGCTCGCGCGCAAGCTCAAGTACCGCGGGTGCAGACTACCTG 240
DB	395 TACACGAGTAGCAGAGCTCGCGCGCAAGCTCAAGTACCGCGGGTGCAGACTACCTG 454
QY	241 TACAACTGTGTGGAGAGACACCGCGGGTGGGGCTTCATCTACCAACGCTTTCGTTTTCTC 300
DB	455 TACAACTGTGTGGAGAGACACCGCGGGTGGGGCTTCATCTACCAACGCTTTCGTTTTCTC 514
QY	301 CTTCCTTTGGTTCCTTGAATTTGTTCAGTGTTTTTACCATTCCTGAGCACACAAATTG 360
DB	515 CTTCCTTTGGTTCCTTGAATTTGTTCAGTGTTTTTACCATTCCTGAGCACACAAATTG 574
QY	361 GCCTCAAGTTCCTTCATCTCGGAGTTCGTGATGATTCGTCTTTGGTTGGAGTTTC 420
DB	575 GCCTCAAGTTCCTTCATCTCGGAGTTCGTGATGATTCGTCTTTGGTTGGAGTTTC 634
QY	421 ATCAATCGAATCTGGTCTGGGGTTGCTGTTCGATATAGAGGATGCGAAGAGACTG 480
DB	635 ATCAATCGAATCTGGTCTGGGGTTGCTGTTCGATATAGAGGATGCGAAGAGAGACTG 694
QY	481 AGGTTTGTCCAAAGCCCTTCGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 540
DB	695 AGGTTTGTCCAAAGCCCTTCGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 754
QY	541 GTTGTTCCTGCAAAACTCAGGGTAATATTTTCCACAGTCTGCACTCAGAGATCTCCGT 600
DB	755 GTTGTTCCTGCAAAACTCAGGGTAATATTTTCCACAGTCTGCACTCAGAGATCTCCGT 814
QY	601 TTCCTACAGATCCTCCGATCGGTGGCATGGACCGAAGGGGAGGCATCTTGGAAATTA 660
DB	815 TTCCTACAGATCCTCCGATCGGTGGCATGGACCGAAGGGGAGGCATCTTGGAAATTA 874
QY	661 GGTTCAGTGGTTATATGCTTCACAGCAAGGAAATTAATACAGCTTCGTATACATAGGATTTTG 720
DB	875 GGTTCAGTGGTTATATGCTTCACAGCAAGGAAATTAATACAGCTTCGTATACATAGGATTTTG 934
QY	721 GFTCTTAATTTTTCCTTTCTCTTCTGCTATCTGGTGGAAAGGATGCCAATAAGAGTTT 780
DB	935 GFTCTTAATTTTTCCTTTCTCTTCTGCTATCTGGTGGAAAGGATGCCAATAAGAGTTT 994
QY	781 TCTACATATGCAGATGCTCTCTGTGGTGGGCAATTAATTCATTTGACAACTATTGGCTATGGA 840
DB	995 TCTACATATGCAGATGCTCTCTGTGGTGGGCAATTAATTCATTTGACAACTATTGGCTATGGA 1054
QY	841 GACAAAATCCCCCTTAACCTTGGCTGGGAAGATTGCTTTCTCGAGGCTTGGACTCTCTTGGC 900

Db 2135 TTATCCAGATCAACTAGTAGTCCCAACATCTCGAGAGGCGCTGCAGTTCATTTCTGACGCAAAAT 2194
Qy 1954 GAGTTTCAGTCCGACAGACTTTCTACGCGCTTAGCCCTACTATCGACAGTCAAGCACACAG 2013
Db 2195 GAGTTTCAGTCCGACAGACTTTCTACGCGCTTAGCCCTACTATCGACAGTCAAGCACACAG 2254
Qy 2014 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTCGCAACCAA 2073
Db 2255 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTCGCAACCAA 2314
Qy 2074 ATAAATACGGCCACCAAGCAGCAGCCCAACAACTTACAGATCCACCTCTCTCCCA 2133
Db 2315 ATAAATACGGCCACCAAGCAGCAGCCCAACAACTTACAGATCCACCTCTCTCCCA 2374
Qy 2134 GCCATCAAGCATCTGCCAGGCGCAGAACTCTGCACCTTAACCTGCAGGCTTACAGAA 2193
Db 2375 GCCATCAAGCATCTGCCAGGCGCAGAACTCTGCACCTTAACCTGCAGGCTTACAGAA 2434
Qy 2194 AGCATTTCTGAGTCAACCACTGCTTGTGCTTCAAGGAAATGTTTCAGTTGCACAG 2253
Db 2435 AGCATTTCTGAGTCAACCACTGCTTGTGCTTCAAGGAAATGTTTCAGTTGCACAG 2494
Qy 2254 TCBAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGCATGGGAGGAGAACTCTG 2313
Db 2495 TCBAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGCATGGGAGGAGAACTCTG 2554
Qy 2314 TTGCTGTCTGTCCATGTCGCGAGGACTTTGGCAAACTTTCTGTGTGCAAAACCTG 2373
Db 2555 TTGCTGTCTGTCCATGTCGCGAGGACTTTGGCAAACTTTCTGTGTGCAAAACCTG 2614
Qy 2374 ATCAGTTCGACCGAGAACTGAATATACAACTTTCAGGAGTGAAGTGGCTCCAGA 2433
Db 2615 ATCAGTTCGACCGAGAACTGAATATACAACTTTCAGGAGTGAAGTGGCTCCAGA 2674
Qy 2434 GCGACCAAGATTTTACCCAAATGGAGGAAATCCAAATGTTTATACATGATGAAG 2493
Db 2675 GCGACCAAGATTTTACCCAAATGGAGGAAATCCAAATGTTTATACATGATGAAG 2734
Qy 2494 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGTCGCGACCGCAGCTGCCAGGAA 2553
Db 2735 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGTCGCGACCGCAGCTGCCAGGAA 2794
Qy 2554 GTCGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGTATCTCAGAGCAATTTGT 2613
Db 2795 GTCGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGTATCTCAGAGCAATTTGT 2854
Qy 2614 AAGCAGAGAAAGTACAGATGCTCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
Db 2855 AAGCAGAGAAAGTACAGATGCTCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908

RESULT 9
ADB78684
ID ADB78684 standard; cDNA; 3074 BP.
XX
AC ADB78684;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human potassium channel subunit mutant cDNA SEQ ID NO:55.
XX
KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephroretic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO2003008574-A1.
XX
PD 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.
XX
XX 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
XX (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin IA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
XX WPI; 2003-239332/23.
XX
XX Identifying predisposition to an ion channel dysfunction, such as
XX periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
XX schizophrenia, anxiety and depression, by detecting encoding-gene
XX mutation events.
XX
XX Claim 6; SEQ ID NO 55; 106pp; English.
XX
XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyrretic,
XX antiarrhythmic, anti-migraine, antidepressant, antiparkinsonian,
XX neuroleptic, tranquiliser, analgesic, nephroretic, antidiabetic, and
XX ion channel agonist, or ion channel antagonist. The methods, isolated
XX nucleic acids, polypeptides, antibody, selective agonist, antagonist or
XX modulator of an ion channel, cells and genetically modified non-human
XX animal, are useful for the diagnosis and treatment of epilepsy and/or a
XX disorder associated with ion channel dysfunction, such as hyper- or hypo-
XX kalemic periodic paralysis, myotonias, malignant hyperthermia,
XX myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
XX disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
XX depression, phobic obsessive symptoms, neuropathic pain, inflammatory
XX pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
XX Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
XX fibrosis, congenital stationary night blindness and total colour
XX blindness. The present sequence represents a mutant cDNA of the
XX invention. The sequence data for this patent is not represented in the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;

Query Match 98.1%; Score 2615.6; DB 10; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2658; Conservative 0; Mismatches 9; Indels 27; Gaps 1;

Qy 1 ATGAAGGATGTGGAGTGGCGCGGCGCAGGAGTGGCTGTAACCTCGGACGCGCCAGGGGC 60
Db 215 ATGAAGGATGTGGAGTGGCGCGGCGCAGGAGTGGCTGTAACCTCGGACGCGCCAGGGGC 274
Qy 61 GACGCGCTGTCTGTGGGACCGCGCGGCGCAGGAGTGGCTGTCGGCGGCGGCGGCTGTG 120
Db 275 GACGCGCTGTCTGTGGGACCGCGCGGCGCAGGAGTGGCTGTCGGCGGCGGCGGCTGTG 334
Qy 121 AGGAGAGAGCGCGCGGCGCAGGAGTGGCTGTCGGCGGCGGCGGCGGCGGCGGCTGTG 180
Db 335 AGGAGAGAGCGCGCGGCGCAGGAGTGGCTGTCGGCGGCGGCGGCGGCGGCGGCTGTG 394
Qy 181 TACACGAGTAGCAGAGTGGCGCGGCGCAGGAGTGGCTGTCGGCGGCGGCGGCGGCGGCTGTG 240
Db 395 TACACGAGTAGCAGAGTGGCGCGGCGCAGGAGTGGCTGTCGGCGGCGGCGGCGGCGGCTGTG 454
Qy 241 TACACGAGTAGCAGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGTG 300
Db 455 TACACGAGTAGCAGAGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGTG 514

QY	301	CTTGTCTTTGGTGTGCTGATTTTGTCTAGTGTCTTTTCTACCATCCTCGAGACACAAAATTG	360	1354	ACTGATGATGATATGATGAAAAAGGATGCGAGTGTGATGTATCAGTGGAGACCTCACC	1413
Db	515	CTTGTCTTTGGTGTGCTGATTTTGTCTAGTGTCTTTTCTACCATCCTCGAGACACAAAATTG	574	1595	ACTGATGATGATATGATGAAAAAGGATGCGAGTGTGATGTATCAGTGGAGACCTCACC	1654
QY	361	GCCTCAAGTTCCTCTTGTATCTCGAGTTCGTGATGATGTCTCTTTTGGTGGATTC	420	1414	CCACCACCTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTTTCTGTTGCAAAACGG	1473
Db	575	GCCTCAAGTTCCTCTTGTATCTCGAGTTCGTGATGATGTCTCTTTTGGTGGATTC	634	1655	CCACCACCTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTTTCTGTTGCAAAACGG	1714
QY	421	ATCATTCGAATCTGCTCGGGTGTCTGTTCGATATAGAGATGGCAAGGAAGACTG	480	1474	AAGTTTAAAGGAAACGTTTACGTCCTATGATCTAAAGATGTCATTGAAACAATATTTCTGCT	1533
Db	635	ATCATTCGAATCTGCTCGGGTGTCTGTTCGATATAGAGATGGCAAGGAAGACTG	694	1715	AAGTTTAAAGGAAACGTTTACGTCCTATGATCTAAAGATGTCATTGAAACAATATTTCTGCT	1774
QY	481	AGGTTTCTCGTCAAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540	1534	GGTCACTCTGGACATGTTCTGTAGAAATTAAGACCTTCAAAACAGCTGTTGATCAAAATCTT	1593
Db	695	AGGTTTCTCGTCAAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	754	1775	GGTCACTCTGGACATGTTCTGTAGAAATTAAGACCTTCAAAACAGCTGTTGATCAAAATCTT	1834
QY	541	GTGTTTCTGCAAAACCTCAGGTTAAATTTTGGCAGCTCTGACCTCAGAACTCTCCGT	600	1594	GGAAGGAGGCAATCAGATCAGATAGAAAGCCGAGAGAAATAACAGCAGAGAACATGAG	1653
Db	755	GTGTTTCTGCAAAACCTCAGGTTAAATTTTGGCAGCTCTGACCTCAGAACTCTCCGT	814	1835	GGAAGGAGGCAATCAGATCAGATAGAAAGCCGAGAGAAATAACAGCAGAGAACATGAG	1894
QY	601	TTCTACAGATCTCCGATGCTCGCATGGATGGACCGAAGGGGAGGCACTTGGAAATTAAGT	660	1654	ACCACAGACGATCTCAGTATGCTCGGTGGTCAAGGTTGAAAAACAGGTACAGTACC	1713
Db	815	TTCTACAGATCTCCGATGCTCGCATGGATGGACCGAAGGGGAGGCACTTGGAAATTAAGT	874	1895	ACCACAGACGATCTCAGTATGCTCGGTGGTCAAGGTTGAAAAACAGGTACAGTACC	1954
QY	661	GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTG	720	1714	ATAGAGTCCAAAGTCCGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	1773
Db	875	GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTG	934	1955	ATAGAGTCCAAAGTCCGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT	2014
QY	721	GTCTCTTATTTTCTGCTCTTCTGTTCTATCTGCTGGAAAGGATGCAATTAAGAGTTT	780	1774	GGCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT	1833
Db	935	GTCTCTTATTTTCTGCTCTTCTGTTCTATCTGCTGGAAAGGATGCAATTAAGAGTTT	994	2015	GGCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT	2074
QY	781	TCTACATATGAGATGCTCTCTGTGGGGCAATTAATCAATGACAACTATTTGGCTATGGA	840	1834	GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCAAAAACAGTGGCTGC	1893
Db	995	TCTACATATGAGATGCTCTCTGTGGGGCAATTAATCAATGACAACTATTTGGCTATGGA	1054	2075	GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCCGCAAAAACAGTGGCTGC	2134
QY	841	GACAAACCTCCCTTAACTTGGCTGGAGATGCTTCTGAGGCTTGGACTCCTTGGC	900	1894	TTATCAGATCAACTAGTCCCAACATCTCGAGAGCCCTGACGTTTCTGAGGCCAAT	1953
Db	1055	GACAAACCTCCCTTAACTTGGCTGGAGATGCTTCTGAGGCTTGGACTCCTTGGC	1114	2135	TTATCAGATCAACTAGTCCCAACATCTCGAGAGCCCTGACGTTTCTGAGGCCAAT	2194
QY	901	ATTTCTTTTCTTGGCACTTCTGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGTACAA	960	1954	GAGTTCAGTCCGACAGATTTTCTACGGCTTACGCTTACTATGACAGTCAAGCAACAG	2013
Db	1115	ATTTCTTTTCTTGGCACTTCTGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGTACAA	1174	2195	GAGTTCAGTCCGACAGATTTTCTACGGCTTACGCTTACTATGACAGTCAAGCAACAG	2254
QY	961	GAAACACCGCCAGAAACACTTTGAGAAAGAGAGAAACCCAGCTGCGCAACCTCATTCAG	1020	2014	GTCCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGGACCAACAAACCAATTTGCAACCAA	2073
Db	1175	GAAACACCGCCAGAAACACTTTGAGAAAGAGAGAAACCCAGCTGCGCAACCTCATTCAG	1234	2255	GTCCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGGACCAACCAACCAATTTGCAACCAA	2314
QY	1021	TGTGTTGGCTAGTTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCA	1080	2074	ATAAATACGGCACCCAGCCAGCCGACCCCAACAACTTTACAGATCCCACTCTCTCCCA	2133
Db	1235	TGTGTTGGCTAGTTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCA	1294	2315	ATAAATACGGCACCCAGCCAGCCGACCCCAACAACTTTACAGATCCCACTCTCTCCCA	2374
QY	1081	CACTTGAAGGCTTGCACACCTGACGCTTACCAA-----	1115	2134	GCATCAAGCATCTGCCAGGCGCAGAAACTCTGACCCCTAACCCCTGACGCTTACAGGAA	2193
Db	1295	CACTTGAAGGCTTGCACACCTGACGCTTACCAA-----	1354	2375	GCATCAAGCATCTGCCAGGCGCAGAAACTCTGACCCCTAACCCCTGACGCTTACAGGAA	2434
QY	1116	---TCGAAAGCTAAGTTTAAAGCGAGTGGCGATGGCTAGCCCGAGGGCCAGAGTAT	1173	2194	AGCATTTCTGACCTCACCACCTCTTGTCCCTCCCAAGGAAATGTTTACAGTTGACAG	2253
Db	1355	AGTCGAAAGCTAAGTTTAAAGCGAGTGGCGATGGCTAGCCCGAGGGCCAGAGTAT	1414	2435	AGCATTTCTGACCTCACCACCTCTTGTTCCTCCCAAGGAAATGTTTACAGTTGACAG	2494
QY	1174	AAGAGCCGACAAAGCTCAGTAGTGACAGGAGTCCCAAGCACCGACATCAAGCCGAG	1233	2254	TCAAATCTCACCAGGACCGTCTTATGAGGAAAGCTTTTACATGAGGAGGAGAACTCTG	2313
Db	1415	AAGAGCCGACAAAGCTCAGTAGTGACAGGAGTCCCAAGCACCGACATCAAGCCGAG	1474	2495	TCAAATCTCACCAGGACCGTCTTATGAGGAAAGCTTTTACATGAGGAGGAGAACTCTG	2554
QY	1234	GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGTTCAACGACCGAACCGCTTCCGGCC	1293	2314	TTGTCCTCTCTGCCATGGTGCAGAGGACTTGGGCAAACTTTTGTCTGTGCAAAACCTG	2373
Db	1475	GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGTTCAACGACCGAACCGCTTCCGGCC	1534	2555	TTGTCCTCTCTGCCATGGTGCAGAGGACTTGGGCAAACTTTTGTCTGTGCAAAACCTG	2614
QY	1294	TGCTGGGCTCAAAAGTTCTCAGCCAAACAGTGTATAGTGTGACACAGCCCTTGGC	1353	2374	ATCAGGTCGACCGAGGAACTGAATATACAACTTTTGTGTCAGGAGTCAAGTGGCTCCAGA	2433
Db	1535	TGCTGGGCTCAAAAGTTCTCAGCCAAACAGTGTATAGTGTGACACAGCCCTTGGC	1594	2615	ATCAGGTCGACCGAGGAACTGAATATACAACTTTTGTGTCAGGAGTCAAGTGGCTCCAGA	2674
QY				2434	GGCAGCCAAAGATTTTACCCTTACGAGGAGAACTCCAAATTTGTTTATACTGATGAAGAG	2493

Db 2675 GGAGGACAAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTATACTGATGAAGAG 2734
QY 2494 GTGGGTCCCGAAGACAGACAGACACATTTTGTATGCGCGACCGCAGCTGCGCAGGAA 2553
Db 2735 GTGGGTCCCGAAGACAGACAGACACATTTTGTATGCGCGACCGCAGCTGCGCAGGAA 2794
QY 2554 GTGGGTCCCGAAGACAGACACATTTTGTATGCGCGACCGCAGCTGCGCAGGAA 2613
Db 2795 GTGGGTCCCGAAGACAGACACATTTTGTATGCGCGACCGCAGCTGCGCAGGAA 2854
QY 2614 AGGCGAGGAAAGTACAGATGCGCTCAGCTTGCCTCAGTCAAACTGAAATTA 2667
Db 2855 AAGGCGAGGAAAGTACAGATGCGCTCAGCTTGCCTCAGTCAAACTGAAATTA 2908

RESULT 10
AAC64371
ID AAC64371 standard; cDNA; 3718 BP.
XX AAC64371;
AC
XX
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW Human; KCNQ5; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ss.

OS Homo sapiens.
XX
XX WO200061606-A1.
PN
XX 19-OCT-2000.
PD
XX 10-APR-2000; 2000WO-US009587.
PF
XX 14-APR-1999; 99US-0129274P.
PR
XX (MERI) MERCK & CO INC.
PA
XX Petrukhin K, Caskey CT, Li W, Metzker ML;
PI
XX WPI; 2000-647417/62.
DR
XX P-PSDB; AAB24241.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
PT dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS Claim 3; Fig 2; 99pp; English.
XX
CC The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
CC which is a voltage-gated potassium channel protein. Human KCNQ5 has
CC ophthalmological, auditory, central nervous system (CNS), cardioactive,
CC anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
CC identifying activators or inhibitors of KCNQ5 protein. These activators
CC and inhibitors are useful for treating Stargardt-like macular dystrophy,
CC cone-rod dystrophy, Salla disease, age-related macular degeneration,
CC other forms of macular degeneration, deafness, epilepsy, and different
CC forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
CC chromosome 6q

SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;

Query Match 94.5%; Score 2521; DB 3; Length 3718;

Best Local Similarity 98.6%; Pred. No. 0;
Matches 2564; Conservative 0; Mismatches 10; Indels 27; Gaps 1;
QY 94 AGCTTTGTTGGCGCGCGCTGCGCTGAGGAGAGCCGCGGGGCAAGCAGGGGCGCGG 153
Db 78 ACTGCTGAGGACTGCGCGCGTGGCTTGGAGGAGAGCCGCGGGGCAAGCAGGGGCGCGG 137
QY 154 ATGAGCTGCTCGGGGAAGCGCTCTCTTACACAGTAGCAGAGCTGCCGGGCAACGTC 213
Db 138 ATGAGCTGCTCGGGGAAGCGCTCTCTTACACAGTAGCAGAGCTGCCGGGCAACGTC 197
QY 214 AAGTACCGCGCGGTGAGAACTACCTGTACAACTGTCTGGAGAGACCCCGCGCTGGCG 273
Db 198 AAGTACCGCGCGGTGAGAACTACCTGTACAACTGTCTGGAGAGACCCCGCGCTGGCG 257
QY 274 TTCACTACACGCTTTGCTTTTCTCTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTT 333
Db 258 TTCACTACACGCTTTGCTTTTCTCTTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTT 317
QY 334 TCTACCATCCCTGAGCACACAAAATTGGCTCAAGTTGCTCTTGATCTCGAGTTGCTG 393
Db 318 TCTACCATCCCTGAGCACACAAAATTGGCTCAAGTTGCTCTTGATCTCGAGTTGCTG 377
QY 394 ATGATTGCTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 453
Db 378 ATGATTGCTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 437
QY 454 CGATATAGAGGATGCAAGGAGAGCTGAGGTTTGTCTGAAAGCCCTTCTGTGTATAGAT 513
Db 438 CGATATAGAGGATGCAAGGAGAGCTGAGGTTTGTCTGAAAGCCCTTCTGTGTATAGAT 497
QY 514 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATTTT 573
Db 498 ACCATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATTTT 557
QY 574 GCCAGTCTGCACTCAGAACTCTCGTTTCTTACAGATCTCCGATGTTGTCGATGGAC 633
Db 558 GCCAGTCTGCACTCAGAACTCTCGTTTCTTACAGATCTCCGATGTTGTCGATGGAC 617
QY 634 CGAAGGAGGAGCCTTGGAATTTACTGGTTTCAGTGGTTTATGCTCAGAGCAAGGAATTA 693
Db 618 CGAAGGAGGAGCCTTGGAATTTACTGGTTTCAGTGGTTTATGCTCAGAGCAAGGAATTA 677
QY 694 ATCAGAGCTTGTACATAGGATTTTGTGTTCTTATTTTTCGTTCTTCTGTTCTATCTG 753
Db 678 ATCAGAGCTTGTACATAGGATTTTGTGTTCTTATTTTTCGTTCTTCTGTTCTATCTG 737
QY 754 GTGAAAAGGATGCCAATAAAGAGTTTCTACATATGAGATGCTCTCTGTGGGGCACA 813
Db 738 GTGAAAAGGATGCCAATAAAGAGTTTCTACATATGAGATGCTCTCTGTGGGGCACA 797
QY 814 ATTACATTGACAACTATTGGCTATGAGACAAACTCCCTTAACCTTGGCTGGGAAGATG 873
Db 798 ATTACATTGACAACTATTGGCTATGAGACAAACTCCCTTAACCTTGGCTGGGAAGATG 857
QY 874 CTTTCTGAGGCTTTGCACTCTCTTGGCATTTCTTTTGTGCACTTCTCTCCCGCATTC 933
Db 858 CTTTCTGAGGCTTTGCACTCTCTTGGCATTTCTTTTGTGCACTTCTCTCCCGCATTC 917
QY 934 GGCTCAGGTTTGTCAATTAAGTACAAGAAACACCGCGAGAAACACTTTTGAGAAAAA 993
Db 918 GGCTCAGGTTTGTCAATTAAGTACAAGAAACACCGCGAGAAACACTTTTGAGAAAAA 977
QY 994 AGGACCCAGCTGCCAAGCTCAATTCAGTGTGTTTGGCGTAGTTACGACGCTCATGAGAA 1053
Db 978 AGGACCCAGCTGCCAAGCTCAATTCAGTGTGTTTGGCGTAGTTACGACGCTCATGAGAA 1037
QY 1054 TCTGTTTCCATTGCAACCTGGAAGCCACACTTTGAAAGGCTTGCACACCTGACCCCTACC 1113
Db 1038 TCTGTTTCCATTGCAACCTGGAAGCCACACTTTGAAAGGCTTGCACACCTGACCCCTACC 1097
QY 1114 AA-----TCAGAAAGCTTAAGTTTAAAGGAGGAGTGCGC 1146
||

Db	1098	AAGAAAGAACAGAGGGAGCATCAAGCAGTCAGAACGCTAAGTTTAAAGGACGAGTGGCG	1157
Qy	1147	ATGCTAGCCCCAGGGCCAGAGTATTAAAGAGCCGACAAGCCTCAGTAGGTGACAGGAG	1206
Db	1158	ATGCTAGCCCCAGGGCCAGAGTATTAAAGAGCCGACAAGCCTCAGTAGGTGACAGGAG	1217
Qy	1207	TCCCCAAGCAGCAGATACAGAGCGAGGAGTCCCAACCAAGTGCAAGAGAGTGGAGC	1266
Db	1218	TCCCCAAGCAGCAGATACAGAGCGAGGAGTCCCAACCAAGTGCAAGAGAGTGGAGC	1277
Qy	1267	TTCAAGCAGCAACCCGCTCCGCGCTCGCTCGCTCAAAAGTCTCAGCCAAAACCA	1326
Db	1278	TTCAAGCAGCAACCCGCTCCGCGCTCGCTCGCTCAAAAGTCTCAGCCAAAACCA	1337
Qy	1327	GTGATAGATGTGACACAGACCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAG	1386
Db	1338	GTGATAGATGTGACACAGACCCCTTGGCACTGATGATGTATATGATGAAAAAGGATGCCAG	1397
Qy	1387	TGTGATGATCAGTGGAAAGACTCACCCACCACTTAAACTGTCAATCGAGCTATCAGA	1446
Db	1398	TGTGATGATCAGTGGAAAGACTCACCCACCACTTAAACTGTCAATCGAGCTATCAGA	1457
Qy	1447	ATTATGAATTTCAATGTTGCAAAACGGAAGTTTAAAGAAAGCTTACGTCCATATGATCTA	1506
Db	1458	ATTATGAATTTCAATGTTGCAAAACGGAAGTTTAAAGAAAGCTTACGTCCATATGATCTA	1517
Qy	1507	AAAGATGTCAATGAAACAATTTCTGCTGGTCACTGTGGAATGTTGTGTAGAAATTAAGC	1566
Db	1518	AAAGATGTCAATGAAACAATTTCTGCTGGTCACTGTGGAATGTTGTGTAGAAATTAAGC	1577
Qy	1567	CTTCAACACAGTGTGATCAATTTCTGGAAGAGGCAAAATCACATCAGATTAAGAGAGC	1626
Db	1578	CTTCAACACAGTGTGATCAATTTCTGGAAGAGGCAAAATCACATCAGATTAAGAGAGC	1637
Qy	1627	CCAGAGAAATAACAGCAGACATCAGACACCAAGATCTCAGTATGCTCGGTGGGTG	1686
Db	1638	CGAGAGAAATAACAGCAGACATCAGACACCAAGATCTCAGTATGCTCGGTGGGTG	1697
Qy	1687	GTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGACTGCTACTAGACATC	1746
Db	1698	GTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGGACTGCTACTAGACATC	1757
Qy	1747	TATCAACAGTCTCTCGGAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATTCAGATC	1806
Db	1758	TATCAACAGTCTCTCGGAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATTCAGATC	1817
Qy	1807	CCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAGATCTT	1866
Db	1818	CCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAGATCTT	1877
Qy	1867	TGGGTTCCGCAAAACAGTGGCTGCTTATCCAGATCAATAGTCCCAACATCTCGAGA	1926
Db	1878	TGGGTTCCGCAAAACAGTGGCTGCTTATCCAGATCAATAGTCCCAACATCTCGAGA	1937
Qy	1927	GGCTCAGTTCATCTCAGCGCAATAGTTCAGTCCAGCATCTTCTACCGCTTAGC	1986
Db	1938	GGCTCAGTTCATCTCAGCGCAATAGTTCAGTCCAGCATCTTCTACCGCTTAGC	1997
Qy	1987	CCTACTATGCAGTCAAGCAACACAGGTGCCAATAGTCAAGCGATGGCTCAGCAGTG	2046
Db	1998	CCTACTATGCAGTCAAGCAACACAGGTGCCAATAGTCAAGCGATGGCTCAGCAGTG	2057
Qy	2047	GCAGCCACCAACACCATTCGAACCAATAATAGCGCACCCCAAGCCAGCAGCCCAACA	2106
Db	2058	GCAGCCACCAACACCATTCGAACCAATAATAGCGCACCCCAAGCCAGCAGCCCAACA	2117
Qy	2107	ACTTTACAGATCCCACTCTCTCCAGGCATCAAGCATCTGCCCCAGCGCCAGAACTCTG	2166
Db	2118	ACTTTACAGATCCCACTCTCTCCAGGCATCAAGCATCTGCCCCAGCGCCAGAACTCTG	2177
Qy	2167	CACCTTAACCTCAGGCTTACAGGAAGATTTCTGAGTCAACACCTGCTTGGC	2226
Db	2178	CACCTTAACCTCAGGCTTACAGGAAGATTTCTGAGTCAACACCTGCTTGGC	2237

Qy	2227	TCCAAGGAAATGTTTCAGTTTCAGTTCACCAAGGACCGTTCTTATGAGGAAA	2286
Db	2238	TCCAAGGAAATGTTTCAGTTTCAGTTCACCAAGGACCGTTCTTATGAGGAAA	2297
Qy	2287	AGCTTTGACATGGGAGGAGAAAACCTCTGTTGTTCTGTCTGTCCATGGTCCGAGGACTTG	2346
Db	2298	AGCTTTGACATGGGAGGAGAAAACCTCTGTTGTTCTGTCTGTCCATGGTCCGAGGACTTG	2357
Qy	2347	GGCAAAATCTTGTCTGTGCAAAACCTTGATCAGGTGACCGAGGAACTGAATATCAAACTT	2406
Db	2358	GGCAAAATCTTGTCTGTGCAAAACCTTGATCAGGTGACCGAGGAACTGAATATCAAACTT	2417
Qy	2407	TCAGGAGTGAAGTCAAGTGGCTCCAGAGGACCAAGATTTTACCCAAATGGAGGAAA	2466
Db	2418	TCAGGAGTGAAGTCAAGTGGCTCCAGAGGACCAAGATTTTACCCAAATGGAGGAAA	2477
Qy	2467	TCCAATTTGTTTATAACTGATGAAGAGTGGTCCGAAAGACAGACAGACATTTT	2526
Db	2478	TCCAATTTGTTTATAACTGATGAAGAGTGGTCCGAAAGACAGACAGACATTTT	2537
Qy	2527	GATCCGCGACCGCAGCTGCCAGGGAAGCTGCTTGCATCAGACTCTCTAAGGACTGGA	2586
Db	2538	GATCCGCGACCGCAGCTGCCAGGGAAGCTGCTTGCATCAGACTCTCTAAGGACTGGA	2597
Qy	2587	AGGTCAAGATCATCTCAGAGCATTTTGAAGCGAGGAAAAGTACAGATGCCCTCAGCTTG	2646
Db	2598	AGGTCAAGATCATCTCAGAGCATTTTGAAGCGAGGAAAAGTACAGATGCCCTCAGCTTG	2657
Qy	2647	CCTCATGTCAAACTGAAATAA	2667
Db	2658	CCTCATGTCAAACTGAAATAA	2678

RESULT 11

AAC64370

ID AAC64370 standard; DNA; 125910 BP.

AC AAC64370;

XX

XX 07-FEB-2001 (first entry)

XX Human KCNQ5 (KCN6q) gene sequence SEQ ID NO:1.

XX Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;

XX Stargardt-like macular dystrophy; cone-rod macular dystrophy;

XX Salla disease; ophthalmological; auditory; central nervous system;

XX cardioactive; anticonvulsant; gastrointestinal; muscular active;

XX age-related macular degeneration; macular degeneration; deafness;

XX epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;

XX gastrointestinal disorder; ds.

XX Homo sapiens.

XX WO200061606-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-US009587.

XX 14-APR-1999; 99US-0129274P.

XX (MERI) MERCK & CO INC.

XX Petrukhin K, Caskey CT, Li W, Metzker ML;

XX WPI; 2000-647417/62.

XX P-PSDB; AAB24241.

XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying

XX inhibitors and activators which can treat e.g. Stargardt-like macular

XX dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.

Claim 3; Fig 1; 99pp; English.

The present sequence represents the human KCNQ5 (also called KCM6q) gene, which encodes a voltage-gated potassium channel protein. Human KCNQ5 has ophthalmological, auditory, central nervous system (CNS), cardioactive, anticonvulsant, gastrointestinal and muscular active activities. Sequences and methods from the present invention are useful for identifying activators or inhibitors of KCNQ5 protein. These activators and inhibitors are useful for treating Stargardt-like macular dystrophy, cone-rod dystrophy, Salla disease, age-related macular degeneration, other forms of macular degeneration, deafness, epilepsy, and different forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders. Stargardt-like macular dystrophy and cone-rod dystrophies are located at chromosome 6q

Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other;

Query Match 36.1%; Score 963.4; DB 3; Length 125910;

Best Local Similarity 99.9%; Pred. No. 6.6e-272;

Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1703	AGGTACAGTCCATAGATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTC	1762
DB	123624	AGGTACAGTCCATAGATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTC	123683
QY	1763	GGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTG	1822
DB	123684	GGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTG	123743
QY	1823	AACAGACATCTGATATCAATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGACAAA	1882
DB	123744	AACAGACATCTGATATCAATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCCGACAAA	123803
QY	1883	ACAGTGGCTGCTTATCCAGATCAATAGTGCACATCTCGAGAGCCCTGCAATTCATTC	1942
DB	123804	ACAGTGGCTGCTTATCCAGATCAATAGTGCACATCTCGAGAGCCCTGCAATTCATTC	123863
QY	1943	TGACGCCAAATGAGTTGAGTCCAGACCTTTTACGCGCTTAGCCCTACTATGCACAGTC	2002
DB	123864	TGACGCCAAATGAGTTGAGTCCAGACCTTTTACGCGCTTAGCCCTACTATGCACAGTC	123923
QY	2003	RAGCAACACAGTGGCAATAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACA	2062
DB	123924	RAGCAACACAGTGGCAATAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACA	123983
QY	2063	TTGCAAAACCAATAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCAC	2122
DB	123984	TTGCAAAACCAATAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCAC	124043
QY	2123	CTCCTCTCCAGCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTTAACCCCTGCAG	2182
DB	124044	CTCCTCTCCAGCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTTAACCCCTGCAG	124103
QY	2183	GCTTACAGAAAGCATTTCTGACGTCAACCTGCTTGTGCTTCCCAAGGAAATGTC	2242
DB	124104	GCTTACAGAAAGCATTTCTGACGTCAACCTGCTTGTGCTTCCCAAGGAAATGTC	124163
QY	2243	AGTTGTCACAGTCAATCTCACCAGGACCGTTCTATGAGGAAAGCTTGCATGGGAG	2302
DB	124164	AGTTGTCACAGTCAATCTCACCAGGACCGTTCTATGAGGAAAGCTTGCATGGGAG	124223
QY	2303	GAGAAACTCTGTGTCTGCTCTCCATGGTGGCCGAGACCTTGGGCAAACTTTGTCTG	2362
DB	124224	GAGAAACTCTGTGTCTGCTCTCCATGGTGGCCGAGACCTTGGGCAAACTTTGTCTG	124283
QY	2363	TGCAAAACCTGATCAGGTGCAGCCAGGAACTGAATATACAACTTTCCAGGATGAGTCAA	2422
DB	124284	TGCAAAACCTGATCAGGTGCAGCCAGGAACTGAATATACAACTTTCCAGGATGAGTCAA	124343
QY	2423	GTGGCTCCAGAGCCAGCAAGATTTTACCCCAATGAGGGAATCCAAATGTTTATAA	2482
DB	124344	GTGGCTCCAGAGCCAGCAAGATTTTACCCCAATGAGGGAATCCAAATGTTTATAA	124403

QY	2483	CTGATGAAGAGTGGTCCCGAAGAGACAGACAGACACACTTTTGTATGCCGACCGCAGC	2542
DB	124404	CTGATGAAGAGTGGTCCCGAAGAGACAGACAGACAGACACTTTTGTATGCCGACCGCAGC	124463
QY	2543	CTGCCAGGAAGCTCCCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTC	2602
DB	124464	CTGCCAGGAAGCTCCCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTC	124523
QY	2603	AGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTCA	2662
DB	124524	AGAGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTCA	124583
QY	2663	AATAA 2667	
DB	124584	AATAA 124588	
RESULT 12			
ACA04855			
ID	ACA04855	standard; cDNA; 582 BP.	
XX	ACA04855;		
XX	28-MAY-2003	(first entry)	
XX		cDNA encoding human membrane associated protein fragment #303.	
XX		Human; ss; gene; microarray; membrane-associated protein; neuropathology;	
KW		immunopathology; pancreatic disease; cancer; diabetes; hyperlipidaemia;	
KW		pancreatic cholera; Alzheimer's disease; Huntington's disease; sarcoma;	
KW		fibrocystic disease; leukaemia; adenocarcinoma; AIDS; allergy; anaemia;	
XX		asthma; gout; dementia.	
OS		Homo sapiens.	
XX		US6492505-B1.	
XX		10-DEC-2002.	
XX		31-JAN-2000; 2000US-00495050.	
XX		01-FEB-1999; 99US-0118318P.	
XX		(INCY-) INCYTE GENOMICS INC.	
XX		Reddy R, Guegler KJ, Au-Young J;	
XX		WPI; 2003-327324/31.	
XX		Combination for research/diagnostic applications and for monitoring	
PT		treatment of e.g., cancer, comprises polynucleotides comprising a	
PT		fragment of gene encoding membrane-associated proteins, receptors or ion	
PT		channels.	
XX		Claim 1; Fig 2; 147pp; English.	
XX		The invention relates to a combination comprising several polynucleotide	
CC		sequences comprising a fragment of gene encoding membrane-associated	
CC		proteins, receptors or ion channels. The combination is useful as a	
CC		probe, for research and diagnostic applications, for monitoring the	
CC		expression of several expressed polynucleotides, in the diagnosis and	
CC		monitoring of treatment of pancreatic disease, cancer, immunopathology or	
CC		neuropathology, for investigating an individual's predisposition to the	
CC		above disease, in genetic or gene expression analysis of polynucleotide	
CC		sequences, to investigate cellular responses to infection or drug	
CC		treatment, as hybridisable array elements in a microarray, to purify a	
CC		subpopulation of mRNAs, cDNAs or genomic fragments in a sample, in	
CC		diagnostics, prognostics and treatment regimens, in drug discovery and	
CC		development, in toxicological and carcinogenicity studies, and in	
CC		forensics or pharmacogenomics, to monitor the progression of disease, to	
CC		monitor the efficacy of treatment, to diagnose the conditions of the	
CC		pancreas e.g. diabetes, pancreatic cholera, hyperlipidaemia or	
CC		fibrocystic disease, to diagnose a cancer e.g. leukaemia, adenocarcinoma	

or sarcoma, to diagnose immunopathologies e.g. AIDS, allergies, anaemia, athma or gout, to diagnose neuropathologies e.g. Alzheimer's disease, dementia or Huntington's disease, to rapidly screen large numbers of candidate drug molecules and as query sequences against GenBank, SwissProt, BLOCKS and PRINTS databases. The combination is employed to fine tune the treatment regimen and thus the expression patterns associated with undesirable side effects are avoided. The present sequence represents a cDNA encoding a fragment of gene encoding human membrane-associated proteins, receptors or ion channels

Sequence 582 BP; 180 A; 157 C; 125 G; 120 T; 0 U; 0 Other;

Query Match 19.1%; Score 509.8; DB 8; Length 582;
Best Local Similarity 99.4%; Pred. No. 2.4e-139;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1594 GGAAAGGCAAAATCAATCATAGTAAGAGCGCGAGAGAAATTAACAGCAGACATGAG 1653
1 GGAAAGGCAAAATCAATCATAGTAAGAGCGCGAGAGAAATTAACAGCAGACATGAG 60

1654 ACCACAGAGATCCAGTATCTCGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1713
61 ACCACAGAGATCTCAGTATCTCGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 120

1714 ATAGAGTCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT 1773
121 ATAGATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT 180

1774 GCCTCAGCGCTCGCTTGGCTTCATCCAGATCCACCTTTTGAATGTGAACACATCT 1833
181 GCCTCAGCGCTCGCTTGGCTTCATCCAGATCCACCTTTTGAATGTGAACACATCT 240

1834 GACTATCAAGGCTGTGGATAGCAAGATCTTTTCGGGTTCGCAACAAACAGTGGCTGC 1893
241 GACTATCAAGGCTGTGGATAGCAAGATCTTTTCGGGTTCGCAACAAACAGTGGCTGC 300

1894 TTATCCAGATCAACTAGTGGCAATCTTCGAGAGCGCTGAGTTCATCTCAGCCCAAT 1953
301 TTATCCAGATCAACTAGTGGCAATCTTCGAGAGCGCTGAGTTCATCTCAGCCCAAT 360

1954 GAGTTCAGTCCGACACTTCTACGGCTTACGCTTACTATGACAGTCAAGCAACACAG 2013
361 GAGTTCAGTCCGACACTTCTACGGCTTACGCTTACTATGACAGTCAAGCAACACAG 420

2014 GTGCCAATTAGTCAAGCGATGGCTCAGAGTGGCAGCCACCAACACCATTCGAACCAA 2073
421 GTGCCAATTAGTCAAGCGATGGCTCAGAGTGGCAGCCACCAACACCATTCGAACCAA 480

2074 ATAAATACGGCCCAAGCCAGCGAGCCCAACCAACTTTTACAGATC 2118
481 ATAAATACGGCCCAAGCCAGCGAG-CCCAACCAACTTTTACAGATC 524

RESULT 13
AAA47618
ID AAA47618 standard; cDNA; 2335 BP.
XX
AC AAA47618;
XX
DT 08-NOV-2000 (first entry)
XX
DE KCNQ4 Potassium channel gene.
XX
KW KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;
KW deafness; proboscis; treatment; therapy; transgenic animal; antibody;
KW agonist; antagonist; tinnitus; hearing loss; neonatal deafness;
KW presbycusis; affective disorder; Alzheimer's disease; anxiety; ataxia;
KW cognitive deficits; compulsive behavior; dementia; depression;
KW Huntington's disease; mania; memory impairment; motor disorders;
KW neurodegenerative disease; Parkinson's disease; Pick's disease;
KW psychosis; schizophrenia; spinal cord damage; stroke; tremor; ds.
XX
OS Homo sapiens.

Key Location/Qualifiers
CDS 83..2170
/*tag= a
/product= "KCNQ4 Potassium channel polypeptide"

WO200044786-A1.
XX
XX 03-AUG-2000.
XX
XX 19-JAN-2000; 2000WO-DK000024.
XX
XX 26-JAN-1999; 99DK-00000076.
XX 19-MAY-1999; 99DK-00000693.
XX
XX (NEUR-) NEUROSEARCH AS.
XX
XX Jentsch TJ;
XX
XX WPI: 2000-548813/50.
XX P-PSDB; AAB01476.
XX
XX Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's diseases.
XX
XX Claim 1; Page 43-48; 65pp; English.
XX
XX Mutations in 3 known genes of the KCNQ branch of the potassium channel gene family underlie inherited cardiac arrhythmias, neonatal epilepsy and in some cases associated with deafness. KCNQ4 has been mapped to the DFN2 locus for autosomal dominant hearing loss, and a dominant negative KCNQ4 mutation that causes deafness in a DFN2 pedigree has been identified. KCNQ4 is the first potassium channel gene underlying non-syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4 protein and the protein itself may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate KCNQ4 expression. The nucleotides may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples and to identify mutations within them, and hence which patients may be in need of restorative therapy. They may also be used to study the expression and function of KCNQ4 polypeptides and their role in metabolism, for example through the production of transgenic animals. The KCNQ4 polypeptides may be used as (agonists and antagonists) of KCNQ4 expression and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate KCNQ4 expression and activity. They may be used in this way to treat tinnitus, loss of hearing (especially progressive hearing loss, neonatal deafness and presbycusis (deafness of the elderly)) and disease or adverse conditions of the central nervous system (CNS) such as affective disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative illness, cognitive deficits, compulsive behavior, dementia, depression, Huntington's disease, mania, memory impairment, motor disorders and dysfunctions, motion disorders, motor disorders, neurodegenerative diseases, Parkinson's disease, Parkinson-like motor disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal cord damage, stroke and/or tremor. Conversely, antisense nucleic acid molecules may be administered to down regulate KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing their expression

Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 18.4%; Score 492; DB 3; Length 2335;
Best Local Similarity 59.3%; Pred. No. 1e-133;
Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

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Tue Apr 12 17:15:11 2005

PR 15-MAR-2002; 2002US-0364529P.
 PR 19-APR-2002; 2002US-0373861P.
 PR 29-APR-2002; 2002US-0376287P.
 PR 12-JUN-2002; 2002US-0388080P.
 PR 24-JUN-2002; 2002US-0390971P.
 PR 03-JUL-2002; 2002US-0394113P.
 PR 10-JUL-2002; 2002US-0394797P.
 PR 21-AUG-2002; 2002US-0404904P.
 PR 23-AUG-2002; 2002US-0405450P.
 PR 04-SEP-2002; 2002US-0408070P.
 PR 06-NOV-2002; 2002US-0424300P.
 PR 05-DEC-2002; 2002US-0431042P.
 PR 05-DEC-2002; 2002US-0431079P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
 PI Stagliano N, Perodin J, Rodrigue-Way A;
 XX P-PSDB; ADE31699.
 DR WPI; 2003-731468/69.
 XX
 PT Identifying a compound capable of treating a cardiovascular disorder
 PT (e.g. atherosclerosis) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 1692, 6169 or 6193
 PT polypeptide or nucleic acid.
 PT
 PS Disclosure; SEQ ID NO 55; 328pp; English.
 XX
 CC The invention relates to a method for identifying a compound capable of
 CC treating a cardiovascular disorder. The present invention identifies the
 CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
 CC 43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
 CC 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 33394, 3484,
 CC 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
 CC 2868, 283, 2534, 9464, 17799, 26686, 43848, 32135, 13208, 2914, 51130,
 CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
 CC 6585 genes in cardiovascular disease states. The methods are useful in
 CC diagnosing, preventing and treating cardiovascular disorders, such as
 CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
 CC restenosis, arterial inflammation, vascular wall remodeling, coronary
 CC microembolism, tachycardia, bradycardia, pressure overload, aortic
 CC bending, coronary artery ligation, vascular heart disease, valvular
 CC disease, including but not limited to, valvular degeneration caused by
 CC calcification, rheumatic heart disease, endocarditis, or complications of
 CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
 CC heart failure, sinus node dysfunction, angina, heart failure,
 CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
 CC including but not limited to, pericardial effusion and pericarditis;
 CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
 CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
 CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
 CC cardiovascular developmental disorders. The methods may also be used for
 CC identifying compounds that modulate cardiovascular disorders. Sequences
 CC given in ADE31644-ADE31769 represent the genes and proteins that may be
 CC regulated by a compound of the invention.
 XX
 XX Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;
 SQ
 Query Match 18.4%; Score 492; DB 10; Length 2335;
 Best Local Similarity 59.3%; Pred. No. 1e-133;
 Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;
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 QY 277 ATCTACACGCTTTCGTTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 336
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-810-796-3

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2662.2	99.8	3111	9	US-09-825-147-3
5	2662.2	99.8	3111	18	US-10-803-268-3
6	2630	98.6	2694	9	US-09-866-020-1
7	2630	98.6	2694	9	US-09-810-796-2
8	2630	98.6	2694	19	US-10-948-493-1
9	2626.4	98.5	3071	9	US-09-810-796-1
10	2625.2	98.4	3137	18	US-10-661-629-1
11	2617.2	98.1	3074	9	US-09-813-148-1

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13	492	18.4	2335	17	US-10-353-690-55	Sequence 55, Appl
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15	489.2	18.3	2273	16	US-10-096-578-88	Sequence 88, Appl
16	475.6	17.8	2169	13	US-10-128-870-22	Sequence 22, Appl
17	475.6	17.8	2169	14	US-10-131-685-22	Sequence 22, Appl
18	472.2	17.7	7411	18	US-10-335-053-6	Sequence 6, Appli
19	472.2	17.7	7420	17	US-10-295-027-281	Sequence 281, App
20	472.2	17.7	7420	18	US-10-643-795A-75	Sequence 75, Appl
21	472.2	17.7	7420	19	US-10-948-518-75	Sequence 75, Appl
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24	465.4	17.5	896	14	US-10-131-685-1	Sequence 1, Appli
25	465	17.4	548	10	US-09-826-734-269	Sequence 269, App
26	452	16.9	575	15	US-10-313-542-305	Sequence 305, App
27	445.2	16.7	5595	18	US-10-820-307-8	Sequence 8, Appli
28	427.4	16.0	1848	18	US-10-744-796-5	Sequence 5, Appli
29	427.2	16.0	2565	13	US-10-128-870-26	Sequence 26, Appl
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39	423.8	15.9	2755	18	US-10-820-307-4	Sequence 4, Appli
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41	423.4	15.9	1425	10	US-09-873-319-313	Sequence 313, App
42	423.4	15.9	1425	16	US-10-116-712-662	Sequence 662, App
43	423.4	15.9	1878	18	US-10-744-796-3	Sequence 3, Appli
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45	423.4	15.9	2619	15	US-10-345-680-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Query Match 100.0%; Score 2667; DB 9; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0;
Matches: 2667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

US-09-825-147-1

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; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kiehl, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
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Query Match 99.8%; Score 2662.2; DB 9; Length 2772;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 |ATGAGGATGTGAGTTCGGGCGGGGAGGGTGTCTGCTGAACTCGGCAGCCCGCAGGGGC| 60
Db 106 |ATGAGGATGTGAGTTCGGGCGGGGAGGGTGTCTGCTGAACTCGGCAGCCCGCAGGGGC| 165
QY 61 |GACGGCTCTACTGCTGGGCAACCGCGCGGCAAGCTTGGTGGCGGCGGCGGTGGCCCTG| 120
Db 166 |GACGGCTCTACTGCTGGGCAACCGCGCGGCAAGCTTGGTGGCGGCGGCGGTGGCCCTG| 225
QY 121 |AGGAGAGCCCGCGGCAAGCAGGGGCGCCGGATGAGCTCTGCTGGGGAAGCCGCTCTCT| 180
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Db 226 |AGGAGAGCCCGCGGCAAGCAGGGGCGCCGGATGAGCTCTGCTGGGGAAGCCGCTCTCT| 285
QY 181 |TACACAGCTTACAGAGCTGCGGCGCACAGTCAAGTACCGGGGGTGCAGAACTACCTG| 240
Db 286 |TACACAGTACAGAGCTGCGGCGCACAGTCAAGTACCGGGGGTGCAGAACTACCTG| 345
QY 241 |TACACAGTCTGAGAGAGACCCCGCGCTGGGGCTTCATCTACACGCTTTCGTTTTC| 300
Db 346 |TACACAGTCTGAGAGAGACCCCGCGCTGGGGCTTCATCTACACGCTTTCGTTTTC| 405
QY 301 |CTTGCTTTTGGTGTCTGATTTTGTCAAGTTCATCATCCCTGAGACACAAATTTG| 360
Db 406 |CTTGCTTTTGGTGTCTGATTTTGTCAAGTTCATCATCCCTGAGACACAAATTTG| 465
QY 361 |GCTCAAGTTCCTCTGATCTGAGTTTGTGATGTTTGTCTTGTGTTTGGTTTGGATTC| 420
Db 466 |GCTCAAGTTCCTCTGATCTGAGTTTGTGATGTTTGTCTTGTGTTTGGTTTGGATTC| 525
QY 421 |ATCATTCGAATCTGCTGCGGGTTCGTTTGTGATATAGAGGATGGCAAGGAAGCTG| 480
Db 526 |ATCATTCGAATCTGCTGCGGGTTCGTTTGTGATATAGAGGATGGCAAGGAAGCTG| 585
QY 481 |AGGTTTGTCTGAAAGCCCTTCTGTTTATAGATACATTTGTTCTTATCGCTTCAATAGCA| 540
Db 586 |AGGTTTGTCTGAAAGCCCTTCTGTTTATAGATACATTTGTTCTTATCGCTTCAATAGCA| 645
QY 541 |GTTGTTTCTGCAAAACTCAGGGTAAATTTTTTGGCAGCTCTGCACTCAGAAAGTCTCCGT| 600
Db 646 |GTTGTTTCTGCAAAACTCAGGGTAAATTTTTTGGCAGCTCTGCACTCAGAAAGTCTCCGT| 705
QY 601 |TTCCTACAGATCCTCCGATGCTGCGCATGGAACGAGGGAGGACATTTGGAATTTACTG| 660
Db 706 |TTCCTACAGATCCTCCGATGCTGCGCATGGAACGAGGGAGGACATTTGGAATTTACTG| 765
QY 661 |GGTTCAGTGGTTTATGCTCAGAGCAAGAAATTAATCAGCTTGGTACATAGGATTTTGG| 720
Db 766 |GGTTCAGTGGTTTATGCTCAGAGCAAGAAATTAATCAGCTTGGTACATAGGATTTTGG| 825
QY 721 |GTTCTTATTTTTCGTTCTTCTGCTATCTGTTGGAAGGATGCAATTAAGAGTTT| 780
Db 826 |GTTCTTATTTTTCGTTCTTCTGCTATCTGTTGGAAGGATGCAATTAAGAGTTT| 885
QY 781 |TCTACATATGAGATGCTCTCTGTTGGGCAAAATTAATTCACAACTATTGGCTATGGA| 840
Db 886 |TCTACATATGAGATGCTCTCTGTTGGGCAAAATTAATTCACAACTATTGGCTATGGA| 945
QY 841 |GACAAAACCTCCCTAACTTGGCTGGGAGATTTGCTTTCTGCAAGGCTTTGCACTCTCTGGC| 900
Db 946 |GACAAAACCTCCCTAACTTGGCTGGGAGATTTGCTTTCTGCAAGGCTTTGCACTCTCTGGC| 1005
QY 901 |ATTTCTTTTCTTGGCACTTCTGCGGCAATTTTGGCTCAGGTTTGGCATTTAAAGTACAA| 960
Db 1006 |ATTTCTTTTCTTGGCACTTCTGCGGCAATTTTGGCTCAGGTTTGGCATTTAAAGTACAA| 1065
QY 961 |GAACAAACCCGCAAGAACACTTTTGAGAAAAGAGAAACCCAGCTGCCAACCTTCATTAG| 1020
Db 1066 |GAACAAACCCGCAAGAACACTTTTGAGAAAAGAGAAACCCAGCTGCCAACCTTCATTAG| 1125
QY 1021 |TGTGTTTGGGTAGTTAGCAGCTGATGAGAAATCTGTTTCCATTTGCAACCTTGAAGCCA| 1080
Db 1126 |TGTGTTTGGGTAGTTAGCAGCTGATGAGAAATCTGTTTCCATTTGCAACCTTGAAGCCA| 1185
QY 1081 |CACTTGAAGGCTTGCACACCTGAGCCCTACCAATCAGAGCTAAAGTTTAAAGAGCCA| 1140
Db 1186 |CACTTGAAGGCTTGCACACCTGAGCCCTACCAATCAGAGCTAAAGTTTAAAGAGCCA| 1245
QY 1141 |GTGCGCATGGCTAGCCCCAGGGGCGCAGAGTATTAAAGCCGCAAGCCCTCAGTAGTGAC| 1200
Db 1246 |GTGCGCATGGCTAGCCCCAGGGGCGCAGAGTATTAAAGCCGCAAGCCCTCAGTAGTGAC| 1305
QY 1201 |AGGAGGTCCCAAGCACCGACATCAGCGAGGGGAGTCCCAACAAAGTGCAGAGAGC| 1260
Db 1306 |AGGAGGTCCCAAGCACCGACATCAGCGAGGGGAGTCCCAACAAAGTGCAGAGAGC| 1365
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2341 GACCTGGCAAAATCTTTGCTGTCGAAACCTGATCAGGTGCAACCGAGGAACCTGAATATA 2400
 2446 GACCTGGCAAAATCTTTGCTGTCGAAACCTGATCAGGTGCAACCGAGGAACCTGAATATA 2505
 2401 CAACCTTCAGGAGGTGAGTCAAGTGGCTCCAGAGGAGCCCAAGATTTTACCCCAATGG 2460
 2506 CAACCTTCAGGAGGTGAGTCAAGTGGCTCCAGAGGAGCCCAAGATTTTACCCCAATGG 2565
 2461 AGGGAATCCAAATCTTTATATCACTGATGAAGAGTGGTCCGAGAGACAGACAGAC 2520
 2566 AGGGAATCCAAATCTTTATATCACTGATGAAGAGTGGTCCGAGAGACAGACAGAC 2625
 2521 ACTTTTGATGCGCGCACCGCAGCTCCAGGGAAGCTGCTTTGCAATCAGACTCTCTAAGG 2580
 2626 ACTTTTGATGCGCGCACCGCAGCTCCAGGGAAGCTGCTTTGCAATCAGACTCTCTAAGG 2685
 2581 ACTGGAAGTCAAGTCACTCTCAGAGCATTTCTAAGGAGGAGAAAGTACAGATGCCCTC 2640
 2686 ACTGGAAGTCAAGTCACTCTCAGAGCATTTCTAAGGAGGAGAAAGTACAGATGCCCTC 2745
 2641 AGCTTGCCCTCATGTCNAACTGAATAA 2667
 2746 AGCTTGCCCTCATGTCNAACTGAATAA 2772

RESULT 3
 US-10-803-268-1
 ; Sequence 1, Application US/10803268
 ; Publication No. US20040157259A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu, Yi
 ; APPLICANT: Kiehe, James Alvin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael C.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Ion Channel Protein and
 ; FILE REFERENCE: LEX-0160-USA
 ; CURRENT APPLICATION NUMBER: US/10/803,268
 ; CURRENT FILING DATE: 2004-03-18
 ; PRIOR APPLICATION NUMBER: US/09/825,147
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/194,255
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2772
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-803-268-1

Query Match 99.8%; Score 2662.2; DB 18; Length 2772;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGAAGATGTTGAGTGGGCGGCGGAGGCTGCTGAACTCGGAGCGCGGCGGCGG 60
 106 ATGAAGATGTTGAGTGGGCGGCGGAGGCTGCTGAACTCGGAGCGCGGCGGCGG 165
 61 GACGCGCTGCTACTGCTGGGCGGCGGAGGCTGCTGAACTCGGAGCGCGGCGGCGG 120
 166 GACGCGCTGCTACTGCTGGGCGGCGGAGGCTGCTGAACTCGGAGCGCGGCGGCGG 225
 121 AGGAGAGCGCGCGGCGGAGGCTGCTGAACTCGGAGCGCGGCGGCGGCGGCGGCTCT 180
 226 AGGAGAGCGCGCGGCGGAGGCTGCTGAACTCGGAGCGCGGCGGCGGCGGCTCTCT 285
 181 TACACAGTACCGAGGCTGCTGAACTCGGAGCGCGGCGGCGGCGGCGGCGGCTCTCT 240
 286 TACACAGTACCGAGGCTGCTGAACTCGGAGCGCGGCGGCGGCGGCGGCGGCTCTCT 345

1261 TGGAGCTTCAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTCAGCCA 1320
 1366 TGGAGCTTCAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTCAGCCA 1425
 1321 AAACAGGTGATGATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATG 1380
 1426 AAACAGGTGATGATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATG 1485
 1381 TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 1486 TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1545
 1441 ATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1546 ATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
 1501 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 1606 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1665
 1561 AAACGCTTCAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTCAGCCA 1620
 1666 AAACGCTTCAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTCAGCCA 1725
 1621 AAGAGCGGAGGAAATTAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTC 1680
 1726 AAGAGCGGAGGAAATTAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTC 1785
 1681 CGGCTGCTCAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTCAGCCA 1740
 1786 CGGCTGCTCAACGACGAAACCGCTTCCGGCCCTCGCTGGCTCAAAAGTCTTCAGCCA 1845
 1741 GACATCTATCAACGACGCTTCCGGAAAGGCTGCTGCTGAGGCTGCTGCTGCTGCTGCT 1800
 1846 GACATCTATCAACGACGCTTCCGGAAAGGCTGCTGCTGAGGCTGCTGCTGCTGCTGCT 1905
 1801 CAGATCCCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
 1906 CAGATCCCACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1965
 1861 GATCTTTGCGGTTCCGCAACAGAGTGGCTGCTTATCCAGATCAACTAGTGGCAACATC 1920
 1966 GATCTTTGCGGTTCCGCAACAGAGTGGCTGCTTATCCAGATCAACTAGTGGCAACATC 2025
 1921 TCGAGAGGCTGCTGAGTTCATTTCTGACGCAAAATGATGATGATGATGATGATGATGATG 1980
 2026 TCGAGAGGCTGCTGAGTTCATTTCTGACGCAAAATGATGATGATGATGATGATGATGATG 2085
 1981 CTTAGCCCTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
 2086 CTTAGCCCTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2145
 2041 GCAGTGGCAGCCACCAACCACTTCAACCAAAATTAATACGCAACCAAGCCAGCAGCC 2100
 2146 GCAGTGGCAGCCACCAACCACTTCAACCAAAATTAATACGCAACCAAGCCAGCAGCC 2205
 2101 CCAACCACTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
 2206 CCAACCACTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2265
 2161 ACTCTGACCCCTAACCTGACGCTTACAGAAAGCATTTCTGACGTCACCACTGCTCTT 2220
 2266 ACTCTGACCCCTAACCTGACGCTTACAGAAAGCATTTCTGACGTCACCACTGCTCTT 2325
 2221 GTTGCTTCCAGGAAATGTTCAAGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2280
 2326 GTTGCTTCCAGGAAATGTTCAAGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2385
 2281 AGGAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 2386 AGGAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2445

QY	241	TACAAAGTGTGCTGAGAGACCCCGGCTGGCGCTTCATCTTACCAACGCTTTCGTTTTCTC	300
Db	346	TACAAAGTGTGCTGAGAGACCCCGGCTGGCGCTTCATCTTACCAACGCTTTCGTTTTCTC	405
QY	301	CTTGTCTTTGGTTGCTTGAATTTGTGACAGTGTGTTTACCAATCCCTGAGACACAAATTTG	360
Db	406	CTTGTCTTTGGTTGCTTGAATTTGTGACAGTGTGTTTACCAATCCCTGAGACACAAATTTG	465
QY	361	GCCTCAAGTTGCTCTTGTATCCCTGGAGTTGCTGATGATGCTGCTTTCGTTTGGAGTTC	420
Db	466	GCCTCAAGTTGCTCTTGTATCCCTGGAGTTGCTGATGATGCTGCTTTCGTTTGGAGTTC	525
QY	421	ATCATTTGCAATCTGGTCTGCGGTTGCTGTTGCGATATAGAGGATGGCAAGGAAGCTG	480
Db	526	ATCATTTGCAATCTGGTCTGCGGTTGCTGTTGCGATATAGAGGATGGCAAGGAAGCTG	585
QY	481	AGTTTGTCTCGAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATGCTTCAATAGCA	540
Db	586	AGTTTGTCTCGAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATGCTTCAATAGCA	645
QY	541	GTGTTTCTTGCAAAACTCAGGTAATATTTTGGCCACGCTGCTGACCTCAGAGTCTCCGT	600
Db	646	GTGTTTCTTGCAAAACTCAGGTAATATTTTGGCCACGCTGCTGACCTCAGAGTCTCCGT	705
QY	601	TTCTACAGATCCTCCGATGTTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTTACTG	660
Db	706	TTCTACAGATCCTCCGATGTTGCGCATGGACCGAAGGGGAGGCACTTGGAAATTTACTG	765
QY	661	GGTTAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGG	720
Db	766	GGTTAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGG	825
QY	721	GTTCCTATTTTTCGTTCTTCTGTTGCTATCTGGTGGAAAGATGCCAATAAAGGTTT	780
Db	826	GTTCCTATTTTTCGTTCTTCTGTTGCTATCTGGTGGAAAGATGCCAATAAAGGTTT	885
QY	781	TCTACATATGCAGATCTCTCTGGTGGGACAAATTTACATTTGCAACTATTTGGCTATGGA	840
Db	886	TCTACATATGCAGATCTCTCTGGTGGGACAAATTTACATTTGCAACTATTTGGCTATGGA	945
QY	841	GACAAACTCCCTAACTGGCTGGGAAGATTTGCTTTCTGAGGCTTTGCACTCTCTTGGC	900
Db	946	GACAAACTCCCTAACTGGCTGGGAAGATTTGCTTTCTGAGGCTTTGCACTCTCTTGGC	1005
QY	901	ATTCTTTCTTTGCACTTCTCGCGCATTTCTGGCTCAGGTTTTCATTTAAAGTACAA	960
Db	1006	ATTCTTTCTTTGCACTTCTCGCGCATTTCTGGCTCAGGTTTTCATTTAAAGTACAA	1065
QY	961	GAACAAACCCGACAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCTCATTTAG	1020
Db	1066	GAACAAACCCGACAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCTCATTTAG	1125
QY	1021	TGTGTTTGGGTTAGTTACGAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGGAAGCA	1080
Db	1126	TGTGTTTGGGTTAGTTACGAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGGAAGCA	1185
QY	1081	CACTTGAAGGCTTGCACACCTGACGCTTACCAATCAGAACTAAGTTTAAAGAGGGA	1140
Db	1186	CACTTGAAGGCTTGCACACCTGACGCTTACCAATCAGAACTAAGTTTAAAGAGGGA	1245
QY	1141	GTGCGATAGGCTAGCCCGGAGGAGGATTTAAGAGCGGACCAAGCCCTCAGTAGGTGAC	1200
Db	1246	GTGCGATAGGCTAGCCCGGAGGAGGATTTAAGAGCGGACCAAGCCCTCAGTAGGTGAC	1305
QY	1201	AGAGGTCCCAAGCAACGACATCACAGCCGAGGAGGCTCCCAACCAAGTGAGAGAGC	1260
Db	1306	AGAGGTCCCAAGCAACGACATCACAGCCGAGGAGGCTCCCAACCAAGTGAGAGAGC	1365
QY	1261	TGAGGCTTCAAGACCGAACCGCTTCCGCGCTCTGCTGCGCTCAAAAGTTCTCAGGCA	1320
Db	1366	TGAGGCTTCAAGACCGAACCGCTTCCGCGCTCTGCTGCGCTCAAAAGTTCTCAGGCA	1425
QY	1321	AAACCAAGTGTAGATGCTGACACAGCCCTTGGCACTGATGATGATATATGATGAAAAAGGA	1380
Db	1426	AAACCAAGTGTAGATGCTGACACAGCCCTTGGCACTGATGATGATATATGATGAAAAAGGA	1485
QY	1381	TGCCAGTGTGATGATCAGTGAAGACCTCACCCACCACTTTAAACTGTCTCAATTCAGCT	1440
Db	1486	TGCCAGTGTGATGATCAGTGAAGACCTCACCCACCACTTTAAACTGTCTCAATTCAGCT	1545
QY	1441	ATCAGAAATTTATCAAAATTTTCATGTTCCAAACCGAAGTTTAAAGGAACGTTACGTCATAT	1500
Db	1546	ATCAGAAATTTATCAAAATTTTCATGTTCCAAACCGAAGTTTAAAGGAACGTTACGTCATAT	1605
QY	1501	GATGTAAGAGATGCTCATTGAAACAATTTCTGCTGGTCACTCGGACATGTTGTGTAATTT	1560
Db	1606	GATGTAAGAGATGCTCATTGAAACAATTTCTGCTGGTCACTCGGACATGTTGTGTAATTT	1665
QY	1561	AAAAAGCTTCAAAACAGCTGTTGATCAAAATTTCTTGGAAAAGGGCAATCAATCAGATAAG	1620
Db	1666	AAAAAGCTTCAAAACAGCTGTTGATCAAAATTTCTTGGAAAAGGGCAATCAATCAGATAAG	1725
QY	1621	AAGAGCCGAGAGAAAAATTAACAGCAGAACATGAGACACAGACGATCTCAGTATGCTCGGT	1680
Db	1726	AAGAGCCGAGAGAAAAATTAACAGCAGAACATGAGACACAGACGATCTCAGTATGCTCGGT	1785
QY	1681	CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGAGCTGCCTACTA	1740
Db	1786	CGGGTGGTCAAGGTTGAAAAACAGGTACAGTCCATAGAGTCCAAAGCTGCCTACTA	1845
QY	1741	GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTGCTTTGGCTTCATTC	1800
Db	1846	GACATCTATCAACAGGTCCTTCGAAAAGGCTCTGCTCAGCCCTGCTTTGGCTTCATTC	1905
QY	1801	CAGATCCCAACCTTTTGAATGTGAAACAGACATCTGACTCAAAAGCCCTGTGGATAGCAAA	1860
Db	1906	CAGATCCCAACCTTTTGAATGTGAAACAGACATCTGACTCAAAAGCCCTGTGGATAGCAAA	1965
QY	1861	GATCTTTGGGTTCCGCAACAAACAGTGGCTCTTATCCAGATCAACTAGTGCCAAATC	1920
Db	1966	GATCTTTGGGTTCCGCAACAAACAGTGGCTCTTATCCAGATCAACTAGTGCCAAATC	2025
QY	1921	TCGAGAGGCTGCTCAGTTCAATTTGAGCCCAATAGATTCAGTGCCGAGACTTTTCTACGG	1980
Db	2026	TCGAGAGGCTGCTCAGTTCAATTTGAGCCCAATAGATTCAGTGCCGAGACTTTTCTACGG	2085
QY	1981	CTTACGCTTACTATGCACAGTCAACCAACACAGGTGCCAATTTAGTCAAAAGCCTGCTCA	2040
Db	2086	CTTACGCTTACTATGCACAGTCAACCAACACAGGTGCCAATTTAGTCAAAAGCCTGCTCA	2145
QY	2041	GCAGTGGCAGCCCAACCAACCAATTTGCAAAACCAATTAACCGCACCCCAAGCCAGCAGC	2100
Db	2146	GCAGTGGCAGCCCAACCAACCAATTTGCAAAACCAATTAACCGCACCCCAAGCCAGCAGC	2205
QY	2101	CCAAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCCAGGCCAGAA	2160
Db	2206	CCAAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCCAGGCCAGAA	2265
QY	2161	ACTCTGACCCCTTAACCTGCAAGCTTACAGGAAGCAATTTCTGAGCTCACCACTGCTCTT	2220
Db	2266	ACTCTGACCCCTTAACCTGCAAGCTTACAGGAAGCAATTTCTGAGCTCACCACTGCTCTT	2325
QY	2221	GTTCCTCCAAAGGAAATTTGTCAGGTTGCACAGTCAAAATCTCCAAAGGAGCCGTTCTATG	2280
Db	2326	GTTCCTCCAAAGGAAATTTGTCAGGTTGCACAGTCAAAATCTCCAAAGGAGCCGTTCTATG	2385
QY	2281	AGGAAAAGCTTTGACATGGGAGGAAACTCTGTTGTCTGTCTGTCCCATGTTGCGGAGAG	2340
Db	2386	AGGAAAAGCTTTGACATGGGAGGAAACTCTGTTGTCTGTCTGTCCCATGTTGCGGAGAG	2445
QY	2341	GACTTTGGGCAAAATTTCTGCTGTGCAAAACCTGATCAGGTGCACCGAGGAACCTGAATATA	2400
Db	2446	GACTTTGGGCAAAATTTCTGCTGTGCAAAACCTGATCAGGTGCACCGAGGAACCTGAATATA	2505
QY	2401	CAACTTTCCAGGAGTGTAGTCAAGTGGCTCCAGAGGAGCAGCAAGATTTTTTACCCCAATGG	2460

Db	2506	CAATTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGCGAGCAAGATTTTACCCCAAAATGG	2565	465	CTTGTCTTTGGTTGCTTGGATTTTGTGCTGCTTGTACCATCCCTGAGCACACAAAATTG	524
Qy	2461	AGGGAATCCAAATTTTATTAACATGATGAAGAGTGGTCCCGAAGAGACAGACAGAC	2520	361	GCCTCAAGTGGCTCTTGATTCCTGAGTTCGTGATGATGCTGCTTTGGTTGGAGTTC	420
Db	2566	AGGGAATCCAAATTTTATTAACATGATGAAGAGTGGTCCCGAAGAGACAGACAGAC	2525	525	GCCTCAAGTGGCTCTTGATTCCTGAGTTCGTGATGATGCTTGGTTGGAGTTC	584
Qy	2521	ACTTTTGAATCGGACGCGACGCTGCGAGGGAAGCTGCTTTGTCATCAGACTCTCTTAAGG	2580	421	ATCATTTCGAATCTGCTGCGGTTGCTGTTGTCATATAGAGATGGCAAGGAAGACTG	480
Db	2626	ACTTTTGAATCGGACGCGACGCTGCGAGGGAAGCTGCTTTGTCATCAGACTCTCTTAAGG	2685	585	ATCATTTCGAATCTGCTGCGGTTGCTGTTGTCATATAGAGATGGCAAGGAAGACTG	644
Qy	2581	ACTGGAAGGTCAAGATCATCTCAGAGCATTTGTAAAGCAGAGAGAAATGATGATGCTC	2640	481	AGGTTTGTCTGAAAGCCCTTCTGCTTATAGATACATTTGTTCTTATGCTTCAATAGCA	540
Db	2686	ACTGGAAGGTCAAGATCATCTCAGAGCATTTGTAAAGCAGAGAGAAATGATGATGCTC	2745	645	AGGTTTGTCTGAAAGCCCTTCTGCTTATAGATACATTTGTTCTTATGCTTCAATAGCA	704
Qy	2641	AGCTTGCCTCATGTCAAACTGAATAA	2667	541	GTGTTTCTGCAAAAACCTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAACTCCGT	600
Db	2746	AGCTTGCCTCATGTCAAACTGAATAA	2772	705	GTGTTTCTGCAAAAACCTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAACTCCGT	764
Db				601	TTCTTACAGATCCTCCGCATGGTGGCATGGACCGAAGGGGAGGCACTTGGAAATTA	660
Db				765	TTCTTACAGATCCTCCGCATGGTGGCATGGACCGAAGGGGAGGCACTTGGAAATTA	824
Qy				661	GGTTCAGTGGTTTATGCTCAAGCAAGGAATTAATCAGAGCTTGGTACATAGATTTTGG	720
Db				825	GGTTCAGTGGTTTATGCTCAAGCAAGGAATTAATCAGAGCTTGGTACATAGATTTTGG	884
Qy				721	GTCTTTATTTTTCGTTCTTCTGTTGCTATCTGTTGGAAGGATGCCAATAAAGATTT	780
Db				885	GTCTTTATTTTTCGTTCTTCTGTTGCTATCTGTTGGAAGGATGCCAATAAAGATTT	944
Qy				781	TCTACATATGACAGATGCTCTGTTGGGGGCAATTAATACATGACAACTATTTGGCTAT	840
Db				945	TCTACATATGACAGATGCTCTGTTGGGGGCAATTAATACATGACAACTATTTGGCTAT	1004
Qy				841	GACAAACTCCCTTAACCTTGGCTGGGAAGATTCCTTCTGCGAGCTTTCACCTCTTGGC	900
Db				1005	GACAAACTCCCTTAACCTTGGCTGGGAAGATTCCTTCTGCGAGCTTTCACCTCTTGGC	1064
Qy				901	ATTTCTTTCTTTCGACCTTCTGCGGCACTTCTGCGGCTTCTGCGCTTGGCTTGGCTT	960
Db				1065	ATTTCTTTCTTTCGACCTTCTGCGGCACTTCTGCGGCTTCTGCGCTTGGCTTGGCTT	1124
Qy				961	GACAACTCCCGGAGAACACTTTGAGAAAGAGAACCCAGCTGCAACCTCATTTCAG	1020
Db				1125	GACAACTCCCGGAGAACACTTTGAGAAAGAGAACCCAGCTGCAACCTCATTTCAG	1184
Qy				1021	TGCTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA	1080
Db				1185	TGCTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA	1244
Qy				1081	CACTTGAAGGCTTTGCACTGCTGAGCCCTACCATCAGAACTTAAGTTTAAAGGAGCA	1140
Db				1245	CACTTGAAGGCTTTGCACTGCTGAGCCCTACCATCAGAACTTAAGTTTAAAGGAGCA	1304
Qy				1141	GTGCGCATGCTAGCTGCGGCGGCGAGAGTATTAAGAGCCGACAAAGCTCAGTAGGTGAC	1200
Db				1305	GTGCGCATGCTAGCTGCGGCGGCGAGAGTATTAAGAGCCGACAAAGCTCAGTAGGTGAC	1364
Qy				1201	AGGAGTCCCCAAGCAGCAGCATCAGCCGAGGGGAGTCCCACTAAGTGCAGAGAGC	1260
Db				1365	AGGAGTCCCCAAGCAGCAGCATCAGCCGAGGGGAGTCCCACTAAGTGCAGAGAGC	1424
Qy				1261	TGGAGCTTCAACAGCCGAAACCGCTTCCGGCCCTCGCTGCGCCCTCAAAAGTTCTCAGCCA	1320
Db				1425	TGGAGCTTCAACAGCCGAAACCGCTTCCGGCCCTCGCTGCGCCCTCAAAAGTTCTCAGCCA	1484
Qy				1321	AAACAGATGATAGATGCTGACACAGCCCTTGGCACTGATGATGATATGATGATAAAGGA	1380
Db				1485	AAACAGATGATAGATGCTGACACAGCCCTTGGCACTGATGATGATATGATGATAAAGGA	1544
Qy				1381	TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1440
Db				1545	TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1604

RESULT 4

US-09-825-147-3
 ; Sequence 3, Application US/09825147
 ; Patent No. US20020042505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu, Yi
 ; APPLICANT: Kieke, James Alvin
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael C.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
 ; TITLE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0160-USA
 ; CURRENT APPLICATION NUMBER: US/09/825,147
 ; CURRENT FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 60/194,255
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 3111
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; ORGANISM: homo sapiens
 ; US-09-825-147-3

Qy	1	ATGAAGGATGTGAGTGGGCGGCGAGGCTGCTGCTGAACTCGGCGAGCGCGGCG	60	Query Match	99.8%;	Score 2662.2;	DB 9;	Length 3111;
Db	165	ATGAAGGATGTGAGTGGGCGGCGGCGAGGCTGCTGCTGAACTCGGCGAGCGCGGCG	224	Best Local Similarity	99.9%;	Pred. No. 0;	Mismatches	3; Indels
Qy	61	GACGGCTGCTACTGCTGGGACCCGCGGCGGCGGCGGCTGCTGCTGAACTCGGCGAGCGCGGCG	120	Matches 2664;	Conservative	0;	Gaps	0;
Db	225	GACGGCTGCTACTGCTGGGACCCGCGGCGGCGGCGGCTGCTGCTGAACTCGGCGAGCGCGGCG	284					
Qy	121	AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGAACTCGGCGAGCGCGGCG	180					
Db	285	AGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGAACTCGGCGAGCGCGGCG	344					
Qy	181	TACACAGTAGCAGAGCTGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGAACTCGGCGAGCGCGGCG	240					
Db	345	TACACAGTAGCAGAGCTGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGAACTCGGCGAGCGCGGCG	404					
Qy	241	TACAACTGTCTGGAGAGACCCCGCGGCTGGGCGGCTTCACTACCAAGCTTTTCTGTTTCTC	300					
Db	405	TACAACTGTCTGGAGAGACCCCGCGGCTGGGCGGCTTCACTACCAAGCTTTTCTGTTTCTC	464					
Qy	301	CTTGTCTTGGTGTGATTTTGTGATTTTCTACCATCTTCTACCATCTTCTACCATCTTCTACCATCTTCT	360					

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QY 1441 ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAGGAAACGTTTACGTCCATAT 1500
Db 1605 ATCAGAAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAGGAAACATTTACGTCCATAT 1664
QY 1501 GATGTAAGAGATGTCATTTGAAACAAATATTTCTGCTGGTCACTCTGACATGTTGTGTAAT 1560
Db 1665 GATGTAAGAGATGTCATTTGAAACAAATATTTCTGCTGGTCACTCTGACATGTTGTGTAAT 1724
QY 1561 AAAAGCCTTCAAAACAGTGTGATCAAAATTTCTTGGAAAGGGCAATTCATCATCAGATAAG 1620
Db 1725 AAAAGCCTTCAAAACAGTGTGATCAAAATTTCTTGGAAAGGGCAATTCATCATCAGATAAG 1784
QY 1621 AAGAGCGAGAGAAAAATAACAGCAGAACATGAGACCAACAGACGATCTCAGTATGTCGGT 1680
Db 1785 AAGAGCGAGAGAAAAATAACAGCAGAACATGAGACCAACAGACGATCTCAGTATGTCGGT 1844
QY 1681 CGGGTGGTCAAGTTTGAAGAAAGGTACAGTCCATAGAGTCAAGCTGAGCTGCCCTACTA 1740
Db 1845 CGGGTGGTCAAGTTTGAAGAAAGGTACAGTCCATAGAAATCCAAGCTGGACTGCCCTACTA 1904
QY 1741 GACATCTATCAACAGAGTCCCTTCGGAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800
Db 1905 GACATCTATCAACAGAGTCCCTTCGGAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1964
QY 1801 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATACAAA 1860
Db 1965 CAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATACAAA 2024
QY 1861 GATCTTTCCGGTTCGCGACAAAACAGTGGTGTCTTATCAGATCAACTAGTGCCAAATC 1920
Db 2025 GATCTTTCCGGTTCGCGACAAAACAGTGGTGTCTTATCAGATCAACTAGTGCCAAATC 2084
QY 1921 TCAGAGAGGCTGCAGTTTCTGAGCCAAATAGTTTCAAGTCCAGAGCTTTCTACGG 1980
Db 2085 TCAGAGAGGCTGCAGTTTCTGAGCCAAATAGTTTCAAGTCCAGAGCTTTCTACGG 2144
QY 1981 CTTAGCCCTACTATGACACAGTCAAGCAACACAGTGTCCCAATTAGTCAAAAGCGATGCTCA 2040
Db 2145 CTTAGCCCTACTATGACACAGTCAAGCAACACAGTGTCCCAATTAGTCAAAAGCGATGCTCA 2204
QY 2041 GCAGTGGCAGCACCACCAACCATTTGCAAAACCAATTAATACGGCACCAAGCCAGCAGCC 2100
Db 2205 GCAGTGGCAGCACCACCAACCATTTGCAAAACCAATTAATACGGCACCAAGCCAGCAGCC 2264
QY 2101 CCAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCGCCAGAA 2160
Db 2265 CCAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCGCCAGAA 2324
QY 2161 ACTCTGACCCCTAACCCCTGAGGCTTTACAGGAAGCATTTTGAACCTCAACCTGCTT 2220
Db 2325 ACTCTGACCCCTAACCCCTGAGGCTTTACAGGAAGCATTTTGAACCTCAACCTGCTT 2384
QY 2221 GTTGCTTCAAGGAAATGTTTCAAGTTGACAGTCAAAATCTCAACGAAGACGTTCTATG 2280
Db 2385 GTTGCTTCAAGGAAATGTTTCAAGTTGACAGTCAAAATCTCAACGAAGACGTTCTATG 2444
QY 2281 AGGAAAGCTTTGACATGGGAGAGAACTCTGTTGCTGCTGTCCTCCATGTCGCGAG 2340
Db 2445 AGGAAAGCTTTGACATGGGAGAGAACTCTGTTGCTGCTGTCCTCCATGTCGCGAG 2504
QY 2341 GACTTGGGCAATCTTTGCTGTGCAAAACCTGATCAGGTGCAACCGAGGAATGAAATATA 2400
Db 2505 GACTTGGGCAATCTTTGCTGTGCAAAACCTGATCAGGTGCAACCGAGGAATGAAATATA 2564
QY 2401 CAACTTTCAAGGAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCCAATGG 2460
Db 2565 CAACTTTCAAGGAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCCAATGG 2624
QY 2461 AGGGATCCAAATTTGTTTAACTGATGAAGAGTGGGTCCCGAGAGACAGACAGAC 2520
Db 2625 AGGGATCCAAATTTGTTTAACTGATGAAGAGTGGGTCCCGAGAGACAGACAGAC 2684
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QY 2521 ACTTTTGATGCCGACCCGAGCGCTGCAGGAGCTGCTTTTGCATCAGACTCTCTAAGG 2580
Db 2685 ACTTTTGATGCCGACCCGAGCGCTGCAGGAGCTGCTTTTGCATCAGACTCTCTAAGG 2744
QY 2581 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTC 2640
Db 2745 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTC 2804
QY 2641 AGCTTGCCTCATGTCAAACTGAAATAA 2667
Db 2805 AGCTTGCCTCATGTCAAACTGAAATAA 2831

RESULT 5
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3

Query Match 99.8%; Score 2662.2; DB 18; Length 3111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2664; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTGCTGAACTCGGCAGCCGCGAGGGC 60
Db 165 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTGCTGAACTCGGCAGCCGCGAGGGC 224
QY 61 GAGCGCTGCTACTGCTGGGCAACCGCGGCGCAGCTTGGTGGCGGCGGTGGCCTG 120
Db 225 GAGCGCTGCTACTGCTGGGCAACCGCGGCGCAGCTTGGTGGCGGCGGTGGCCTG 284
QY 121 AGGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGCGGGAAGCGCTCTCT 180
Db 285 AGGAGAGCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGCGGGAAGCGCTCTCT 344
QY 181 TACAGAGTAGCAGAGCTGCCGGCGCAACGTCAGATCCGGGGGTGAGAACTACCTG 240
Db 345 TACAGAGTAGCAGAGCTGCCGGCGCAACGTCAGATCCGGGGGTGAGAACTACCTG 404
QY 241 TACAACGTGCTGAGAGAGACCCCGCGGCTGAGCTTACCTACACGCTTTCGTTTCTC 300
Db 405 TACAACGTGCTGAGAGAGACCCCGCGGCTGAGCTTACCTACACGCTTTCGTTTCTC 464
QY 301 CTTGCTTTGGTGTGATTTTGTAGTGTGTTTCTACCATCCCTGAGCACACAAATTTG 360
Db 465 CTTGCTTTGGTGTGATTTTGTAGTGTGTTTCTACCATCCCTGAGCACACAAATTTG 524
QY 361 GCCTCAAGTTGCTCTTGAATCCTGAGTTGCTGATGATGTGCTTGTGTTGAGTTTC 420
Db 525 GCCTCAAGTTGCTCTTGAATCCTGAGTTGCTGATGATGTGCTTGTGTTGAGTTTC 584
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QY	421	ATCATTGGAATCTGGTCTGGGGTTGCTGTGTCGATATAGAGATGGCAAGAGACTG	480	1501	GATGTAAAGATGTCAATGAAACAATATTCTGCTCATCTGGACATGTTGTGTAGAAATT	1560
Db	585	ATCATTGGAATCTGGTCTGGGGTTGCTGTGTCGATATAGAGATGGCAAGAGACTG	644	1665	GATGTAAAGATGTCAATGAAACAATATTCTGCTCATCTGGACATGTTGTGTAGAAATT	1724
QY	481	AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540	1561	AAAAGCCTTTCAAACACGTTGTTGATCAAAATCTTGGAAAAGGGCAAAATCACATCAGATAAG	1620
Db	645	AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	704	1725	AAAAGCCTTTCAAACACGTTGTTGATCAAAATCTTGGAAAAGGGCAAAATCACATCAGATAAG	1784
QY	541	GTGTTTCTGCAAAAACACGAGGTAATATTTTGGCAGCTGTCACATCAGAGTCTCCGT	600	1621	AAGAGCCGAGAGAAAATAACAGCAGAAATGAGACCAACAGACGATCTCAGTATGCTCGGT	1680
Db	705	GTGTTTCTGCAAAAACACGAGGTAATATTTTGGCAGCTGTCACATCAGAGTCTCCGT	764	1785	AAGAGCCGAGAGAAAATAACAGCAGAAATGAGACCAACAGACGATCTCAGTATGCTCGGT	1844
QY	601	TTCCTACAGATCTCCGATCGTGGCATGACACGAGGGGAGGACACTTGGAAATTAATG	660	1845	CGGTGGTCAAGGTTGAAAACAAGGTACAGTCCATAGAGTCCAAAGCTGAGCTGCTACTA	1740
Db	765	TTCCTACAGATCTCCGATCGTGGCATGACACGAGGGGAGGACACTTGGAAATTAATG	824	1741	GACATCTATCAACAGGTCCTTCGGAAGGCTCTGCTCAGCCCTGCTTGGCTTCAATTC	1800
QY	661	GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTG	720	1905	GACATCTATCAACAGGTCCTTCGGAAGGCTCTGCTCAGCCCTGCTTGGCTTCAATTC	1964
Db	825	GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTG	784	1801	CAGATCCCACTTTGAAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA	1860
QY	721	GTTCCTATTTTTCGTCCTTCTGCTCTATCTGTTGGAAGAGATGCCAATAAAGAGTTT	780	1965	CAGATCCCACTTTGAAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGATAGCAAA	2024
Db	885	GTTCCTATTTTTCGTCCTTCTGCTCTATCTGTTGGAAGAGATGCCAATAAAGAGTTT	944	1861	GATCTTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAACTC	1920
QY	781	TCTACATATGAGATGCTCTCTGTTGGGGCAAAATTAATCAATTCACAACTATTTGGCTATGGA	840	2025	GATCTTTTCGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGGCCAACTC	2084
Db	945	TCTACATATGAGATGCTCTCTGTTGGGGCAAAATTAATCAATTCACAACTATTTGGCTATGGA	1004	1921	TCGAGAGGCTGAGTTCATTTCTGACGCCAAATGAGTTCAGTGCCCGAGACTTCTTACGCG	1980
QY	841	GACAAAACCTCCCTAACTTGGCTGGGAGATGCTTTCTGAGGCTTTGCACTCTCTGGC	900	2085	TCGAGAGGCTGAGTTCATTTCTGACGCCAAATGAGTTCAGTGCCCGAGACTTCTTACGCG	2144
Db	1005	GACAAAACCTCCCTAACTTGGCTGGGAGATGCTTTCTGAGGCTTTGCACTCTCTGGC	1064	1981	CTTAGCCCTACTATGACAGTCAAGCAACACAGGTGCCAATTTAGTCAAAAGCGATGCTCA	2040
QY	901	ATTCTTTCTTTGCACTTCTCTCGGCAATCTTGGCTCAGGTTTGGCAATTAAGATACAA	960	2145	CTTAGCCCTACTATGACAGTCAAGCAACACAGGTGCCAATTTAGTCAAAAGCGATGCTCA	2204
Db	1065	ATTCTTTCTTTGCACTTCTCTCGGCAATCTTGGCTCAGGTTTGGCAATTAAGATACAA	1124	2041	GCAGTGGCAGCCCAACACCATTTGCAACCAATTAATACGCCCAACCCAGCCAGCAGCC	2100
QY	961	GAAACAACCGCCAGAAAACATTTGAGAAAAGAGAACCCAGCTGCCAACCCTCAATCAG	1020	2205	GCAGTGGCAGCCCAACACCATTTGCAACCAATTAATACGCCCAACCCAGCCAGCAGCC	2264
Db	1125	GAAACAACCGCCAGAAAACATTTGAGAAAAGAGAACCCAGCTGCCAACCCTCAATCAG	1184	2101	CCAACTATTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGCCAGCCAGAA	2160
QY	1021	TGTGTTTGGGTAAGTACGAGCTGATGAGAAATCTGTTCCATTCGCAACCTGGAAGCCA	1080	2265	CCAACTATTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGCCAGCCAGAA	2324
Db	1185	TGTGTTTGGGTAAGTACGAGCTGATGAGAAATCTGTTCCATTCGCAACCTGGAAGCCA	1244	2161	ACTCTGACCCCTAAACCTTGACAGGTTACAGAAAGATTTCTGACGTCAACCACTGCTCTT	2220
QY	1081	CACCTGAAGCCCTTGACACCTCAGCCCTACCAATCAGAACTAAGTTTAAAGAGCGA	1140	2325	ACTCTGACCCCTAAACCTTGACAGGTTACAGAAAGATTTCTGACGTCAACCACTGCTCTT	2384
Db	1245	CACCTGAAGCCCTTGACACCTCAGCCCTACCAATCAGAACTAAGTTTAAAGAGCGA	1304	2221	GTTGCCCTCAAAGGAAAATGTTTACAGTTGACAGTCAAAATCTCACCAGGACCCGTTCTATG	2280
QY	1141	GTGCGCATGGCTAGCCCGAGGGCCAGATTAATTAAGAGCCGACAGCCCTCAGTAGTGAC	1200	2385	GTTGCCCTCAAAGGAAAATGTTTACAGTTGACAGTCAAAATCTCACCAGGACCCGTTCTATG	2444
Db	1305	GTGCGCATGGCTAGCCCGAGGGCCAGATTAATTAAGAGCCGACAGCCCTCAGTAGTGAC	1364	2281	AGGAAAAGCTTTGACATGGGAGGAGAACTCTGTTGTTCTGCTGCCATGGTCCCGAAG	2340
QY	1201	AGGAGTCCCAAGCACCGACATCACAGCCGAGGCGAGTCCCAACCAAGTGCAGAGAGC	1260	2445	AGGAAAAGCTTTGACATGGGAGGAGAACTCTGTTGTTCTGCTGCCATGGTCCCGAAG	2504
Db	1365	AGGAGTCCCAAGCACCGACATCACAGCCGAGGCGAGTCCCAACCAAGTGCAGAGAGC	1424	2341	GACTTGGGCAAAATCTTTGTTCTGTCGAAAACCTGATCAGTTCGACCGAGGACTCAATATA	2400
QY	1261	TGGAGCTTCAACGACCGAACCCTGCTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT	1320	2505	GACTTGGGCAAAATCTTTGTTCTGTCGAAAACCTGATCAGGTCGACCGAGGAACTGAATATA	2564
Db	1425	TGGAGCTTCAACGACCGAACCCTGCTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT	1484	2401	CAACTTTTCAGGGAGTGAAGTGAAGTGGCTCCAGAGGCGAGCCAAAGATTTTATCCCAATGG	2460
QY	1321	AAACAGTATGATGTCGACAGACCCCTTGGCACTGATGATGATGATGATGATGATGATGATG	1380	2565	CAACTTTTCAGGGAGTGAAGTGAAGTGGCTCCAGAGGCGAGCCAAAGATTTTATCCCAATGG	2624
Db	1485	AAACAGTATGATGTCGACAGACCCCTTGGCACTGATGATGATGATGATGATGATGATGATG	1544	2461	AGGGAATCCAAATTTGTTTATTAACATGATGAAGAGTGGTCCCGAAGAGACAGACAGAC	2520
QY	1381	TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1440	2625	AGGGAATCCAAATTTGTTTATTAACATGATGAAGAGTGGTCCCGAAGAGACAGACAGAC	2684
Db	1545	TGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1604	2521	ACTTTTGTGTCGCGCACCCGAGCCCTGCCAGGGAAGCTGCTTTTGCATCAGACTCTCTAAGG	2580
QY	1441	ATCAGAAATTAATTAATTTTATGTTTGAACAGGAGTTTAAAGGAAAGCTTACGTCATAT	1500	2685	ACTTTTGTGTCGCGCACCCGAGCCCTGCCAGGGAAGCTGCTTTTGCATCAGACTCTCTAAGG	2744
Db	1605	ATCAGAAATTAATTAATTTTATGTTTGAACAGGAGTTTAAAGGAAACATTTACGTCATAT	1664	2581	ACTGGAAGGTCAACGATCATCTCAGAGCATTTTGAAGGAGGAGAAATGATCAGATGCCCTC	2640

Db 2745 ACTGGAAGGTACGATCTCTCAGAGCAATTTGTAAGGCAGGAGAGAAAGTACAGATGCGCTC 2804
Qy 2641 AGCTTCCTCATGTCAAACTGAAATAA 2667
Db 2805 AGCTTCCTCATGTCAAACTGAAATAA 2831

RESULT 6

US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNOS POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1

Query Match 98.6%; Score 2630; DB 9; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;
Qy 1 ATGAAGGATGTGGAGTCGGGCGGGGAGGGTGTCTGAACTCGGCAGCCGCGAGGGGC 60
Db 1 ATGAAGGATGTGGAGTCGGGCGGGGAGGGTGTCTGAACTCGGCAGCCGCGAGGGGC 60
Qy 61 GACGGCTCTACTGTCTGGGACCCCGCGGGGCGGAGCGCTTGGTGGCGGGCGGGTGGCTG 120
Db 61 GACGGCTCTACTGTCTGGGACCCCGCGGGGCGGAGCGCTTGGTGGCGGGCGGGTGGCTG 120
Qy 121 AGGGAGAGCGCGGGGCAAGCAGAGGGGCGCGGATGAGCTGTCTGGGGAAGCGCTCTCT 180
Db 121 AGGGAGAGCGCGGGGCAAGCAGAGGGGCGCGGATGAGCTGTCTGGGGAAGCGCTCTCT 180
Qy 181 TACACAGTAGCCAGAGCTGCCGGGCGCAACGTCAAGTACCGGGGTGCAGAACTACCTG 240
Db 181 TACACAGTAGCCAGAGCTGCCGGGCGCAACGTCAAGTACCGGGGTGCAGAACTACCTG 240
Qy 241 TACACAGTCTGAGAGAGACCCCGGGGCTGGGCTGATCTACACGCTTCTGTTTCTC 300
Db 241 TACACAGTCTGAGAGAGACCCCGGGGCTGGGCTGATCTACACGCTTCTGTTTCTC 300
Qy 301 CTGTGCTTTGGTGTCTGATTTTGTTCAGTGTCTTCTTACCATCCCTGAGCACAAATTTG 360
Db 301 CTGTGCTTTGGTGTCTGATTTTGTTCAGTGTCTTCTTACCATCCCTGAGCACAAATTTG 360
Qy 361 GCCTCAAGTGTCTTGTATCTCGGAGTTCGTGATGATTCGTCTTGTGTTGGAGTTC 420
Db 361 GCCTCAAGTGTCTTGTATCTCGGAGTTCGTGATGATTCGTCTTGTGTTGGAGTTC 420
Qy 421 ATCATTGCAATCTGTCTCGGGTTCGTCTTGTTCGATATAGAGATGGAAGAACTG 480
Db 421 ATCATTGCAATCTGTCTCGGGTTCGTCTTGTTCGATATAGAGATGGAAGAACTG 480
Qy 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATGTTCTTATCGCTTCAATAGCA 540
Db 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATGTTCTTATCGCTTCAATAGCA 540

Qy 541 GTTGTCTTGCAGAACTCAGGGTAATAATTTTTGCCACGTCTGCACTCAGAACTCTCCGT 600
Db 541 GTTGTCTTGCAGAACTCAGGGTAATAATTTTTGCCACGTCTGCACTCAGAACTCTCCGT 600
Qy 601 TTCCTACAGATCCTCGGATGTGGCATGGAACGAGGGGAGGCACTTGGAAATTTACTG 660
Db 601 TTCCTACAGATCCTCGGATGTGGCATGGAACGAGGGGAGGCACTTGGAAATTTACTG 660
Qy 661 GGTTCAGTGTGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGG 720
Db 661 GGTTCAGTGTGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGG 720
Qy 721 GTTCTTATTTTTCGCTTTCTTCTATCTGTGTGGAAGAAAGATGCCAATAAAGAGTTT 780
Db 721 GTTCTTATTTTTCGCTTTCTTCTATCTGTGTGGAAGAAAGATGCCAATAAAGAGTTT 780
Qy 781 TCTACATATGAGATGCTCTCTGTGGTGGGCGACAAATTTACATTGCACTATTGGCTATGGA 840
Db 781 TCTACATATGAGATGCTCTCTGTGGTGGGCGACAAATTTACATTGCACTATTGGCTATGGA 840
Qy 841 GACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTTGCACCTCCTTGGC 900
Db 841 GACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTTGCACCTCCTTGGC 900
Qy 901 ATTTCTTTTTCGCACTTCTCTGCCGCGCATTTTGGCTCAGGTTTTCATTAAAGATACAA 960
Db 901 ATTTCTTTTTCGCACTTCTCTGCCGCGCATTTTGGCTCAGGTTTTCATTAAAGATACAA 960
Qy 961 GAAACACCGCGCAGAAACACTTTTGAAGAAAGAACCCAGCTGCGCAACCTCATTCAG 1020
Db 961 GAAACACCGCGCAGAAACACTTTTGAAGAAAGAACCCAGCTGCGCAACCTCATTCAG 1020
Qy 1021 TGTGTTTGGCGTAGTTTACGACCTCATGAGAAATCTGTTTCCATTCGCACTCGGAAGCCA 1080
Db 1021 TGTGTTTGGCGTAGTTTACGACCTCATGAGAAATCTGTTTCCATTCGCACTCGGAAGCCA 1080
Qy 1081 CACTTGAAGGCGCTTGCACACCTGCGAGCCCTACAA----- 1115
Db 1081 CACTTGAAGGCGCTTGCACACCTGCGAGCCCTACCAAGAAAGAACAGGGGAAGCATCAAGC 1140
Qy 1116 ---TCAGAGCTTAAGTTTAAAGAGCGAGTGCAGCTAGCCATGGTCCAGGGGCCAGAGTATT 1173
Db 1141 AGTCAGAGCTTAAGTTTAAAGAGCGAGTGCAGCTAGCCATGGTCCAGGGGCCAGAGTATT 1200
Qy 1174 AAGAGCGCACAAAGCTCAGTAGTGCAGAGAGGTCCCAAGCACCGACATCACAGCCGAG 1233
Db 1201 AAGAGCGCACAAAGCTCAGTAGTGCAGAGAGGTCCCAAGCACCGACATCACAGCCGAG 1260
Qy 1234 GGCAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGGAAACCGCTTCCGGCCC 1293
Db 1261 GGCAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGGAAACCGCTTCCGGCCC 1320
Qy 1294 TGGCTGGCGCTCAAAAGTTCTCAGCCAAAACAGTGCAGTATGCTGACACAGCCCTTGGC 1353
Db 1321 TGGCTGGCGCTCAAAAGTTCTCAGCCAAAACAGTGCAGTATGCTGACACAGCCCTTGGC 1380
Qy 1354 ACTGATGATGTATATGATGAAAAGATGCGCAGTGTGATGATCAGTGAAGACCTTCACC 1413
Db 1381 ACTGATGATGTATATGATGAAAAGATGCGCAGTGTGATGATCAGTGAAGACCTTCACC 1440
Qy 1414 CCACCACTTAAACTGTCTATTCGAGCTATCAGAAATTTGAAATTTTTCATGTTGCAAAACGG 1473
Db 1441 CCACCACTTAAACTGTCTATTCGAGCTATCAGAAATTTGAAATTTTTCATGTTGCAAAACGG 1500
Qy 1474 AAGTTTAAAGAAACGTTAGCTCCATATCATGTAAAAGATGTCATTGGAACAATTTCTGCT 1533
Db 1501 AAGTTTAAAGAAACGTTAGCTCCATATGATGTAAAAGATGTCATTGGAACAATTTCTGCT 1560
Qy 1534 GGTCTATCTGGACATGCTGTGTAGAAATTTAAAGCCCTTCAAAACGCTTGTGATCAAAATCTT 1593
Db 1561 GGTCTATCTGGACATGCTGTGTAGAAATTTAAAGCCCTTCAAAACGCTTGTGATCAAAATCTT 1620
Qy 1594 GGAAAGGGCAATCACATCAGATTAAGAGAGCGGAGAGAAATAACAGCAGAACATGAG 1653

QY 661 GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 720
DB 661 GGTTCAGTGGTTATGCTCAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 720
QY 721 GTTCTTATTTTTCGTCCTTCTGTCATCTCGTGGAAAGGATGCCAATAAGAGTTT 780
DB 721 GTTCTTATTTTTCGTCCTTCTGTCATCTCGTGGAAAGGATGCCAATAAGAGTTT 780
QY 781 TCTACATATGCAGATGCTCTCGTGGGACAAATACATTTGCAACATTTGCTGCTATGA 840
DB 781 TCTACATATGCAGATGCTCTCGTGGGACAAATACATTTGCAACATTTGCTGCTATGA 840
QY 841 GACAAATCTCCCTAACTTGGCTGGGAAGATTCTTCTGCAGGCTTGGCACTCTTGGC 900
DB 841 GACAAATCTCCCTAACTTGGCTGGGAAGATTCTTCTGCAGGCTTGGCACTCTTGGC 900
QY 901 ATTCTCTTCTTGCACCTCTCGTGGGACAAATACATTTGCAACATTTGCTGCTATGA 960
DB 901 ATTCTCTTCTTGCACCTCTCGTGGGACAAATACATTTGCAACATTTGCTGCTATGA 960
QY 961 GAAACACCGCCAGAAACACTTTGAGAAAGGAACCCAGCTGCCAACCTCATTTAG 1020
DB 961 GAAACACCGCCAGAAACACTTTGAGAAAGGAACCCAGCTGCCAACCTCATTTAG 1020
QY 1021 TGTGTTTGGGTAAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAAGCCA 1080
DB 1021 TGTGTTTGGGTAAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAAGCCA 1080
QY 1081 CACTTGAAGCCTTGCACACCTGCGAGCCCTACAA----- 1115
DB 1081 CACTTGAAGCCTTGCACACCTGCGAGCCCTACAAAGAAAGAAACAAAGGGAAGCATCAAGC 1140
QY 1116 --TCAGAACGTAAGTTTAAAGAGCAGTCCGATGCTAGCCCGAGGGGCCAGATTT 1173
DB 1141 AGTCAGAACGTAAGTTTAAAGAGCAGTCCGATGCTAGCCCGAGGGGCCAGATTT 1200
QY 1174 AAGAGCCGCAAGCCTCAGTAGTGACAGGAGTCCCAAGCACCGACATCAAGCCGAG 1233
DB 1201 AAGAGCCGCAAGCCTCAGTAGTGACAGGAGTCCCAAGCACCGACATCAAGCCGAG 1260
QY 1234 GGCAGTCCCAACCAAGTCAGAAAGAGCTGGAGCTTCAACGACCGCTTCCGGCCC 1293
DB 1261 GGCAGTCCCAACCAAGTCAGAAAGAGCTGGAGCTTCAACGACCGCTTCCGGCCC 1320
QY 1294 TCGCTCGGCTCAAAAGTTCTCAGCCAAACAGATGATAGCTGACACAGCCCTTGGC 1353
DB 1321 TCGCTCGGCTCAAAAGTTCTCAGCCAAACAGATGATAGCTGACACAGCCCTTGGC 1380
QY 1354 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATGATGAGGAGACCTCACC 1413
DB 1381 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATGATGAGGAGACCTCACC 1440
QY 1414 CCACCACTTAAACTGTCTATTCAGCTATCAGAAATATGAAATTTCAATTTGCAAAACGG 1473
DB 1441 CCACCACTTAAACTGTCTATTCAGCTATCAGAAATATGAAATTTCAATTTGCAAAACGG 1500
QY 1474 AAGTTTAAAGAAACGTTTACGTCATATGATGATGATGATGATGATGATGATGATGATGAT 1533
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DB 1561 GGTCTATCTGGACATGTTGTGAGAAATTAAGCCTTCAACACGCTTGGATCAAAATTTCT 1620
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DB 1621 GGAAGAGGCAATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1654 ACCACAGAGCATCTCAGTATGCTCGGTGGTCAAGGTTCAAGGTTCAAGGTTCAAGGTTCA 1713
DB 1681 ACCACAGAGCATCTCAGTATGCTCGGTGGTCAAGGTTCAAGGTTCAAGGTTCAAGGTTCA 1740

QY 1714 ATAGAGTCCAAAGCTGGAGCTGCTTACTAGACATCTATCAACAGGTCCTTCGAAAGGCTCT 1773
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QY 1774 GGCCTAGCCCTCGCTTTGGCTTCAATTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1833
DB 1801 GGCCTAGCCCTCGCTTTGGCTTCAATTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1860
QY 1834 GACTATCAAGCCCTGTGTGATAGCAAGATCTTTGGGTTCCGACAAACAGTGGCTGC 1893
DB 1861 GACTATCAAGCCCTGTGTGATAGCAAGATCTTTGGGTTCCGACAAACAGTGGCTGC 1920
QY 1894 TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTTCAGTTCATTTCTGACGCCAAAT 1953
DB 1921 TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTTCAGTTCATTTCTGACGCCAAAT 1980
QY 1954 GAGTTCAAGTCCGAGACTTTCTAGCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2013
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QY 2014 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACTTTACAGATCCCACTCTCCCA 2073
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QY 2074 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2133
DB 2101 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
QY 2134 GCATCAAGCATCTGCCAGGCGAGAACTCTGCACCTTAAACCTGCAGGCTTACAGGAA 2193
DB 2161 GCATCAAGCATCTGCCAGGCGAGAACTCTGCACCTTAAACCTGCAGGCTTACAGGAA 2220
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DB 2221 AGCATTTCTGAGCTCAGCAGCTCTGTTGCTTCCAGGAAATCTTTCAGGTTGCACAG 2280
QY 2254 TCAAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2313
DB 2281 TCAAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
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DB 2341 TTGCTGCTGTCCTGATGTCGAGGACTTTGGGAAATCTTTGCTGTCGAAACCTG 2400
QY 2374 ATCAGTCCAGCAGGAACTGAATATACAACTTTCAGGAGTGAGTCAAGTGGCTCCAG 2433
DB 2401 ATCAGTCCAGCAGGAACTGAATATACAACTTTCAGGAGTGAGTCAAGTGGCTCCAG 2460
QY 2434 GGCAGCCAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTATTAATGATGAAGAG 2493
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QY 2494 GTGGGTCCGAAAGACAGACAGACACTTTTGTATGCGGACCGCAGGCTGCGCAGGAA 2553
DB 2521 GTGGGTCCGAAAGACAGACAGACACTTTTGTATGCGGACCGCAGGCTGCGCAGGAA 2580
QY 2554 GCTGCTTTGATCAGACTCTTAAGGACTGAAAGTCAAGTCACTCTCAGAGCATTTGT 2613
DB 2581 GCTGCTTTGATCAGACTCTTAAGGACTGAAAGTCAAGTCACTCTCAGAGCATTTGT 2640
QY 2614 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
DB 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694

RESULT 8

US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DMORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T

```

; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KNO5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-493-1

Query Match 98.6%; Score 2630; DB 19; Length 2694;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2667; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 ATGAAGGATGTGAGTTCGGGCGGGGCGAGGCTGCTGAACTCGGCAGCCCGCAGGGGC 60
DB 1 ATGAAGGATGTGAGTTCGGGCGGGGCGAGGCTGCTGAACTCGGCAGCCCGCAGGGGC 60
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QY 241 TACACAGTAGCAGAGCTGCGGGGCAACGTCAGTAGTCCGGCGGGTCCAGAACTACCTG 300
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DB 661 GGTTCAAGTGTATGCTCAGCAAGGAATTAATCAGCTTGGTACATAGATTTTGG 720
QY 721 GTTCTTATTTTGGTCTTCTGCTATCTGTTGAAAGGATGCCAATAAGAGTTT 780
DB 721 GTTCTTATTTTGGTCTTCTGCTATCTGTTGAAAGGATGCCAATAAGAGTTT 780

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841 GACAAAACCTCCCTTAACCTTGGCTGGGAAAGATTGCTTTCTGCAAGGCTTTGCACTCTCTGGC 900
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901 ATTTCTTTCTTTGCACTTCTCTGCGGCATTTCTGCTCAGGTTTTCATTAAGAGTACAA 960
901 ATTTCTTTCTTTGCACTTCTCTGCGGCATTTCTGCTCAGGTTTTCATTAAGAGTACAA 960
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1801 GCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
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1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTTCGGTTCCGACAAAACAGTGCTGC 1920
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1921 TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCAATCTCGCGCCAAAT 1980
1954 GAGTTCAAGTCCAGAGCTTTTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2013
1981 GAGTTCAAGTCCAGAGCTTTTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2040
2014 GTGCCAATTAGTCAAGAGGATGCTCAGAGTGGGAGCCACCAACACATTCGAACCAA 2073
2041 GTGCCAATTAGTCAAGAGGATGCTCAGAGTGGGAGCCACCAACACATTCGAACCAA 2100
2074 ATAAATACGGCACCAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2133
2101 ATAAATACGGCACCAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
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2461 GCAGGCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATTAATCTGATGAAG 2520
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2581 GCTGCCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGTCAATCTCAGAGCAATTTGT 2640
2614 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
2641 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2694

RESULT 9
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-1

Query Match 98.5%; Score 2626.4; DB 9; Length 3071;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
QY 1 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTCTGAACTCGGACGCGCCAGGGGC 60
DB 10 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTCTGAACTCGGACGCGCGAGGGGC 69
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DB 70 GAGGCTCTGTACTGTGCGGCACCCGCGCGGCGAGCTTTGGTGGGCGCGGCGGTGCGCTG 129
QY 121 AGGAGAGCGCGCGGCGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAAGCGCTCTCT 180
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QY 301 CTGTGCTTGGTGTGATTTGTGCTGAGTTTGTACCATCTCTGAGCAGCAAAATTTG 360
DB 310 CTGTGCTTGGTGTGATTTGTGCTGAGTTTGTACCATCTCTGAGCAGCAAAATTTG 369
QY 361 GCCTCAAGTGTCTGTGATCTGAGTTCGATGATTTGTGCTGCTTTGGAGTTTC 420
DB 370 GCCTCAAGTGTCTGTGATCTGAGTTCGATGATTTGTGCTGCTTTGGAGTTTC 429
QY 421 ATCAATTCGAATCTGTCTGCGGGTGTCTGTGCTGATATAGAGGATGGAAGAACTG 480
DB 430 ATCAATTCGAATCTGTCTGCGGGTGTCTGTGCTGATATAGAGGATGGAAGAACTG 489
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DB 490 AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCA 549
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QY 721 GTTCTTATTTTTCGCTTCTTCTGCTATCTGTTGGGAAAGGATGCCAATAAAGAGTTT 780
DB 730 GTTCTTATTTTTCGCTTCTTCTGCTATCTGTTGGGAAAGGATGCCAATAAAGAGTTT 789
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1954	QY	GAGTTTCAGTGCCACAGACTTTCTACCGGTTAGCCCTACTATGCAAGCTCAAGCACACAG	2013
1990	Db	GAGTTTCAGTGCCACAGACTTTCTACCGGTTAGCCCTACTATGCAAGCTCAAGCACACAG	2049
2014	QY	GTGCCAAATTAGTCAAAAGCATGGCTCAGCAGTGGCAGCACCAACACATTTGCAAAACCAA	2073
2050	Db	GTGCCAAATTAGTCAAAAGCATGGCTCAGCAGTGGCAGCACCAACACATTTGCAAAACCAA	2109
2074	QY	ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCGCACCTCTCTCCCA	2133
2110	Db	ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCGCACCTCTCTCCCA	2169
2134	QY	GCATCAAGGATCTGCCACGGCAGAACTCTGCACCCTAAACCTTCAGGCTTACAGGAA	2193
2170	Db	GCATCAAGGATCTGCCACGGCAGAACTCTGCACCCTAAACCTTCAGGCTTACAGGAA	2229
2194	QY	AGCAATTTCTGACGTCAACCACTGCCTTGTGTGCTCCAAGGAAATGTTCAGTTGTCACAG	2253
2230	Db	AGCAATTTCTGACGTCAACCACTGCCTTGTGTGCTCCAAGGAAATGTTCAGTTGTCACAG	2289
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2290	Db	TCAAATCTCACCAAGGACCGTTCATGAGGAAAGCTTTGACATGGAGAGAGAACTCTG	2349
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2350	Db	TTGTCTCTGTGCCATGTGTCGCGAAGGACTTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2409
2374	QY	ATCAGTGTGACCGAGGAACTGAATATACAACCTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2433
2410	Db	ATCAGTGTGACCGAGGAACTGAATATACAACCTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2469
2434	QY	GGCAGCCAAGATTTTATACCCCAATGGAGGGAATCCAAATTTGTTATACTGATGAAGAG	2493
2470	Db	GGCAGCCAAGATTTTATACCCCAATGGAGGGAATCCAAATTTGTTATACTGATGAAGAG	2529
2494	QY	GTGGTCCGGAAGAGACAGACACAGACATTTTGTGTCGCCACCGCAGCTGCCAGGAA	2553
2530	Db	GTGGTCCGGAAGAGACAGACACAGACATTTTGTGTCGCCACCGCAGCTGCCAGGAA	2589
2554	QY	GCTGCCTTTGTCATCAGACTCTCTAAGGACTGGAGGTCAAGTCACTCAGAGCATTTGT	2613
2590	Db	GCTGCCTTTGTCATCAGACTCTCTAAGGACTGGAGGTCAAGTCACTCAGAGCATTTGT	2649
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2650	Db	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTGCAACCTGAATAA	2703

RESULT 10
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1

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; PUBLICATION NO.: US20040200703A1
;
; GENERAL INFORMATION:
;
; APPLICANT: JENTSCH, Thomas
;
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
;
; FILE REFERENCE: 2815-0236P
;
; CURRENT APPLICATION NUMBER: US/10/661,629
;
; CURRENT FILING DATE: 2003-09-15
;
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 1
;
; LENGTH: 3137
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
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; FEATURE:
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; NAME/KEY: CDS
;
; LOCATION: (1)..(2691)
;
; US-10-661-629-1

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Query Match 98.4%; Score 2625.2; DB 18; Length 3137;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 2664; Conservative 0; Mismatches 3; Indels 27; Gaps 1;

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910	ATTTCTTTCCTTGCACTTCCTCGCGGCATTCTTGCTCAGGTCTTTGATTAAAGTAGTACAA	969
Qy		
961	GAAACAACGGCCAGAAAAACATTTTGAGAAAAGAAGAACCCAGCTGCCAACCCTCATTCAG	1020
Db		
970	GAAACAACGGCCAGAAAAACATTTTGAGAAAAGAAGAACCCAGCTGCCAACCCTCATTCAG	1029
Qy		
1021	TGTGTTTGGCGTAGTTAACCGACTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCCA	1080
Db		
1030	TGTGTTTGGCGTAGTTAACCGACTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCCA	1089
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Qy		
1174	AAGAGCCGACAAGCCTCAGTAGTGTGACAGAGGTCCCAGCACCGACATCACAGCCGAG	1233
Db		
1210	AAGAGCCGACAAGCCTCAGTAGTGTGACAGAGGTCCCAGCACCGACATCACAGCCGAG	1269
Qy		
1234	GGCAGTCCCACCAAGTGACAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC	1293
Db		
1270	GGCAGTCCCACCAAGTGACAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC	1329
Qy		
1294	TCGCTGGCGCCTCAAAAGTTCTCAGCCAAAACCAAGTGATGATGCTGACACAGCCCTTGGC	1353
Db		
1330	TCGCTGGCGCCTCAAAAGTTCTCAGCCAAAACCAAGTGATGATGCTGACACAGCCCTTGGC	1389
Qy		
1354	ACTGATGATGATATGATGATAAAGAGATGCCAGTGTGATGATCACTGGAAGACCTCACC	1413
Db		
1390	ACTGATGATGATATGATGATAAAGAGATGCCAGTGTGATGATCACTGGAAGACCTCACC	1449
Qy		
1414	CCACCACCTTAAAACTGTCAITTCGAGCTATCAGAAATTTGAAATTTCAATGTTGCAAAACGG	1473
Db		
1450	CCACCACCTTAAAACTGTCAITTCGAGCTATCAGAAATTTGAAATTTCAATGTTGCAAAACGG	1509
Qy		
1474	AAGTTTAAGAAAACTGTACGTCCATATGATGATAAAGATGTCATTCGAACAATTTCTGCT	1533
Db		
1510	AAGTTTAAGAAAACTGTACGTCCATATGATGATAAAGATGTCATTCGAACAATTTCTGCT	1569
Qy		
1534	GGTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAACACGTTGATCAAAATTCCT	1593
Db		
1570	GGTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAACACGTTGATCAAAATTCCT	1629
Qy		
1594	GGAAAGGGCAAAATCACATCAGATAAGAAGCCGAGAGAAAATAACAGCAGAACATGAG	1653
Db		
1630	GGAAAGGGCAAAATCACATCAGATAAGAAGCCGAGAGAAAATAACAGCAGAACATGAG	1689
Qy		
1654	ACCA CAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGTTGGA AAAACAGGTACAGTCC	1713
Db		
1690	ACCA CAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGTTGGA AAAACAGGTACAGTCC	1749
Qy		
1714	ATAGAGTCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTCTTCGGA AAGGCTCT	1773
Db		
1750	ATAGAAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTCTTCGGA AAGGCTCT	1809
Qy		
1774	GCCTCAGCCCTCGCTTTTGGCTTCATTCAGATCCCACTTTTGAATGTGGAACAGACATCT	1833
Db		
1810	GCCTCAGCCCTCGCTTTTGGCTTCATTCAGATCCCACTTTTGAATGTGGAACAGACATCT	1869
Qy		
1834	GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC	1893
Db		
1870	GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGCACAAAAACAGTGGCTGC	1929
Qy		
1894	TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCCTGCGAGTTCA TTTGACGCCAAAT	1953
Db		
1930	TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCCTGCGAGTTCA TTTGACGCCAAAT	1989

QY 1 ATGAAGGATGTGGAGTCGGGCGGGCAGGGTGTCTGTGAACCTCGCGAGCCGCGCAGGGG 60
DB |||||
1 ATGAAGGATGTGGAGTCGGGCGGGCAGGGTGTCTGTGAACCTCGCGAGCCGCGCAGGGG 60
QY 61 GACGGCTGTCTACTGTCTGGGACACCGCGGGGCCACGCTTGGTGGCGGGCGGGTGGCCCTG 120
DB |||||
61 GACGGCTGTCTACTGTCTGGGACACCGCGGGGCCACGCTTGGTGGCGGGCGGGTGGCCCTG 120
QY 121 AGGGAGAGCGCGCGGGCAAGCAGAGGGGGCGGAGCTGTCTGGGAAGCGCTCTCT 180
DB |||||
121 AGGGAGAGCGCGGGCAAGCAGAGGGGGCGGAGCTGTCTGGGAAGCGCTCTCT 180
QY 181 TACACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGGGGTGCAGAACTACCTG 240
DB |||||
181 TACACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGGGGTGCAGAACTACCTG 240
QY 241 TACAACGTCGTGGAGAGACCCCGGGCTGGGGTGTCTATCAACGCTTGGTTTCTC 300
DB |||||
241 TACAACGTCGTGGAGAGACCCCGGGCTGGGGTGTCTATCAACGCTTGGTTTCTC 300
QY 301 CTGTGCTTGGTGTGATTTGTTCAGTGTCTTCTACCATCCCTGAGCACACAAATG 360
DB |||||
301 CTGTGCTTGGTGTGATTTGTTCAGTGTCTTCTACCATCCCTGAGCACACAAATG 360
QY 361 GCTCAAGTTGCTTGTATCTCGAGTTCGTGATGATTTGTCTTGGTTGGAGTTTC 420
DB |||||
361 GCTCAAGTTGCTTGTATCTCGAGTTCGTGATGATTTGTCTTGGTTGGAGTTTC 420
QY 421 ATCATTCGAATCTGGTCTGGGGTTCGTGTGTGATAGAGGATGGCAAGAGACTG 480
DB |||||
421 ATCATTCGAATCTGGTCTGGGGTTCGTGTGTGATAGAGGATGGCAAGAGACTG 480
QY 481 AGSTTGTCTCGAAGCCCTCTGTGTATAGATACCATTTCTTATCCGCTTCAATAGCA 540
DB |||||
481 AGSTTGTCTCGAAGCCCTCTGTGTATAGATACCATTTCTTATCCGCTTCAATAGCA 540
QY 541 GTTGTCTTGCAGAACTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAACTCTCGT 600
DB |||||
541 GTTGTCTTGCAGAACTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAACTCTCGT 600
QY 601 TTCTCAGATCCTCGGATGTGGCGATGGACCGAAGGGGAGGACATTGGAAATTTACTG 660
DB |||||
601 TTCTCAGATCCTCGGATGTGGCGATGGACCGAAGGGGAGGACATTGGAAATTTACTG 660
QY 661 GGTTCAGTGTATGTCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGATTTTGG 720
DB |||||
661 GGTTCAGTGTATGTCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGATTTTGG 720
QY 721 GTTCTTATTTTTCGTTCTTCTGTCTATCTGGTGGAAAGGATGCCAATAAAGATTT 780
DB |||||
721 GTTCTTATTTTTCGTTCTTCTGTCTATCTGGTGGAAAGGATGCCAATAAAGATTT 780
QY 781 TCTACATATGCAGATGTCTGTGGGGGACAAATTAATTGACAACTATTGGCTATGGA 840
DB |||||
781 TCTACATATGCAGATGTCTGTGGGGGACAAATTAATTGACAACTATTGGCTATGGA 840
QY 841 GACAAACTCCCTAACTTGGCTGGGAGATTTCTTCTGAGGCTTTCACCTCTTGGC 900
DB |||||
841 GACAAACTCCCTAACTTGGCTGGGAGATTTCTTCTGAGGCTTTCACCTCTTGGC 900
QY 901 ATTTCTTCTTGTGCACTTCTTGGCTCAGGTTTGGCTCAGGTTTGGCTCAGGTTTGG 960
DB |||||
901 ATTTCTTCTTGTGCACTTCTTGGCTCAGGTTTGGCTCAGGTTTGGCTCAGGTTTGG 960
QY 961 GAACAAACCGCGCAGAAACATTTGAGAAAGAGAAACCGAGCTGCGCAACCTCATTCAG 1020
DB |||||
961 GAACAAACCGCGCAGAAACATTTGAGAAAGAGAAACCGAGCTGCGCAACCTCATTCAG 1020
QY 1021 TGTGTTGGGTAGTTACCGAGCTGATGAAATCTGTTTCCATTTGCAACCTGGAGCCA 1080
DB |||||
1021 TGTGTTGGGTAGTTACCGAGCTGATGAAATCTGTTTCCATTTGCAACCTGGAGCCA 1080

QY 1081 CACTTGAAGCCCTTGACACACCTGCGAGCCCTTACCAA----- 1115
DB |||||
1081 CACTTGAAGCCCTTGACACACCTGCGAGCCCTTACCAAAGAAAGAAACAGGGGAGCATCAAGC 1140
QY 1116 ---TCAAGAGCTAAGCTTTTAAGAGCGAGTGCAGTGGCTAGCCCNAGGGGCCAGAGTATT 1173
DB |||||
1141 AGTCAGAGCTAAGCTTTTAAGAGCGAGTGCAGTGGCTAGCCCNAGGGGCCAGAGTATT 1200
QY 1174 AAGAGCCGACAAAGCCCTCAGTAGTGCAGGAGGTCCCAAGCAACCGACATCAAGCCGAG 1233
DB |||||
1201 AAGAGCCGACAAAGCCCTCAGTAGTGCAGGAGGTCCCAAGCAACCGACATCAAGCCGAG 1260
QY 1234 GCGAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACGACCGAAACCCGCTTCCGGCCC 1293
DB |||||
1261 GCGAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACGACCGAAACCCGCTTCCGGCCC 1320
QY 1294 TCGCTGCGCCTCAAAGTTCTCAGCCAAACAGTGATAGATGCTGACACAGCCCTTGGC 1353
DB |||||
1321 TCGCTGCGCCTCAAAGTTCTCAGCCAAACAGTGATAGATGCTGACACAGCCCTTGGC 1380
QY 1354 ACTGATGATGATATGATGAAAAAGATGCCAGTGTGATGATCAGTGGAAGACCTCACC 1413
DB |||||
1381 ACTGATGATGATATGATGAAAAAGATGCCAGTGTGATGATCAGTGGAAGACCTCACC 1440
QY 1414 CCACCACTTAAACCTGTATTGAGCTATCAGAAATTAAGAAATTTTCAATGCAAAACCG 1473
DB |||||
1441 CCACCACTTAAACCTGTATTGAGCTATCAGAAATTAAGAAATTTTCAATGCAAAACCG 1500
QY 1474 AAGTTTAAGGAAACGTTAGTCCATATGATGAAAAAGATGTCATTTGAAACAAATTTCTGCT 1533
DB |||||
1501 AAGTTTAAGGAAACATTAAGTCCATATGATGAAAAAGATGTCATTTGAAACAAATTTCTGCT 1560
QY 1534 GGTCACTTGGACATGTTGTGTAGAAATTAAGACCTTCAACACAGCTGTTCATCAAAATCTT 1593
DB |||||
1561 GGTCACTTGGACATGTTGTGTAGAAATTAAGACCTTCAACACAGCTGTTCATCAAAATCTT 1620
QY 1594 GGAAAGGGCAATCACATCAGATAAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1653
DB |||||
1621 GGAAAGGGCAATCACATCAGATAAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1680
QY 1654 ACCACAGAGATCTCAGTATGCTCGGTGGGTGGTTCAGGTTTGAANAACAGGTACAGTCC 1713
DB |||||
1681 ACCACAGAGATCTCAGTATGCTCGGTGGGTGGTTCAGGTTTGAANAACAGGTACAGTCC 1740
QY 1714 ATAGAGTCCAAGCTGGCTAGCTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1773
DB |||||
1741 ATAGAGTCCAAGCTGGCTAGCTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1800
QY 1774 GCTCAGCCCTCGCTTGGCTTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1833
DB |||||
1801 GCTCAGCCCTCGCTTGGCTTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
QY 1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGCAACAAACAGTGGCTGC 1893
DB |||||
1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGCAACAAACAGTGGCTGC 1920
QY 1894 TTATCCAGATCAACTAGTGCCAAACATCTCAGAGGCTGCAGTTCATTTCTGACGCAAT 1953
DB |||||
1921 TTATCCAGATCAACTAGTGCCAAACATCTCAGAGGCTGCAGTTCATTTCTGACGCAAT 1980
QY 1954 GAGTTTCAAGTCCAGACTTTCTACGCGTTCAGCCCTTACCTATGACAGTCAAGCAACAG 2013
DB |||||
1981 GAGTTTCAAGTCCAGACTTTCTACGCGTTCAGCCCTTACCTATGACAGTCAAGCAACAG 2040
QY 2014 GTGCCAATTTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACCACTTCGCAACCAA 2073
DB |||||
2041 GTGCCAATTTAGTCAAGCGATGGCTCAGCAGTGGCAGCCCAACACCACTTCGCAACCAA 2100
QY 2074 ATAAATACGGCAACCCAGCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2133
DB |||||
2101 ATAAATACGGCAACCCAGCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2160
QY 2134 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAACCTGCGAGGCTTACAGGAA 2193

Db	2161	GCATCAAGCATCTGCCAGCGCAGAACTCTGCACCTTAACCTGCGAGCTTTACAGGAA	2220	
Qy	2194	AGATTTCTGACGTCAACCACTGCTTGTTCCTCCAAAGGAAATGTTTCAAGTTGCACAG	2253	
Db	2221	AGCATTTCTGACGTCACCACTGCTTGTTCCTCCAAAGGAAATGTTTCAAGTTGCACAG	2280	
Qy	2254	TCAAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAAACTCTG	2313	
Db	2281	TCAAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAAACTCTG	2340	
Qy	2314	TTGTCTGTCTGCCATGTCGCAAGGACTTGGGCAAACTTTGCTCTGTGCAAACTTG	2373	
Db	2341	TTGTCTGTCTGCCATGTCGCAAGGACTTGGGCAAACTTTGCTCTGTGCAAACTTG	2400	
Qy	2374	ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA	2433	
Db	2401	ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA	2460	
Qy	2434	GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATAAATGATGAAGAG	2493	
Db	2461	GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATAAATGATGAAGAG	2520	
Qy	2494	GTGGTCCCGAAGACAGACAGACACACTTTTGTATGTCGCGCAGCGCTGCCAGGGAA	2553	
Db	2521	GTGGTCCCGAAGACAGACAGACACACTTTTGTATGTCGCGCAGCGCTGCCAGGGAA	2580	
Qy	2554	GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT	2613	
Db	2581	GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAGAGCAATTTGT	2640	
Qy	2614	AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTATGTCAAACTGAATAA	2667	
Db	2641	AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTATGTCAAACTGAATAA	2694	
RESULT 11				
US-09-813-148-1				
; Sequence 1, Application US/09813148				
; Patent No. US20020076809A1				
; GENERAL INFORMATION:				
; APPLICANT: STEINMEYER, Klaus				
; APPLICANT: LERCHE, Christian				
; APPLICANT: SCHERER, Constanze				
; APPLICANT: SEEBOHM, Guiscard				
; APPLICANT: BUSCH, Andreas E.				
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCN05, A NEW TARGET FOR DISEASES OF CEN				
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM				
; FILE REFERENCE: 38005-119				
; CURRENT APPLICATION NUMBER: US/09/813,148				
; CURRENT FILING DATE: 2001-03-21				
; PRIOR APPLICATION NUMBER: DE 100 13 732.6				
; PRIOR FILING DATE: 2000-03-21				
; PRIOR APPLICATION NUMBER: US 60/194,041				
; PRIOR FILING DATE: 2000-04-03				
; NUMBER OF SEQ ID NOS: 6				
; SOFTWARE: Patent in version 3.0				
; SEQ ID NO 1				
; LENGTH: 3074				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-09-813-148-1				
Query Match				
Best Local Similarity 98.1%; Score 2617.2; DB 9; Length 3074;				
Matches 2659; Conservative 0; Mismatches 8; Indels 27; Gaps 1;				
Qy	1	ATGAAGGATGTGAGTCCGGGCGGCGAGGGTGTCTGTAACCTCGGACGCCGCGAGGGC	60	
Db	215	ATGAAGGATGTGAGTCCGGGCGGCGAGGGTGTCTGTAACCTCGGACGCCGCGAGGGC	274	
Qy	61	GACGGCTGTACTGTCTGGGACCCGCGCGGCGACCGCTTGGTGGCGGCGGTGGCTG	120	

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QY 1174 AAGAGCCGCAAGCCTCAGTAGTGACAGAGGTCCCCAAGCACCGACATCAAGCCGAG 1233
DB 1415 AAGAGCCGCAAGCCTCAGTAGTGACAGAGGTCCCCAAGCACCGACATCAAGCCGAG 1474
QY 1234 GGCAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1293
DB 1475 GGCAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1534
QY 1294 TCGTCGGCTCAAAAGTTCTCAGCCCAAAACACGATGATAGCTGACACAGCCCTTGGC 1353
DB 1535 TCGTCGGCTCAAAAGTTCTCAGCCCAAAACACGATGATAGCTGACACAGCCCTTGGC 1594
QY 1354 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATCAGTGAAGACCTTACC 1413
DB 1595 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATCAGTGAAGACCTTACC 1654
QY 1414 CCACACTTAAACTGTCTATTCGAGCTATCAGAAATATGAAATTCATGTTGCAAAACGG 1473
DB 1655 CCACACTTAAACTGTCTATTCGAGCTATCAGAAATATGAAATTCATGTTGCAAAACGG 1714
QY 1474 AAGTTTAAAGAAACGTTACGTCCATATGATGATAAAGATGTCATTGAAACAATATCTGCT 1533
DB 1715 AAGTTTAAAGAAACATTTACGTCCATATGATGATAAAGATGTCATTGAAACAATATCTGCT 1774
QY 1534 GGTCTATCTGGACATGTTGTGTAGAATTAAAGCCTTCAAAACAGCTTTCATCAAAATTCCT 1593
DB 1775 GGTCTATCTGGACATGTTGTGTAGAATTAAAGCCTTCAAAACAGCTTTCATCAAAATTCCT 1834
QY 1594 GGAAGAGGCAATCAATCAGATAGAAAGAGCCGAGAGAAATTAACAGCAGAAATGAG 1653
DB 1835 GGAAGAGGCAATCAATCAGATAGAAAGAGCCGAGAGAAATTAACAGCAGAAATGAG 1894
QY 1654 ACCAGAGAGCTCAGTATGCTCGTCCGGTGGTCAAGTTTGAAGAGAGTACAGTCC 1713
DB 1895 ACCAGAGAGCTCAGTATGCTCGTCCGGTGGTCAAGTTTGAAGAGAGTACAGTCC 1954
QY 1714 ATAGAGTCCAAGTGGCTGCTACTAGACATCTATCAACAGTCTCTCGGAAGGCTCT 1773
DB 1955 ATAGAGTCCAAGTGGCTGCTACTAGACATCTATCAACAGTCTCTCGGAAGGCTCT 2014
QY 1774 GCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCCAACCTTTTGAATGTGAACAGACATCT 1833
DB 2015 GCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCCAACCTTTTGAATGTGAACAGACATCT 2074
QY 1834 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCGCAAAACAGTGGCTGC 1893
DB 2075 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCGCAAAACAGTGGCTGC 2134
QY 1894 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTGCACTTCAATTCGACGCCAAT 1953
DB 2135 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTGCACTTCAATTCGACGCCAAT 2194
QY 1954 GAGTTCAAGTCCAGACTTTTACGGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2013
DB 2195 GAGTTCAAGTCCAGACTTTTACGGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2254
QY 2014 GTGCCAATTTAGTCAAGCGATGGCTCAGAGTGGCAGCCACCAACCAATTCGAACCA 2073
DB 2255 GTGCCAATTTAGTCAAGCGATGGCTCAGAGTGGCAGCCACCAACCAATTCGAACCA 2314
QY 2074 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2133
DB 2315 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2374
QY 2134 GCCATCAAGCATCTGCCAGGCAGAACTCTGCACCTTAAACCTTCAGAGCTTACAGAA 2193
DB 2375 GCCATCAAGCATCTGCCAGGCAGAACTCTGCACCTTAAACCTTCAGAGCTTACAGAA 2434
QY 2194 AGCATTTCTGAGCTCACCACCTGCCTTGTGCTCCAGGAAATGTTTCAGGTTGCACAG 2253
DB 2435 AGCATTTCTGAGCTCACCACCTGCCTTGTGCTCCAGGAAATGTTTCAGGTTGCACAG 2494
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QY 2254 TCAATCTCAACAAGACCGTTCTATGAGAAAGCTTTGACATGGAGGAGAAACTCTG 2313
DB 2495 TCAATCTCAACAAGACCGTTCTATGAGAAAGCTTTGACATGGAGGAGAAACTCTG 2554
QY 2314 TTGTCTGTCTGCCATGTCGGAAGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2373
DB 2555 TTGTCTGTCTGCCATGTCGGAAGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2614
QY 2374 ATCAGTCCAGCAGGAACTGAATATACAACTTTCAGGAGTGAGTCAAGTGGCTCCAG 2433
DB 2615 ATCAGTCCAGCAGGAACTGAATATACAACTTTCAGGAGTGAGTCAAGTGGCTCCAG 2674
QY 2434 GGCAGCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTATTAATCTGATGAAGAG 2493
DB 2675 GGCAGCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTATTAATCTGATGAAGAG 2734
QY 2494 GTGGTCCGGAAGACAGACAGACACTTTTGTATGCCGACCCGAGGCTGCCAGGAA 2553
DB 2735 GTGGTCCGGAAGACAGACAGACACTTTTGTATGCCGACCCGAGGCTGCCAGGAA 2794
QY 2554 GCTGCTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAAGTCAAGTCAAGTCTG 2613
DB 2795 GCTGCTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAAGTCAAGTCAAGTCTG 2854
QY 2614 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2667
DB 2855 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAA 2908
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RESULT 12

US-10-313-542-303

; Sequence 303, Application US/10313542

; Publication No. US20030120057A1

; GENERAL INFORMATION:

; APPLICANT: Roopa, Reddy

; APPLICANT: Guegler, Karl, J.

; APPLICANT: Au-Young, Janice

; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED

; FILE REFERENCE: PA-0013 US

; CURRENT APPLICATION NUMBER: US/10/313,542

; CURRENT FILING DATE: 2002-12-05

; PRIOR APPLICATION NUMBER: US/09/495,050

; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/118,318

; PRIOR FILING DATE: 1999-02-01

; NUMBER OF SEQ ID NOS: 305

; SOFTWARE: PERL Program

; SEQ ID NO 303

; LENGTH: 582

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20030120057A1 4970006CT1

US-10-313-542-303

Query Match 19.1%; Score 509.8; DB 15; Length 582;
Best Local Similarity 99.4%; Pred. No. 1.7e-146;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 1594 GGAAGGGGCAATCAATCAGATGAAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1653
DB 1 GGAAGGGGCAATCAATCAGATGAAGAGCCGAGAGAAATTAACAGCAGAACATGAG 60
QY 1654 ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAGAGTTGAAAAACAGTACAGTCC 1713
DB 61 ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAGAGTTGAAAAACAGTACAGTCC 120
QY 1714 ATAGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGCTCT 1773
DB 121 ATAGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGCTCT 180
QY 1774 GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCAACCTTTTGAATGTGAACAGATCT 1833
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181 GCCTCAGCCCTGCTTTGGCTTCAATCCAGATCCACCTTTGAATGTGAACAGATCT 240
1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 1893
241 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGACAAAACAGTGGCTGC 300
1894 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTCGAGTTCAATTTGAGCCCAAT 1953
301 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTCGAGTTCAATTTGAGCCCAAT 360
1954 GAGTTAGTCCGACACTTTTACGGCTTACCTACTATGACAGTCAAGCAACAG 2013
361 GAGTTAGTCCGACACTTTTACGGCTTACCTACTATGACAGTCAAGCAACAG 420
2014 GTGCCAATTAGTCAAGGATGGCTCAGCAGTGGCAGCCACCAACACATTTGCAACCAA 2073
421 GTGCCAATTAGTCAAGGATGGCTCAGCAGTGGCAGCCACCAACACATTTGCAACCAA 480
2074 ATAATACGGACCCCAAGCCAGAGCCCAACCAACTTTACAGATC 2118
481 ATAATACGGACCCCAAGCCAGAGCCCAACCAACTTTACAGATC 524

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RESULT 13
US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Ferodin, Jacqueline
; APPLICANT: Rodigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 5848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17793, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MPI02-018PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-353-690-55

Query Match      18.4%; Score 492; DB 17; Length 2335;
Best Local Similarity 59.3%; Pred. No. 1.4e-140;
Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

QY 217 TACCGCGGGTGCAGAACTACCTGTACAAAGTGTGGAGAGACCCCGGGCTGGCGTTC 276
DB 320 TACCGCGGGTGCAGAACTACCTGTACAAAGTGTGGAGAGACCCCGGGCTGGCGTTC 379
QY 277 ATCTACCAAGCTTTGTTTTTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 336
DB 380 GTCTACCAAGCTTTGTTTTTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 439
QY 337 ACCATCCCTGAGCACAAAAATTTGGCTCAAGTTGCTTCTTGTATCTGAGTTCGTGATG 396
DB 440 ACTATCCAGGAGCACCAGGAACCTTGCCAAACAGAGTGTCTCTCATCTTGGAAATTCGTGATG 499
QY 397 ATTGTGCTTTGGTTTGGAGTTCATATTCGAAATCTGCTGCTGCGGTTGCTGTTGCTGA 456
DB 500 ATCGTGGTTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCGCCGATGCTGCTGCCGC 559
QY 457 TATAGAGGATGGCAAGAAAGACTGAGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATAC 516
DB 560 TACCGAGGATGGCAGGGTTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTCATCGACTTC 619
QY 517 ATTGTTTCTTATCGCTTCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATATTTGTC 576
DB 620 ATCGTGTTCGTGGCTTCGGTGGCGCTCATCGCCGCGGGTACCCAGGGCAACATCTTCGCC 679
QY 577 ACCTGCACTCAGAACTCTCCGTTTCCCTACAGATCTCTCGCATGTGCGCATGAGCCGA 636
DB 680 ACCTCGCGCTGCGCAGCATGCGCTTCTCTCAAGATCTCTGCGCATGTGCGCATGAGCCGC 739
QY 637 AGGGAGGCACTTGGAAATTTACTGGGTTTCAGTGGTTTATGCTCACAGCAAGAAATTAATC 696
DB 740 CGCGCGGCACTTGGAAAGTCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGAGAGCTGATC 799
QY 697 ACAGCTTGTATACATAGAAATTTTGGTTTCTTATTTTCTGTTCTTCTGTTCTATCTGTTG 756
DB 800 ACCGCTTGTATACATAGAAATTTTGGTTTCTTATTTCTGCTTCTTCTGTTCTACCTGCCC 859
QY 757 GAAAGAGTGCATAAAGAGTTTCTTACATATGACAGATGCTCTCTGTTGGGGCACAAAT 816
DB 860 GAGAGAGGAGCAACTCCGACTTCTCTCTAGCGCGACTCGCTCTGTTGGGGACGAT 919
QY 817 ACATTGACAACTATTGGCTATGAGAGCAAACTCCCTTAATCTGGCTGGGAAGATTGCTT 876
DB 920 ACATTGACAACTATTGGCTATGAGAGCAAACTCCCTTAATCTGGCTGGGAAGATTGCTT 979
QY 877 TCTGAGGCTTGGCACTCTTGGCAATTTCTTTTGTGCACTTCTCTGCGGCAATTTCTTGGC 936
DB 980 GCTGTGCTTTCGCTTACTGCGGCAATCTCTTCTTCTGCTGCTGCTGCGGCAATCTTAGGC 1039
QY 937 TCAGGTTTTCATTAAGAGTACAAGAAACACACCGCCAGAAACACTTTTGAGAAAGAGG 996
DB 1040 TCCGGCTTTCGCTTGAAGTTCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGG 1099
QY 997 AACCCAGTGGCAACCTCATTCAGTGTGTTTGGCGTAGTACGCGAGCTGATGAGAAATCT 1056
DB 1100 ATCGCGGAGCCCAACCTCATTCAGGCTGCTTGGCGCTGTTACTCAACGATATGAGCGCG 1159
QY 1057 GTTTCATTTGCAACTGGAAGCCACACTTTGAAGGCTTTGACAC 1100
DB 1160 GCCTACCTGACAGCCACCTGTTACTTACTTACAGATATCTCTCCCATCTTTCAGAGAGCTG 1219
QY 1101 ----- 1100
DB 1220 GCCCTTGTGAGCAGTGCACCGGCGCCGCAATGGGGGCTTACGCGCCCTGAGGTG 1279

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QY 1101 ----- 1100
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QY 1101 -----CTGAGCCCTACCAATCAGAAGCTAAGTTTAAAGGAGCGA 1140
Db 1340 CGCGCGGCGAGCACCTCTCTCCCTTGGGGAAGCAGCGGATGGGCATCAAGACCCG 1399
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QY 1195 GTGACAGAGGTCCCAAGCACCAGACATCACAGCCGAGG---GAGTCCCAACCAAGTG 1251
Db 1460 ACAATGCCACCTCCCAAGCAGGAGAGGTGGTGAGGCCACAGCCCGACCAAGTG 1519
QY 1252 CAGAGAGCTGAGCTTCAACGACCGAACCCGCTTCCGCGCTTGGTGGCTCAAAAGT 1311
Db 1520 CAAAAGAGCTGAGCTTCAATGACCGCACCCGCTTCCGGGCTCTCTGAGACTC----- 1573
QY 1312 TCTCAGCCAAACAGTATAGTGTGACACAGCCCTTGGCAGCTGATGATATATAT 1371
Db 1574 -----AAACCCGCACTCTGCTGAGGATGCCCC---CTCAGAGGAAGTAGCAGAG 1621
QY 1372 GAAAAGGATGCCAGTGTGATGTATCAGTGAAGACCTCACCCCACTTAAACTGTC 1431
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QY 1432 ATTGAGCTATCAGAAATATGAAATTTCAATGTTGAAAACGGAAGTTTAAAGAAACGTTA 1491
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QY 1552 TGTAGAAATTAAGCCCTTCAACACAGCTGTTGATCAAAATTTTGGAAAAGGGC---AAATC 1608
Db 1802 GSCCGGATCAAGAGCTCGAATCTCGGTGGACCAATTTGTGGTTCGGGGCCCGGGAC 1861
QY 1609 ACATCAGATAGAAGAGCGGAGAGAAATAACAGCAGAACATGAGACACAGACGATCTC 1668
Db 1862 AGGAAGGCCCGGAGAAAGGCGACAAAGGGCGCTCCGACGCGAGGTGGTGGATGAAATC 1921
QY 1669 ACTATGCTCGGTCGGTGTGCTGAGTTGAABACAGGTACAGTCCATAGAGTCCAGCTG 1728
Db 1922 AGCATGATGGAGCGGTGCTCAAGGTGGAGAGAGGTCGATCCATCGAGCACAAGCTG 1981
QY 1729 GACTGCTACTAGACATCTATCAACAGGTCTCTTCGGAAGGCTCTGCGCTCAGCCCTCGCT 1788
Db 1982 GACCTGCTGTGGCTTCTATTTCGCGCTGCTGC-----GCTTGGCACCTCGGCCAGC 2035
QY 1789 TTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1848
Db 2036 CTGGGCGCGGTGCAAGTGGCTGTTCGACCCCGACATCACCTCGGACTTACCAGCCCT 2095
QY 1849 GTGGATAGCAAGATCTTTCCGGTTCCGCAACAA 1882
Db 2096 GTGGACCGAGGACATCTCCCTCTCCGACAGA 2129

RESULT 14

US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; CURRENT FILING DATE: 2004-05-20

; PRIOR APPLICATION NUMBER: 09/492,361

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2335

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: gene

; LOCATION: (1)..(2335)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (83)..(2170)

US-10-850-928-1

Query Match 18.4%; Score 492; DB 19; Length 2335;

Best Local Similarity 59.3%; Pred. No. 1.4e-140;

Matches 1087; Conservative 0; Mismatches 555; Indels 192; Gaps 7;

QY 217 TACCGCGGGTGACAACTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGGGTTC 276

Db 320 TACCGCGCTGCAGAACTGGGTCTACAACTGCTGGAGCGCCCGCGCTGGGGCTTC 379

QY 277 ATCTACCAAGCTTTTCCTCTCTCTTTTGGTTGCTTGAATTTGTAGTGTTCCT 336

Db 380 GTCTACCAAGCTTTTCCTCTCTCTTTTGGTTGCTTGAATTTGTAGTGTTCCT 439

QY 337 ACCATCCCTGAGCACAACAAATGGCTTCAAGTTCCTTTCATCTCGAGTTTCGTGATG 396

Db 440 ACTATCCAGGAGCACAGGAACCTTGCCAAACAGAGTCTCTCTCATCTTGGAAATTCGTGATG 499

QY 397 ATTGCTGCTTTGTTTGGTTCAGTTCATCATTCGAACTCTGCTCGGGTTCGCTGTCGA 456

Db 500 ATGCTGGTTTCGGCTTGGAGTACATCGTCCGGTCTGGTCCGCGGATGCTGCTGCCGC 559

QY 457 TATAGAGATGGCAAGAGACTGAGTTCCTCGAAAGCCCTTCTGTGTTATAGATACC 516

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 1101 ----- 1100
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 1340 CGGGCGGCGACGACTCTCTTCTGCGCTGGGGAAGCAGCGGATGGGCATCAAGACCGC 1399
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 1252 CAGAGAGCTGAGCTTCAACAGCAGAACCCCGCTTCCGGCCCTCGCTCGCGCTCAAAAGT 1311
 1520 CAAGAAGCTGGAGCTTCAATGACCGCAGCCGCTTCCGGGCTCTCTGAGACTC----- 1573
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 1574 -----AAACCCCGCACCTCTGCTGAGGATGCCC---CCTCAGAGGAAGTACAGAG 1621
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 1802 GCGCGGATCAAGAGCTTGCNAATCGGGTGGACCAATTTGTGGTGGGGCGCGCGGAC 1861
 1609 ACATCAGATGAAGAGCGGAGAGAAATAACAGCAGAACATGAGACACACAGCATCTC 1668
 1862 AGGAAGCGCGGAGAGAGGCGCAAGAGGGGCCCTCCGACCGCGAGGTGTGATGAAATC 1921
 1669 AGTATGCTCGGTGGGTGAGAGTGAAGAGGTTGAAAGAGTACAGTCCATAGAGTCAAGCTG 1728
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 1729 GACTGCTCTAGACATCTATCAACAGAGTCTTTGGAAAGGCTCTCGCTCAGCCCTCGGT 1788
 1982 GACTGCTGTTGGGCTTCTATTCGCGCTGCTGC-----GCTCTGGCACCTCGGCCAGC 2035
 1789 TTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1848
 2036 CTGGGCGCGGTGAGTGGCGCTGTTGACCCCGCAGCATACCTCCGACTACACAGCCCT 2095
 1849 GTGATAGCAAGATCTTTGGGTTCCGACAAA 1882
 2096 GTGACCAAGGACATCTCGTCTCCGACAGA 2129

RESULT 15

US-10-096-578-88
 ; Sequence 88, Application US/10096578
 ; Publication NO. US20030165874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Leppert, Mark F.
 ; APPLICANT: Charlier, Carole
 ; APPLICANT: Singh, Nanda
 ; TITLE OF INVENTION: KNO2 AND KNO3 - POTASSIUM CHANNEL GENES WHICH ARE
 ; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
 ; FILE REFERENCE: 2323-160
 ; CURRENT APPLICATION NUMBER: US/10/096,578
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: US 09/177,650
 ; PRIOR FILING DATE: 1998-10-23
 ; PRIOR APPLICATION NUMBER: US 60/063,147
 ; PRIOR FILING DATE: 1997-10-24
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 88
 ; LENGTH: 2273
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2271)
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(2273)
 ; OTHER INFORMATION: n may be any nucleotide except at position
 ; OTHER INFORMATION: 272 at which n may be t, c or g.
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(757)
 ; OTHER INFORMATION: Xaa may be: S or R at 18, 19 and 69; V, A, E or G
 ; OTHER INFORMATION: at 31; D or E at 33; S, P, T or A at 39; I, T, N or
 ; OTHER INFORMATION: S at 52; F, L, I, M or V at 53; S, P, T or A at 64;
 ; OTHER INFORMATION: P at 68; L, S or W at 91; R at 365; V at 509 and 516.
 ; OTHER INFORMATION:
 US-10-096-578-88

Query Match 18.3%; Score 489.2; DB 16; Length 2273;
 Best Local Similarity 57.0%; Pred. No. 1e-139;
 Matches 1020; Conservative 2; Mismatches 667; Indels 99; Gaps 4;
 QY 64 GGCCTGCTACTGTGGGCACCGCGCGCCACGCTTGGTGGCGCGCGCGTGGCGGAGG 123
 DB 67 GGCCTGCTGGGGTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
 QY 124 GAGAGCGCGCGCGGCAAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 183
 DB 127 GCGGGCTCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
 QY 184 ACAGTAGCCAGAGCTGCCGCGCGCAACGTCAGTACCGCGCGCGCGCGCGCGCGCG 243
 DB 187 GGACCGGGAAGCG 246
 QY 244 AACGTGCTGAGAGACCG 303
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 QY 304 GTCTTTGGTTCCTTGAATTTTGTCTAGTGTTCCTACCTTCTACCTTCTACCTTCT 363
 DB 307 GTTCTCTCTGCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 366
 QY 364 TCAAGTGCCTTCTGATCTCGAGTTCGTGATGATGTCGTCCTTGTGTTTGGAGTTCATC 423
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 DB 487 TTTGCGAGGAGCCGCTTCTGTGATGATATCATGGTGGTGGTGGTGGTGGTGGTGG 546

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Qy	664	TCAGTGGTTTATGCT	TCACAGACAAGGAATTAATCACAGCTTTGGTACATAGAGATTTTGGTT	723
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Qy	784	ACATATGCAGATGCTCT	CTGGTGGGGCACAAATACATTTGACAACTATTGGCTATGGAGAC	843
Db	787	ACCTACGCAGATGAC	CTCTGGTGGGCTCATCACCTTGACGACCATTGGCTACGGGGAC	846
Qy	844	AAAACCTCCCATACT	TGGCTGGGAAGATGCTTTCTGACGGCTTTGCATCTCTTGGCAT	903
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Qy	904	TCCTTTCTTTGCATCT	CTCTGCGGGCATTTCTTTGGCTCAGGTTTTTGCATTA	963
Db	907	TCGTTCTTTCTCT	TCCTGGCTGGCATTTTGGGATTCGGGCTTTGCCCTTGAAGATCCAAGAG	966
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Qy	1133	AGGAGCGAGTGGCAG	TGGCTAGGCCCCAGGGCCAGAGTATTAAGAGCCGCAAGCCCTCAG	1192
Db	1207	CTCACCTTCAGGAAG	GAGCCACAGCCATCACAAAGCCCGGAGCATGGGCTGCC	1266
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Db	1267	AAGGGAAGGGGTCT	CTCCCAAGGCCAGCCGCTCGGCGGTCCCCCAGTGGGATCAGAGT	1326
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Qy	1288	CGGCGCTCGCTCGC	CTCAAAAGTTTCTACGCCAAAACCAAGTATGATGCTGACACAGCC	1347
Db	1387	CGCCAGGCTTTCG	GCATCAAGGGTGTGCAATCCCGGAGAAATTCAGAAAGCAAGCCCTC	1446
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 09:10:16 ; Search time 8429.33 Seconds
(without alignments)
12043.352 Million cell updates/sec

Title: US-09-810-796-3
Perfect score: 2667
Sequence: 1 atgaagatgtggagtcggg.....ctcatgtcaactgaataa 2667

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2653.6	99.5	2733	9 AY407013	Homo sapi
2	2142.2	80.3	2729	9 AY407015	Mus muscu
3	1859.2	69.7	2014	9 AY407014	Pan trogl
4	1351.4	50.7	2276	3 AK033079	Mus muscu
C 5	670.6	25.1	797	6 CD629762	
6	637.2	23.9	658	2 BE158938	MR0-HT04J
C 7	636.2	23.9	732	6 CD629756	55049343J
C 8	625.2	23.4	742	6 CD629754	55049327J
C 9	595.2	22.3	678	6 CD629758	
C 10	592.2	22.2	717	6 CD629766	55049391J
11	583.6	21.9	691	6 CD629755	55049343H
12	570.2	21.4	744	6 CB244389	UT-M-FY0-
C 13	567.6	21.3	714	6 CD629760	55049359J
C 14	559.6	21.0	724	6 CD629752	55049303J
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C 16	549.6	20.6	628	5 BX917798	EX917798
17	536.4	20.1	547	4 BI034993	QV2-NN200
C 18	530.8	19.9	570	4 BI033850	QV2-NN200
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22	520	19.5	624	6 CD629751	55049303H
23	516.8	19.4	584	2 AW049888	UT-M-BH1-
24	513.8	19.3	635	6 CD629759	55049359H

25	508.8	19.1	643	6 CD629763	55049383H
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31	467.2	17.5	895	5 BU187082	AGENCOURT
32	466.8	17.5	1571	3 AK040190	Mus muscu
33	454.8	17.1	997	2 BB609854	BB609854
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39	403	15.1	517	4 BF954375	QV2-NN004
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C 44	378.4	14.2	477	8 AZ443500	IM0238H18
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407013.1 GI:39762984
VERSION
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
ORIGIN
Query Match 99.5%; Score 2653.6; DB 9; Length 2733;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2656; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
1 ATGAAGGATGTGAGTCGGCGCGGAGGGTCTGCTGAACCTCGGACGCCCGAGGGC 60
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2733 bp DNA linear GSS 15-DEC-2003
Homo sapiens KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
AY407013.1 GI:39762984
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2733)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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/db_xref="taxon:9606"
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/gene="KCNQ5"
/locus_tag="HCM2749"

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Db 127 GACGGCTGTACTGCTGGGCACCCGCGCCACCGTCTGGTGGCGCGCGTGGCGCTG 186
Qy 121 AGGAGAGCCCGCGGGGCAAGCAGGGGGCCGGGATGAGCTGTGGGGAAGCGCTCTCT 180
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Qy 1081 CACTTGAAGGCTTGGACACTGAGCCCTTACCNAATCAGAGCTTAAGTTTGAAGGAGCGA 1140
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Qy 1141 GTGCGCATGGCTAGCCCGAGGGGCCAGAGTATTAAAGCCGACAGAGCCTCAGTAGGTGAC 1200
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Qy 1201 AGGAGTCCCCAAGCACCGACATCAAGCCGAGGGCAGTCCCACAAAGTGCGAAGAGC 1260
Db 1267 AGGAGTCCCCAAGCACCGACATCAAGCCGAGGGCAGTCCCACAAAGTGCGAAGAGC 1326
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Qy 1561 AAAAGCCTTCAACACAGTGTTCATTAATCTTGGAAAGGGCAATCATCAGATAAG 1620
Db 1627 AAAAGCCTTCAACACAGTGTTCATTAATCTTGGAAAGGGCAATCATCAGATAAG 1686
Qy 1621 AAGAGCCGAGAGAAATAACAGCAGAAACATGAGACCAAGATCTCAGTATGCTCGGT 1680
Db 1687 AAGAGCCGAGAGAAATAACAGCAGAAACATGAGACCAAGATCTCAGTATGCTCGGT 1746
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Qy 1801 CAGATCCACCTTTGAAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 1860
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 QY 1921 TCAGAGGCTGCGAGTTCATTTCTGAGCGCAATAGTTTCAGTCCCGCAGACTTTTACGGG 1980
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 QY 2641 AGTTGCTCATGTCAAACTGAAATTA 2667
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 LOCUS Pan troglodytes KCMQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY407014
 VERSION AY407014.1 GI:39762985
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE
 1 (bases 1 to 2014)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 2014)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 TITLE Location/Qualifiers
 JOURNAL 1..2014
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 SOURCE

[illegible]

QY	2447	TTTACCCCAAATGAGGGAATCCAAATGTTTATTAACATGATGAAGAGGTGGTCCCGAAG	2506
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Db	1621	CAGACTCTCTAAGGACTGGAAGTGCAGGTCATCTCAGAACATTTGTGAAGACAGAGACA	1680
QY	2627	GTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAAATTA	2667
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RESULT 5

CD629762/c

LOCUS CD629762 797 bp mRNA linear EST 12-JAN-2004

DEFINITION 5504936701 FLP Homo sapiens cDNA, mRNA sequence.

ACCESSION CD629762

VERSION CD629762.1 GI:40278028

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 797)

TITLE Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

JOURNAL Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

COMMENT Genomics 84 (1), 205-210 (2004)

Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

Location/Qualifiers

1..797

/organism="Homo sapiens"

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/note="vector: pDrive Cloning Vector"

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Best Local Similarity 95.0%; Pred. No. 1.2e-180;

Matches 725; Conservative 0; Mismatches 9; Indels 29; Gaps 2;

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QY	1201	AGGAGTGCCCAAGCACCGACATCACAGCGGCGAGTCCCAACCAAGTGCAGAGAGC	1260
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QY	1261	TGGAGCTTTCACAGCACCGAACCCCGCTTCGCGCCCTTCGCTGCGCCTCAAAAAGTTCTCAGCCA	1320

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
1..732
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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Query Match 23.9%; Score 636.2; DB 6; Length 732;
Best Local Similarity 95.4%; Pred. No. 9.3e-171;
Matches 699; Conservative 0; Mismatches 3; Indels 31; Gaps 3;
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Db 732 CATTGAGTGTGTTGGCGTAGTTAAGCGAGCTGATGAGAAATCTGTTCCATTGCAACCT 673
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Db 672 GGNAGCCACACTTGAAGGCTTCGACACCTGCGAGCCTACCCCAAGAAAGAACAGGGGGA 613
QY 1113 -----CAATCAGAAGCTAAGTTTAAAGGAGCGAGTGGCGATGGCTAGCCCCAGGGG 1163
Db 612 AGCATCAAGCAGTCAGAGCTAAGTTTAAAGGAGCGAGTGGCGATGGCTAGCCCCAGGGG 553
QY 1164 CCAGAGTATTAGAGCGGACGAGCTCAGTAGTGACAGGAGTCCCAAGCACCAGAT 1223
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QY 1284 CTTCCGGCCCTCGCTCGGCTCAAAAGTCTCAGCCAAACCCAGTGAATGATGCTGACAC 1343
Db 432 CTTCCGGCCCTCGCTCGGCTCAAAAGTCTCAGCCAAACCCAGTGAATGATGCTGACAC 373
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Db 312 AGACCTCAGCCCAACCACTTAAACTGTCAATTCAGCTATCAGAAATATGAAATTTTCATGT 253
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Db 192 ATATTCTGCTGCTCATCGACATGTTGTAGAAATTAAGGCTTCAACACAGTGTGA 133
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Db 132 TCAAAATTTCTGAAAAGGGCAATACATCAGATAGAAGAGCCGAGAGAAATACACG 73
QY 1644 AGAACATGAGACACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGTTTGAAGAAACA 1703
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Db 13 GGTACAGTCCATA 1

RESULT 8
CD429754/c
LOCUS CD429754 742 bp mRNA linear EST 12-JAN-2004
DEFINITION 550493327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629754
VERSION CD629754.1 GI:40278020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

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Best Local Similarity 94.7%; Pred. No. 1.4e-167;
Matches 701; Conservative 0; Mismatches 8; Indels 31; Gaps 4;
QY 1016 TTCAGTGTGTTTGGGCTAGTTACGCGAGCTGATGAGAAATCTGTTCCATTGCAACCTGGA 1075
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QY 1076 AGCCACACTTGAAGGCTTGCACACTGCGAGCTTCAACCAAGAAAGAAACCAAGGGGAAGCA 624
Db 683 AGCCACACTTGAAGGCTTGCACACTGCGAGCTTCAACCAAGAAAGAAACCAAGGGGAAGCA 1166
QY 1116 -----TCAGAAGCTAAGTTTAAAGAG -CGAGTGCATGGCTAGGCCAGGGGCCA 564
Db 623 TCAGAAGCTAAGTTTAAAGAGCGGAGTGGCATGGCTAGGCCAGGGGCCA 564
QY 1167 GAGTATTAAAGCCGACCAAGCTCAGTAGGTGACAGGAGTCCCAAGCAGCATCAC 1226
Db 563 GAGTATTAAAGCCGACCAAGCTCAGTAGGTGACAGGAGTCCCAAGCAGCATCAC 504
QY 1227 AGCCAGGGCAGTCCCAAGAGTGCAGAGCTGGAGCTTCAAGCAGCAGACCGCTT 1286
Db 503 AGCCAGGGCAGTCCCAAGAGTGCAGAGCTGGAGCTTCAAGCAGCAGACCGCTT 444
QY 1287 CGGCGCTCGCTCGCCCTCAAAAGTTCTCAGCAAAACCCAGTGATAGTGTGACACAGC 1346
Db 443 CGGCGCTCGCTCGCCCTCAAAAGTTCTCAGCAAAACCCAGTGATAGTGTGACACAGC 384
QY 1347 CTTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1406
Db 383 CTTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 324
QY 1407 CTTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1466
Db 323 CTTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 264
QY 1467 AAAACCGAAGTTTAAAGGAAACGTTACGTCATATGATGATGATGATGATGATGATGATG 1526
Db 263 AAAACCGAAGTTTAAAGGAAACGTTACGTCATATGATGATGATGATGATGATGATGATG 204
QY 1527 TTTCTGCTGCTCATCTGGACATGTTGTAGTAATTAAGGCTTCAACACAGTGTGATCA 1586

Db 203 TTCTGCTGGTCACTGACATGTTGTGTAGAAATTAAGACCTTCAAAACACGTGTGATCA 144
QY 1587 AATTCTTGAAAGGCGCAATACATCAGATAAGAGAGCGGAGAGAAAATAACAGCAGA 1646
Db 143 AATTCTTGAAAGGCGCAATACATCAGATAAGAGAGCGGAGAGAAAATAACAGCAGA 84
QY 1647 ACATGAGACCAACAGACGATCTCAGTATGCTCGGTGCGG-TGGTCAAGGTTGAAAACAGG 1705
Db 83 ACATGAGACCAACAGACGATCTCAGTATGCTCGGTGCGGTTGGTCAAGGTTGAAAACAGG 24
QY 1706 TACAGTCCATAGATCCCAAG 1725
Db 23 TACAGTCCATAGATCCCTAG 4

RESULT 9
CD629758/c 678 bp mRNA linear EST 12-JAN-2004
LOCUS
DEFINITION 55049351J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629758
VERSION CD629758.1 GI:40278024

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 678)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
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/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 22.3%; Score 595; DB 6; Length 678;
Best Local Similarity 99.0%; Pred. No. 6.3e-159;
Matches 609; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Db 618 CAAGCAGTCAGAGCTTAAGTTTAAAGGAGCGAGTGGCATGGCTAGCCCGAGGGCCAGA 559
QY 1169 GTATTAAAGCGCAGCAAGGCTCAGTAGGTGACAGAGGTCCCAAGCAGCCGACATCACAG 1228
Db 558 GTATTAAAGCGCAGCAAGGCTCAGTAGGTGACAGAGGTCCCAAGCAGCCGACATCACAG 499
QY 1229 CCGAGGGCAGTCCCAACCAAGTGCAGAGAGTGTGAGCTTCAACGACCGACCGCTTCC 1288
Db 498 CCGAGGGCAGTCCCAACCAAGTGCAGAGAGTGTGAGCTTCAACGACCGACCGCTTCC 439
QY 1289 GGCCCTCGTGGCCTCAAAAGTTCTCAGCCAAACCAAGTGTAGATGTCTGACACAGCC 1348
Db 438 GGCCCTCGTGGCCTCAAAAGTTCTCAGCCAAACCAAGTGTAGATGTCTGACACAGCC 379
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QY 1409 TCACCCCAACACTTAAACCTGCTTCAGGCTATCAGATTATGAATTTCAATTTGCA 1468
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QY 1589 TTCTTGAAAAGGCGCAATACATCAGATAAGAGAGCGGAGAGAAAATAACAGCAGAAC 1648
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QY 1709 AGTCCATAGATCCCA 1723
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RESULT 10
CD629766/c

LOCUS
DEFINITION 55049319J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629766
VERSION CD629766.1 GI:40278032

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 717)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES
source
1..717
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/db_xref="taxon:9606"
/clone_lib="FLP"
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ORIGIN

Query Match 22.2%; Score 592.2; DB 6; Length 717;
Best Local Similarity 94.6%; Pred. No. 4.1e-158;
Matches 678; Conservative 0; Mismatches 8; Indels 31; Gaps 5;
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QY 1091 CTTTGCAACCTGAGCCCTTACCAA-----TCAGAAGC 1123
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QY 1124 TAAGTT-TTAAGGAGCGAGTGGCATGGCTAGCCCCAGGGCCAGAGTATTAAAGCC-G 1181
Db 597 TAAGTTTAAAGGAGCGAGTGGCATGGCTAGCCCCAGGGCCAGAGTATTAAAGCCGG 538
QY 1182 ACAAGCCTCAGTAGTGAACAGAGTCCCAGACCCAGATCACAGCCGAGGCGAGTCC 1241
Db 537 ACAAGCCTCAGTAGTGAACAGAGTCCCAGACCCAGATCACAGCCGAGGCGAGTCC 478
QY 1242 CACCAAGTAGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGCGCCTCGCTCG 1301

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Qy	1542	GGACATGTTGTGTAGAATTAAGAGCCCTTCA - AACACGTTGTGATCAAAATTTCTGGAAAAG	1600
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LOCUS CD629755 691 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049343H1 FLP Homo sapiens cDNA. mRNA sequence.

Accession	U0629755
Version	CD629755.1
Keywords	GI:40278021
Source	EST.
Organism	Homo sapiens (human)
Reference	Homo sapiens
Authors	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Title	1 (bases 1 to 691)
Journal	Fu, G. K., Wang, J. T., Yang, J., Au-Young, J. and Stuve, L. L.
Comment	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
	Genomics 84 (1), 205-210 (2004)
	Contact: Fu GK
	Incyte Genomics, Inc.
	3160 Porter Dr., Palo Alto, CA 94304, USA
	Tel: 6508454102
	Email: gfu@incyte.com.

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FEATURES
source
1. .691
Location/Qualifiers
email: ghu@zincysce.com
/organism="Homo sapiens"
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Db	181	AAACACTTTT	CAGAAAAG	AAGAAC	CCAGCTGC	CAACCTCA	TTCAGTGT	TTTTCGCGTAGT	240
Qy	1036	TACGCAGCTG	ATGAGAAAT	CTGTTT	CCATTGCA	ACCTTGA	AGGCCAC	ACTTTGAAGGCC	1095
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Qy	1096	CACACTGCA	GGCCCTAC	CCAA-----	TCAGAGCT	TAAGT	1128		
Db	301	CACACTGCA	GGCCCTAC	CCAAAGAA	AGAAAC	CAAGGGAA	GAGCAT	CAAGCAGT	360
Qy	1129	TTTAAAGGAG	CGAGTGC	GCATGGCT	TAGCC	CAGGGCC	CAGAGT	ATTAAAGAC	1188
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Db	420	TCAGTAGT	GCAAGG	AGTCCCC	AAGCAC	CGAAT	CACAGCCGA	-GGCGAGT	479
Qy	1248	AGTGCAGAG	AGCTGG	AGCTTT	CAACGAC	CGAA	CCCGCTT	CCGGCCCT	1307
Db	480	AGTGCAGAG	AGCTGG	AGCTTT	CAACGCG	CGAA	CCCGCTT	CCGGCCCT	539
Qy	1308	AAGTTCTC	AGCAAA	ACCAGT	GATAGT	CTGAC	CAGCCCTT	GGCACT	1367
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CB244389	VERSION	AUTHORS
LOCUS	KEYWORDS	TITLE
DEFINITION	SOURCE	JOURNAL
	ORGANISM	COMMENT

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 UI-W-FYO-cdq-c-03-0-UI.r1 NIH BMAP_FYO Mus musculus cDNA clone
 IMAGE:6832924 5', mRNA sequence.
 CB244389
 CB244389.1 GI:28366033
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 744)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Straussberg, Ph.D.
 Email: cgarbs-r@mail.nih.gov

Email: c9gpos-remail.llnl.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5,
Location/Qualifiers
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/notes="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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ORIGIN

Query Match 21.4%; Score 570.2; DB 6; Length 744;
Best Local Similarity 85.6%; Pred. No. 8.7e-152; Mismatches 106; Indels 0; Gaps 0;
Matches 632; Conservative 0;

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DB 7 CTGTCGGCTCAGCACAAACAGCGGCTGTTAACGAGTCCAGCAGTCCCAATCTCA 66

QY 1924 AGAGCCCTGCAGTTCAATTCGAGCGCAATAGATTGAGTGCAGCTTTCTACGGCTT 1983
DB 67 AGAGCCCTGCAGTTCAATTCGAGCGCAATAGATTGAGTGCAGCTTTCTACGGCTT 126

QY 1984 AGCCCTACTATGCAGTCAAGCAGACAGAGTGCATTAATAGTCAAGGATGGCTCAGCA 2043
DB 127 AGCCCTACTATGCAGCAGCAGTACCCAGGATACCATGATCAAAATGACGGCTCTCC 186

QY 2044 GTGGCAGCCACCAACACCATTCGAAACAAATATAATAGCGCACCCCAAGCCAGCAGCCCA 2103
DB 187 GTGGTAGCCACCAATAACATTGCAACCAATAGCGCGCACCCCAAGCCAGCAGCCCA 246

QY 2104 ACACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCGCAGAACT 2163
DB 247 ACACTTTACAGATCCCTCTCTCTCGGCCATCAAGCAGCTTGTCCAGGCGCAGAACT 306

QY 2164 CTGCACCTTAACCTGCGAGGTTACAGGAAAGCATTTCTGACGTCAACCACTGCTCTGTT 2223
DB 307 CTGCTCTCAACCCACCGGCTTACAGAGAGTATTTCTGATGTCACCACTGCTGTTGT 366

QY 2224 GCCTCCAAAGGAAATGTTTCAGTTGTCAGAGTCAAACTCTCACCAGGACCGTTCTATGAG 2283
DB 367 GCCTCCAAAGGAAATGTTTCAGTTGTCAGAGTCAAACTCTCACCAGGACCGTTCCCTGAG 426

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DB 427 AAAAGTTTGCATGGGAGGAAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 486

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DB 487 TTGGGCAATCTCTGTGTGTCACAACTGATCAGTCCAGAGAACTGACCTTACAG 546

QY 2404 CTTTCAGGAGTGTGAGTCAAGTGGCTCCAGAGCAGCCAAAGATTTTTCACCAATGGAG 2463
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QY 2464 GAATCCAAATGTTTATACTGATCAAGAGTGGTCCGAGAGCAGACAGACACT 2523
DB 607 GAATCCAAATGTTTATACTGATCAGGAGGTCNGGTGCGAGAGACAGAACTACT 666

QY 2524 TTTGATGCCGACCGCAGCTGCCAGGAAGCTGCTTTTGATCAGACTCTCTTAAGGACT 2583
DB 667 TTTGACGGACCCACCGCTCGGGGAGGCTGCTTTCTCATCAGACTCTCTTAGGACT 726

QY 2584 GGAAGGTCACGATCAATCT 2601
DB 727 GGAAGGTCACGGTCAATCT 744

RESULT 13
CD629760/c
LOCUS CD629760 714 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049359J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629760
VERSION CD629760.1 GI:40278026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 714)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
FEATURES
source
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ORIGIN

Query Match 21.3%; Score 567.6; DB 6; Length 714;
Best Local Similarity 98.3%; Pred. No. 4.8e-151; Mismatches 9; Indels 1; Gaps 1;
Matches 584; Conservative 0;

QY 1109 CTACCAATCAGAACCTAAGTTTAAAGGAGCGAGTGCATGGCTAGCCAGGCGGCCAGA 1168
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QY 1169 GTATTAAAGCGCGACAAGCCCTCAGTAGTGACAGAGGTTCCCAAGCACCCACATCAG 1228
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QY 1229 CCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAA-CGACCGAACCCGCTTC 1287
DB 494 CCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAAAGCGACCGAACCCGCTTC 435

QY 1288 CGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCAAAACCCAGTAGATGCTGACACGCC 1347
DB 434 CGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCAAAACCCAGTAGATGCTGACACGCC 375

QY 1348 CTTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1407
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DB 314 CTCACCCACCACTTAAACCTGCTATTCGAGCTATCAGAAATATGAAATTTTCATGTTGCA 255

QY 1468 AAACGGAAGTTTAAAGGAAACGTTACGTCATATGATGATGATGATGATGATGATGATGAT 1527
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QY 1528 TCTCTGCTCATCTGGACATGTTGTGATAGATTTAAAGCCTTCAACACGCTGTTGATCAA 1587

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Db	61	CTAACCCCTGAGGCTTACAGAGAAAGATTTCTGACGTCACACCTGCTTTGTTCCTCCA	120
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Job time : 8438.33 secs

STIC-Biotech/ChemLib

150642

From: Bunner, Bridget
Sent: Wednesday, April 06, 2005 2:08 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:
1. the amino acid sequence of SEQ ID NO: 5 - 888777

CRF

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STAFF USE ONLY

Searcher:
Searcher Phone: 2-
Date Searcher Picked up:
Date Completed:
Searcher Prep/Rev. Time:
Online Time:

Type of Search

NA#: AA#:
Interference: SPDI:
S/L: Oligomer:
Encode/Transl:
Structure#: Text:
Inventor: Litigation:

Vendors and cost where applicable

STN:
DIALOG:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2005, 16:33:11 ; Search time 44 Seconds
(without alignments)
1506.554 Million cell updates/sec

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Perfect score: 4547
Sequence: 1 MKDVESGRVLLNSAARG.....SICKAGESTDALSLPHVCLK 888

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4547	100.0	923	4	US-09-825-147-2
2	4527.5	99.6	897	4	US-09-590-304-2
3	4527.5	99.6	932	4	US-09-813-148-2
4	4300.5	94.6	854	4	US-09-590-304-7
5	1985	43.7	695	4	US-09-590-304-6
6	1985	43.7	695	4	US-09-492-361-2
7	1985	43.7	696	4	US-09-813-148-6
8	1980	43.5	676	4	US-09-949-016-7694
9	1792	39.4	844	4	US-09-813-148-4
10	1792	39.4	844	4	US-09-590-304-4
11	1792	39.4	844	4	US-09-492-361-34
12	1790.5	39.4	722	4	US-09-105-058C-23
13	1788.5	39.3	930	4	US-09-177-650-96
14	1787.5	39.3	871	4	US-09-105-058C-20
15	1783	39.2	872	4	US-09-177-650-2
16	1759	38.7	757	4	US-09-177-650-89
17	1587.5	34.9	854	4	US-09-105-058C-27
18	1587.5	34.9	872	4	US-09-177-650-7
19	1587.5	34.9	872	4	US-09-813-148-5
20	1587.5	34.9	872	4	US-09-590-304-5
21	1587.5	34.9	872	4	US-09-492-361-35
22	1535.5	33.8	870	4	US-09-177-650-91
23	1207.5	26.6	300	4	US-09-105-058C-4
24	1207.5	26.6	300	4	US-09-105-058C-6
25	1188	26.1	807	4	US-09-177-650-3
26	1102	24.2	676	3	US-09-135-021-2
27	1102	24.2	676	3	US-09-135-020-2

28	1102	24.2	676	3	US-09-135-010A-2	Sequence 2, Appli
29	1102	24.2	676	3	US-09-444-871-2	Sequence 2, Appli
30	1102	24.2	676	3	US-09-634-920-2	Sequence 2, Appli
31	1102	24.2	676	4	US-09-597-735-2	Sequence 2, Appli
32	1102	24.2	676	4	US-09-444-295-2	Sequence 2, Appli
33	1102	24.2	676	4	US-09-597-732-2	Sequence 2, Appli
34	1102	24.2	676	4	US-09-597-731-2	Sequence 2, Appli
35	1102	24.2	676	4	US-09-813-148-3	Sequence 3, Appli
36	1102	24.2	676	4	US-09-590-304-3	Sequence 3, Appli
37	1102	24.2	676	4	US-09-840-125-2	Sequence 3, Appli
38	1102	24.2	676	4	US-09-492-361-33	Sequence 33, Appli
39	1100.5	24.2	605	4	US-09-105-058C-24	Sequence 24, Appli
40	1092.5	24.0	677	4	US-09-177-650-4	Sequence 4, Appli
41	1091.5	24.0	581	3	US-09-135-021-80	Sequence 80, Appli
42	1091.5	24.0	581	3	US-09-135-010A-116	Sequence 116, App
43	1091.5	24.0	581	4	US-09-597-735-116	Sequence 116, App
44	1091.5	24.0	581	4	US-09-597-732-116	Sequence 116, App
45	1091.5	24.0	581	4	US-09-597-731-116	Sequence 116, App

ALIGNMENTS

RESULT 1
US-09-825-147-2
; Sequence 2, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCES: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 923
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-825-147-2

Query Match 100.0%; Score 4547; DB 4; Length 923;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKDVESGRVLLNSAARGDGLLLGTRATLGGGGGLRESRRGGQARMSLLGKPLS	60
Db	36	MKDVESGRVLLNSAARGDGLLLGTRATLGGGGGLRESRRGGQARMSLLGKPLS	95
Qy	61	YTSQSCRNVKRVQVLYNVLPRGNAFIYHAFVFLVFGCLLSVFTIPEHTKL	120
Db	96	YTSQSCRNVKRVQVLYNVLPRGNAFIYHAFVFLVFGCLLSVFTIPEHTKL	155
Qy	121	ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPFCVIDITVLIASIA	180
Db	156	ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPFCVIDITVLIASIA	215
Qy	181	VSAKTOGNIFATSALESRLFLQILRMVDRRGTTWKLGSVVYAHSKELITAWYIGFL	240
Db	216	VSAKTOGNIFATSALESRLFLQILRMVDRRGTTWKLGSVVYAHSKELITAWYIGFL	275
Qy	241	VLIFSSFLVYLVEKDANKFSTYADALWNGTITLTITTYGDKTPLTWLGRLLSAGFALLG	300
Db	276	VLIFSSFLVYLVEKDANKFSTYADALWNGTITLTITTYGDKTPLTWLGRLLSAGFALLG	335

Qy	301	ISFFALPAGILGSGFALKVQEOHROKHFKERPNPAANLIQCVWRSVAADEKSVSIATWKP	360
Db	336	ISFFALPAGILGSGFALKVQEOHROKHFKERPNPAANLIQCVWRSVAADEKSVSIATWKP	395
Qy	361	HLKALHTCSPNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDTITAEGSPTKVQKS	420
Db	396	HLKALHTCSPNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDTITAEGSPTKVQKS	455
Qy	421	WSPNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDLTPPLKTVIRA	480
Db	456	WSPNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDLTPPLKTVIRA	515
Qy	481	IRIMKHFVAKKFKETLRPYDKVIOYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK	540
Db	516	IRIMKHFVAKKFKETLRPYDKVIOYSAGHLDMLCRIKSLQTRVDQILGKGQITSDK	575
Qy	541	KSREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKSGSALALASF	600
Db	576	KSREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKSGSALALASF	635
Qy	601	QIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNEFSAQTFYA	660
Db	636	QIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNEFSAQTFYA	695
Qy	661	LSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPPPLPAIKHLPRPE	720
Db	696	LSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPPPLPAIKHLPRPE	755
Qy	721	TLHPNPAGLQBSISDVTTCLVASKENVQVQASNLTKDRSMRKSPDMGGETLLSVCPMPVK	780
Db	756	TLHPNPAGLQBSISDVTTCLVASKENVQVQASNLTKDRSMRKSPDMGGETLLSVCPMPVK	815
Qy	781	DLGKSLSVQNLIRSTEELNIQLSGESSGSRGSDQFYPKWRESKLFITDEVGPEETETD	840
Db	816	DLGKSLSVQNLIRSTEELNIQLSGESSGSRGSDQFYPKWRESKLFITDEVGPEETETD	875
Qy	841	TFDAAPQAPAREAAAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK	888
Db	876	TFDAAPQAPAREAAAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK	923
RESULT 2			
US-09-590-304-2			
; Sequence 2, Application US/09590304			
; Patent No. 6649371			
; GENERAL INFORMATION:			
; APPLICANT: JENTSCH, Thomas			
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANN			
; FILE REFERENCE: 2815-0136P			
; CURRENT APPLICATION NUMBER: US/09/590,304			
; CURRENT FILING DATE: 2000-06-09			
; NUMBER OF SEQ ID NOS: 10			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 2			
; LENGTH: 897			
; TYPE: PR1			
; ORGANISM: Homo sapiens			
US-09-590-304-2			
Query Match 99.6%; Score 4527.5; DB 4; Length 897;			
Best Local Similarity 98.9%; Pred. No. 0;			
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;			
Qy	1	MKDVSGRGVLLNSAARGDGLLLGTRAAATLGGGGGLRESRGKQAGARMSLLGKPLS	60
Db	1	MKDVSGRGVLLNSAARGDGLLLGTRAAATLGGGGGLRESRGKQAGARMSLLGKPLS	60
Qy	61	YTSQSCRNKVRQYVQNLVNLPRPGWAFIYHAFVLLVFGCLLSVFSTIPEHTKL	120
Db	61	YTSQSCRNKVRQYVQNLVNLPRPGWAFIYHAFVLLVFGCLLSVFSTIPEHTKL	120
Qy	121	ASSCLLILEFVMIVVFGLEFIIRISAGCCCRYRGWQGLRFPKPCFVIDTIVLIASTA	180

Db	121	ASSCLLILEFVMIVVFGLEFIIRISAGCCCRYRGWQGLRFPKPCFVIDTIVLIASTA	180
Qy	181	VVSATQGNIPATSAIRSRFLQIILRMVMDRRGGTGWLLGSAVVAHAKSKEKITANIYIGFL	240
Db	181	VVSATQGNIPATSAIRSRFLQIILRMVMDRRGGTGWLLGSAVVAHAKSKEKITANIYIGFL	240
Qy	241	VLISSFLVYLVEKQANKEFSTYADALMWGITTLTIGYGDKTPLTWLGRLLSAGFALLG	300
Db	241	VLISSFLVYLVEKQANKEFSTYADALMWGITTLTIGYGDKTPLTWLGRLLSAGFALLG	300
Qy	301	ISFFALPAGILGSGFALKVQEOHROKHFKERPNPAANLIQCVWRSVAADEKSVSIATWKP	360
Db	301	ISFFALPAGILGSGFALKVQEOHROKHFKERPNPAANLIQCVWRSVAADEKSVSIATWKP	360
Qy	361	HLKALHTCSPNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDTITAEGSPTKVQKS	420
Db	361	HLKALHTCSPNQKLSFKERVRMASPRGQSIKSRQASVGDRRSPSTDTITAEGSPTKVQKS	420
Qy	412	GSPTKVQKSWSPNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDLTP	471
Db	421	GSPTKVQKSWSPNDRTRFRPSRLKSSQPKPVIDADTALGTDVDEKCCQCDVSVDLTP	480
Qy	472	PPLKTVIRAIRIMKHFVAKKFKETLRPYDKVIOYSAGHLDMLCRIKSLQTRVDQIL	531
Db	481	PPLKTVIRAIRIMKHFVAKKFKETLRPYDKVIOYSAGHLDMLCRIKSLQTRVDQIL	540
Qy	532	GKQITSDKSKREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKSGS	591
Db	541	GKQITSDKSKREKITAHEHTDDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKSGS	600
Qy	592	ASALALASFQIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILT	651
Db	601	ASALALASFQIPPFCEQTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILT	660
Qy	652	EFSAQTFYALSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPP	711
Db	661	EFSAQTFYALSPTMHSQATQVPIQSQDGSAAVATNTIANQINTAPKPAAPTTLQIPPP	720
Qy	712	AIKHLPRPETLHPNPAGLQBSISDVTTCLVASKENVQVQASNLTKDRSMRKSPDMG	771
Db	721	AIKHLPRPETLHPNPAGLQBSISDVTTCLVASKENVQVQASNLTKDRSMRKSPDMG	780
Qy	772	LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGESSGSRGSDQFYPKWRESKLFITDE	831
Db	781	LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGESSGSRGSDQFYPKWRESKLFITDE	840
Qy	832	VGPEETETDTFDAAPQAPAREAAAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK	888
Db	841	VGPEETETDTFDAAPQAPAREAAAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK	897

RESULT 3

US-09-813-148-2

; Sequence 2, Application US/09813148

; Patent No. 6617131

; GENERAL INFORMATION:

; APPLICANT: STEINMEYER, Klaus

; APPLICANT: LERCHER, Christian

; APPLICANT: SCHERER, Constanze

; APPLICANT: SEEBOHM, Guiscard

; APPLICANT: BUSCH, Andreas E.

; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN

; FILE REFERENCE: 38005-119

; CURRENT APPLICATION NUMBER: US/09/813,148

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: DE 100 13 732.6

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/194,041

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-2

Query Match 99.6%; Score 4527.5; DB 4; Length 932;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRKQKGARMSLLGKPLS 60
DB 36 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRKQKGARMSLLGKPLS 95
QY 61 YTSQSCRRNVKRRYQNYLYNVLPRGWFYHAFVFLVFGCLLSVFSPIPHETKL 120
DB 96 YTSQSCRRNVKRRYQNYLYNVLPRGWFYHAFVFLVFGCLLSVFSPIPHETKL 155
QY 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCVDTIVLIASIA 180
DB 156 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCVDTIVLIASIA 215
QY 181 VVSAKTQGNIFATSALRSRFLQILRMVRMDRRGGTWKLLGSVYVAHSKELITAWIGFL 240
DB 216 VVSAKTQGNIFATSALRSRFLQILRMVRMDRRGGTWKLLGSVYVAHSKELITAWIGFL 275
QY 241 VLIFFSFLVYLVEKANKPESTYADALWNGTITLTIGYGDKTPLTWLGRLLSAGFALLG 300
DB 276 VLIFFSFLVYLVEKANKPESTYADALWNGTITLTIGYGDKTPLTWLGRLLSAGFALLG 335
QY 301 ISFFALPAGILSGFALKVQEQHROKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
DB 336 ISFFALPAGILSGFALKVQEQHROKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 395
QY 361 HLKALHTCSPT-----NOKLSFKERVMA SPRQSISKRSQASVGDRRSPSTITAE 411
DB 396 HLKALHTCSPTKEQGEASSQKLSFKERVMA SPRQSISKRSQASVGDRRSPSTITAE 455
QY 412 GSPTKVQKSWSPNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 471
DB 456 GSPTKVQKSWSPNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 515
QY 472 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYVSAGHLDMLCRIKSLQTRVDQIL 531
DB 516 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYVSAGHLDMLCRIKSLQTRVDQIL 575
QY 532 GKQITSDKKSREKI TAEHETTTDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKGS 591
DB 576 GKQITSDKKSREKI TAEHETTTDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKGS 635
QY 592 ASALALASFOIPPFCEQTSQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPTN 651
DB 636 ASALALASFOIPPFCEQTSQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPTN 695
QY 652 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIIPPLP 711
DB 696 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIIPPLP 755
QY 712 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKGS 771
DB 756 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKGS 815
QY 772 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSSSGSRGSDQFPYKWRKSLFTIDEE 831
DB 816 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSSSGSRGSDQFPYKWRKSLFTIDEE 875
QY 832 VGPETETDTFDDAOPAREAAAFASLSLRGCRSSQSICKAGESTDALSLPHVKLK 888
DB 876 VGPETETDTFDDAOPAREAAAFASLSLRGCRSSQSICKAGESTDALSLPHVKLK 932

RESULT 4
US-09-590-304-7

; Sequence 7, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-304-7

Query Match 94.6%; Score 4300.5; DB 4; Length 854;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 841; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRKQKGARMSLLGKPLS 60
DB 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRKQKGARMSLLGKPLS 60
QY 61 YTSQSCRRNVKRRYQNYLYNVLPRGWFYHAFVFLVFGCLLSVFSPIPHETKL 120
DB 61 YTSQSCRRNVKRRYQNYLYNVLPRGWFYHAFVFLVFGCLLSVFSPIPHETKL 120
QY 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCVDTIVLIASIA 180
DB 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRLPARKPCVDTIVLIASIA 180
QY 181 VVSAKTQGNIFATSALRSRFLQILRMVRMDRRGGTWKLLGSVYVAHSKELITAWIGFL 240
DB 181 VVSAKTQGNIFATSALRSRFLQILRMVRMDRRGGTWKLLGSVYVAHSKELITAWIGFL 240
QY 241 VLIFFSFLVYLVEKANKPESTYADALWNGTITLTIGYGDKTPLTWLGRLLSAGFALLG 300
DB 241 VLIFFSFLVYLVEKANKPESTYADALWNGTITLTIGYGDKTPLTWLGRLLSAGFALLG 300
QY 301 ISFFALPAGILSGFALKVQEQHROKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
DB 301 ISFFALPAGILSGFALKVQEQHROKHFEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
QY 361 HLKALHTCSPT-----NOKLSFKERVMA SPRQSISKRSQASVGDRRSPSTITAE 411
DB 361 HLKALHTCSPTKEQGEASSQKLSFKERVMA SPRQSISKRSQASVGDRRSPSTITAE 420
QY 412 GSPTKVQKSWSPNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 471
DB 421 GSPTKVQKSWSPNDRTRFRPSRLKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 480
QY 472 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYVSAGHLDMLCRIKSLQTRVDQIL 531
DB 481 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDVKDVIQYVSAGHLDMLCRIKSLQTRVDQIL 540
QY 532 GKQITSDKKSREKI TAEHETTTDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKGS 591
DB 541 GKQITSDKKSREKI TAEHETTTDLSMLGRVVKVQVQVQIESKLDCLLDIYQOVLKGS 600
QY 592 ASALALASFOIPPFCEQTSQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPTN 651
DB 601 ASALALASFOIPPFCEQTSQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPTN 660
QY 652 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIIPPLP 711
DB 661 EFSAQTFYALSPTHSQATQVPIQSQSGSAVAATNTIANQINTAPKPAAPTTLQIIPPLP 720
QY 712 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKGS 771
DB 721 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVQVQVQIESKLDCLLDIYQOVLKGS 780
QY 772 LSVCPMPVKDLGKLSLVQNLIRSTEELNIQLSGSSSGSRGSDQFPYKWRKSLFTIDEE 831

QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLIS-ISRVSSTNM 694

RESULT 7
US-09-813-148-6
; Sequence 6, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEBOHM, Guiseard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CNS
; FILE REFERENCE: 38005-119
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US/09/813,148
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 696
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-6

Query Match 43.7%; Score 1985; DB 4; Length 696;
Best Local Similarity 60.3%; Pred. No. 4.8e-171;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

QY 35 GGGGGLRESRRGQARMISLIGKPL-----SYTSSQSCRRNVKRRVQNYL 80
Db 37 GGGGSPR-----RLGLGSLPPGAPLPFGSGSGACQORSAAHKRYRRLQNVW 87

QY 81 YNVLEPRGWAFYHAFVFLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIWVFGLEF 140
Db 88 YNVLEPRGWAFYHVFIFLLVFSCLVLSVLSIQEHOELANECLLILEFVMIWVFGLEY 147

QY 141 IIRWSAGCCCRVGMQGRRLRFARKPCVIDITVLIAIVSAKTQGNIFATSLRSLR 200
Db 148 IVRWSAGCCCRVGMQGRFRFARKPCVIDIFVVASVAVIAAGTQGNIFATSLRSMR 207

QY 201 FLOILRMVRDRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKF 260
Db 208 FLOILRMVRDRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVLAEKDANSDF 267

QY 261 STYADALWNGTITLTIGYGDKTPLTWGLRLLSAGFALLGISFPFALPAGILSGFALKVQ 320
Db 268 SSYADSLWNGTITLTIGYGDKTPLTWGLRVLAAGFALLGISFPFALPAGILSGFALKVQ 327

QY 321 EQRQKHFEKRRNPAANLIQCVRWSYAAD-EKSVSIATW----- 358
Db 328 EQRQKHFEKRRNPAANLIQAARWLYSTDMRAYLTATWYIYDYSILPSFRELALLFEHVQ 387

QY 359 -----KPHLKALHT----- 388

Db 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRPGSTSCFCGESSRNGIKDIRMSSQR 447

QY 389 QSIKSRQ--ASVGDRRSPSTDTIAEG-SPTKVOKSWSFNDRTRFRPSLRKSSQPKPVID 445
Db 448 RTGFSKQHLAPPTMPTSPSEQVEATSPTKVOKSWSFNDRTRFRASRLR-----KPTS 502

QY 446 ADTALGTDVYDEKCCQCVDSVEDLTPPLKTVIRAIRIMKPHVAKRKFETLTPYDKOV 505
Db 503 AEDA-PSEEAEEKSYQELTVDIMPVAKTVIRSIIRLFLVAKRKFETLTPYDKOV 561

QY 506 IEQYSAGHLDMLCRIKSLQTRVDQIIVGRG--PDGRKAREKDGKPSDAEVDLSMGRV 619
Db 678 SVSAQTLIS-ISRVSSTNM 694

Db 562 IEQYSAGHLDMLCRIKSLQTRVDQIIVGRG--PDGRKAREKDGKPSDAEVDLSMGRV 619
QY 563 VKVEKQVQSIKSLDCLDIYQQVLRKGSASALALASFOIPPECEQTSYQSPVDSKOL 622
Db 620 VKVEKQVQSIKSLDCLDIYQQVLRKGSASALALASFOIPPECEQTSYQSPVDSKOL 677

QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLIS-ISRVSSTNM 694

RESULT 8
US-09-949-016-7694
; Sequence 7694, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7694
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7694

Query Match 43.5%; Score 1980; DB 4; Length 676;
Best Local Similarity 60.3%; Pred. No. 1.3e-170;
Matches 409; Conservative 75; Mismatches 102; Indels 92; Gaps 13;

QY 35 GGGGGLRESRRGQARMISLIGKPL-----SYTSSQSCRRNVKRRVQNYL 80
Db 18 GGGGSPR-----RLGLGSLPPGAPLPFGSGSGACQORSAAHKRYRRLQNVW 68

QY 81 YNVLEPRGWAFYHAFVFLVFGCLILSVFSTIPEHTKLASSCLLILEFVMIWVFGLEF 140
Db 69 YNVLEPRGWAFYHVFIFLLVFSCLVLSVLSIQEHOELANECLLILEFVMIWVFGLEY 128

QY 141 IIRWSAGCCCRVGMQGRRLRFARKPCVIDITVLIAIVSAKTQGNIFATSLRSLR 200
Db 129 IVRWSAGCCCRVGMQGRFRFARKPCVIDIFVVASVAVIAAGTQGNIFATSLRSMR 188

QY 201 FLOILRMVRDRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKF 260
Db 189 FLOILRMVRDRGGTWKLLGSVVYAHSKELITAWYIGFLVLIFASFLVLAEKDANSDF 248

QY 261 STYADALWNGTITLTIGYGDKTPLTWGLRLLSAGFALLGISFPFALPAGILSGFALKVQ 320
Db 249 SSYADSLWNGTITLTIGYGDKTPLTWGLRVLAAGFALLGISFPFALPAGILSGFALKVQ 308

QY 321 EQRQKHFEKRRNPAANLIQCVRWSYAAD-EKSVSIATW----- 358
Db 309 EQRQKHFEKRRNPAANLIQAARWLYSTDMRAYLTATWYIYDYSILPSFRELALLFEHVQ 368

QY 359 -----KPHLKALHT----- 388

Db 369 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRPGSTSCFCGESSRNGIKDIRMSSQR 428

QY 389 QSIKSRQ--ASVGDRRSPSTDTIAEG-SPTKVOKSWSFNDRTRFRPSLRKSSQPKPVID 445
Db 429 RTGFSKQHLAPPTMPTSPSEQVEATSPTKVOKSWSFNDRTRFRASRLR-----KPTS 483

QY 446 ADTALGTDVYDEKGCQCVSVEDLTPPLKTVIRAIIMKEHVAKKFKETLRPYDVKD 505
Db 484 AEDA-PSEEAESKYSQCELTVDVDDIMPAKVTRIRIRILKFLVAKKFKETLRPYDVKD 542
QY 506 IEQVSAGHLDMLCRIKSLQTRVDQIILGKGQITSDKKSRE---KITAEHETTTDLMLGRV 562
Db 543 IEQVSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKDGKPSDAEVDSEISMGRV 600
QY 563 VKVEKQVQSTESKDCLLDIYQOVLKRGKSASALALASFOIPPECCROTSDYQSPVDKDL 622
Db 601 VKVEKQVQSTESKDCLLDIYQOVLKRGKSASALALASFOIPPECCROTSDYQSPVDKDL 658
QY 623 SGSAQNSGCLSRSTSANI 640
Db 659 SVSAQTLIS-ISRVSSTNM 675

RESULT 9
US-09-813-148-4
; Sequence 4, Application US/098113148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: SCHERER, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-4

Query Match 39.4%; Score 1792; DB 4; Length 844;
Best Local Similarity 49.5%; Pred. No. 2.3e-153;
Matches 406; Conservative 88; Mismatches 179; Indels 148; Gaps 24;

QY 17 AARGDGLLLGTRAAATLGGGGGLRGRGKQARMSSLLGKPLSYTSSQSCRRNVKTRV 76
Db 34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP-----PKRNAFYRKL 77
QY 77 QNLYNVLERPRGWAFFIYHAFVFLVFCCLILSVFSTIPEHTKLASSCLLILEFVMIWVF 136
Db 78 QNLYNVLERPRGWAFFIYHAFVFLVFCCLILSVFSTIPEHTKLASSCLLILEFVMIWVF 137
QY 137 GLEFIIRWSAGCCRYRGWGRLFARKPCFVIDTIVLIASIAVVSAGTQGNIFATSAL 196
Db 138 GVEFYFVIRWAAGCCRYRGWGRLFARKPCFVIDTIVLIASIAVLAAGSGNVFATSAL 197
QY 197 RSLRFQILRMVMDRRGGTWKLLGSGVVAHSEKELITAWYIGLPLVFPSSFLVYLVEKDA 256
Db 198 RSLRFQILRMVMDRRGGTWKLLGSGVVAHSEKELITAWYIGLPLVFPSSFLVYLVEKDA 257
QY 257 NKEFSTYADALMWGTTTLTIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILSGGFA 316
Db 258 NDHFDYADALMWGTTTLTIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILSGGFA 317
QY 317 LKVOEQHRQKHFEKRNPAANLIQCVWRSYAAD-----EKSYSIAWTK--PH 361
Db 318 LKVOEQHRQKHFEKRNPAANLIQCVWRSYAAD-----EKSYSIAWTK--PH 377
QY 362 LKALHTC-----SPNQKLSFKERVVRASPRGQSKRSQASVGD-- 400

Db 378 LNQLLELLNLKSKGLAFKOPPPSP-SOKVSLKDRV-FSSPRGVAAGKGSFQAQTV 435
QY 401 RRSSTDTAEGSTPKVOKSWSFNDRFRSLKSSQPKPVIDADTALGTDDVDYDEKG 460
Db 436 RRSPSADQSLSDSPSKVPKSWSGDRGRARQAFRIKGAASRQNSE-EASLPGEDIVDDKS 494
QY 461 COCDVSVEDLTPPLKTVIRAIIMKEHVAKKFKETLRPYDVKDVIIEQYSAGHLDMLCRI 520
Db 495 CPCEFTVEDLTPGLKVSIRAVCMRFLVSKKFKESLRPYDVMVDVIEQYSAGHLDMLCRI 554
QY 521 KSLQTRVDQIILGKGQITSDKKSREKITAEHETTTDLMLGRVVKVEKQVQSTESKDCLL 580
Db 555 KSLQSRVDQIVGRGPAITD-KDRTKGPAEALPELPSMMGLGKVEKQVLSMEKKLDFLV 613
QY 581 DIYQOVLKRGKSASALALASFOIPPECC-----EQTSDYQSPVDSKLSGSAQNSGC 631
Db 614 NIYMO---RMG-----IPPTETAYFGAKEPEPEAPYHSPEDSRE---HVDRHGC 657
QY 632 LSRSTSANISRGLQFILTPNEFSQATFYALSPTMHSQATQVPIQSOS-----DGSAVA 683
Db 658 IVKIVRSSSTG-----QKNFSAPP--AAPP-----VQCPSTSMQPSHPRQGHGTS 703
QY 684 ATNTIANQINTAPKPAATTLQI-----PP-----PLP 711
Db 704 PVGDHGSILVRIPPPPAHERSISAYGGGNRASMEFLRQDTPGCRPEGTLRDSDTSISIP 763
QY 712 AIKHLPRPETHLPNPAQLQESISDVTTCLVASKENKVVQVQS 752
Db 764 SYDHH-----EELERSFSGF--SISQ-----SKENLDALNS 791

RESULT 10
US-09-590-304-4
; Sequence 4, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590,304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-304-4

Query Match 39.4%; Score 1792; DB 4; Length 844;
Best Local Similarity 49.5%; Pred. No. 2.3e-153;
Matches 406; Conservative 88; Mismatches 179; Indels 148; Gaps 24;

QY 17 AARGDGLLLGTRAAATLGGGGGLRGRGKQARMSSLLGKPLSYTSSQSCRRNVKTRV 76
Db 34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA-----GKP-----PKRNAFYRKL 77
QY 77 QNLYNVLERPRGWAFFIYHAFVFLVFCCLILSVFSTIPEHTKLASSCLLILEFVMIWVF 136
Db 78 QNLYNVLERPRGWAFFIYHAFVFLVFCCLILSVFSTIPEHTKLASSCLLILEFVMIWVF 137
QY 137 GLEFIIRWSAGCCRYRGWGRLFARKPCFVIDTIVLIASIAVVSAGTQGNIFATSAL 196
Db 138 GVEFYFVIRWAAGCCRYRGWGRLFARKPCFVIDTIVLIASIAVLAAGSGNVFATSAL 197
QY 197 RSLRFQILRMVMDRRGGTWKLLGSGVVAHSEKELITAWYIGLPLVFPSSFLVYLVEKDA 256
Db 198 RSLRFQILRMVMDRRGGTWKLLGSGVVAHSEKELITAWYIGLPLVFPSSFLVYLVEKDA 257
QY 257 NKEFSTYADALMWGTTTLTIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILSGGFA 316
Db 258 NDHFDYADALMWGTTTLTIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILSGGFA 317


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QY 317 LKVOEQHROKHFKEKRRNPAAANLIQCWRSYAAD-----EKSYSIATWK--PH 361
Db 318 LKVOEQHROKHFKEKRRNPAAAGLIQSAWRFYATNLSRTDLHSTWQYVERTVTPMYRLIPP 377
QY 362 LKALHTC-----SPTNOKLSFKERVEMASPRGOSIKSROASVGD-- 400
Db 378 LKQLELLRNLSKSLGAFKDPPEPSP-SQKVSCLKDRV-FSSPRGVAAGKSGSPQAQTV 435
QY 401 RRSPTDITAEQSPTKQKSWSPNDTRFRPSLRKSSQPKVIDADTALGTDDVYDEKG 460
Db 436 RRSFSAQSLESDFSQKVPKSWSPGDRSRAQAFRIKGAASRQNSE-EASLPGEDIVDDKS 494
QY 461 CQCDVSVELTTPKLTIVIRAIRIMKHFVAKRKETLRPYDVVDVIEQYSAGHLDMLCRI 520
Db 495 CPCEFTVEDLTPLGLKVSIRAVCMRFLVSKRKFKESLRPYDVMDVIEQYSAGHLDMLCRI 554
QY 521 KSLQTRVDQILGQITSDKSKREKITAHEHTDDLSMLGRVVKVKEQVOSIESKLDCLL 580
Db 555 KSLQSRVDQIVGRGPAITD-KDRTKGPAEALPEDFSMGRLGKVKQVLSMEKKLDLFLV 613
QY 581 DIYOQVLRKGSASALASAFQIPPEFC-----EQTSQYOSPVDSKDLGSAQNSGC 631
Db 614 NIYMQ--RMG-----IPTEAYFGAKEPEPAPPYHSPEDSRE--HVDRHGC 657
QY 632 LRSSTANISRGLOFILTPEFSAQTFYALSPTWHSQATQVPIQS-----DGSAVA 683
Db 658 IVKIVRSSSTG-----QKNFSAPP--AAPP-----VQCPSTSMQPOSHPRQGHGTS 703
QY 684 ATNTIANQINTAPKPAAPTTLQI-----PP-----PLP 711
Db 704 PVGDHGLSVRIPPPAAHRSLSAYGGNRSASMEFLRQEDTPGCRPEGTLRDSDTSISIP 763
QY 712 AIKHLPRPETLHPNPAGLQESISDVTTCLVASKENVOVAQS 752
Db 764 SVDH-----BELEKSFSGF--SISQ-----SKENLDALNS 791

RESULT 12
US-09-492-361-34
; Sequence 34, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492,361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 34
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-492-361-34

Query Match 39.4%; Score 1792; DB 4; Length 844;
Best Local Similarity 49.5%; Pred. No. 2.1e-153;
Matches 406; Conservative 89; Mismatches 179; Indels 148; Gaps 24;

QY 17 AARGDGLLIGTRAAATLGGGGGLRESRRKGQARMSSLLGKPLSYTSSQSCRNVYRRV 76
Db 34 STRDGALLIAGSEAPK---RGSILSKPRAGGAGA---GKP-----PKENAFYRKL 77
QY 77 QNLYNVLERPRGWAFTYHAFVLLVFGCLILSVFSTIPHTKLASSCLLILFVIMVVF 136
Db 78 QNLYNVLERPRGWAFTYHAFVLLVFGCLILSVFSTIPHTKLASSCLLILFVIMVVF 137
QY 137 GLFIFIRIWAGCCCRVGRQGRRLRPFKPCFVIDTILIASIAVVSAKTQGNIFATSAL 196
Db 138 GVEYFVRWIAAGCCCRVGRQGRRLRPFKPCFVIDTILIASIAVLAAGQGNVIFATSAL 197

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Query Match 39.4%; Score 1790.5; DB 4; Length 722;
Best Local Similarity 55.0%; Pred. No. 2.4e-153;

; Sequence 20, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanz, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-105-058C-20

Query Match 39.3%; Score 1787.5; DB 4; Length 871;
Best Local Similarity 47.9%; Pred. No. 6.2e-153;
Matches 406; Conservative 89; Mismatches 178; Indels 175; Gaps 24;

Qy 17 AARGDGLLLGTRAAATLGGGGGLRESRRKGKARMSLLGKLPLSYTSSQSCRNVKYRVV 76
Db :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
34 STDGALLTAGSEAPK---RGSILSKPRAGAGA-----GKP-----PKRNAFYRL 77
Qy 77 QNYLYNVLPRGWAFYHAYFVFLVFCLLSVSFTPEHTKLASSCLILLLEFMIVVF 136
Db ||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
78 QNFYNVLPRGWAFYHAYFVFLVFCLLSVSFTPEHTKLASSCLILLLEFMIVVF 137
Qy 137 GLPFIIRWSAGCCCRYGWGRQLRFARKPCVIDITVLIIASIAVVSAKTQNIPATSAL 196
Db |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
138 GVEYFVRWAAGGCCRYRWGRGLRKPFARKPCVIDITVLIIASIAVLAAGSQGNVPATSAL 197
Qy 197 RSLRFLQILRMVMRDRRGCTWKLLGVVAHSKELITAWIGFLVLIIFSSLVYLIVEKDA 256
Db ||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
198 RSLRFLQILRMIMRDRRGCTWKLLGVVAHSKELITAWIGFLVLIIFSSLVYLAEKE 257
Qy 257 NKEFFSTYADALMWGTTLTTIGYDKTPLTWTWLGRLLSAGFALLGISFPALPAIGLGSGFA 316
Db |:|:|:|:|:|:~::~|||:||||:||||:||||:||||:||||:||||:||||:|
258 NDHFDTYADALMWGLTTLTTIGYDKYPQTWNNGRLAATFTLIGVSFPALPAIGLGSGFA 317
Qy 317 LKVQHROKHFKERKNRNPANLIQCWRYSAAD-----EKSVSTATWK---- CSP--TNOKL 375
Db |::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
378 TYGASRLIPLNOLELRNLKSGLAFRKDPPPEPSKSPCGPGICGCPCGRSSOKV 437
Qy 376 SFKERVMASPRGOSIKRSQASVGDD--RRSPSTDITAEGSPTKVKQSFWNDRTFRPSL 433
Db ||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
438 SLKDRV-FSSPRGVAAGKSPOAVTVSRPADQSLEDSPSKVPKSWFGDRSRAQA 496
Qy 434 RLKSSQPVIDADTALGTDVDVDEKGCODSVEDLTPPLKTVTIRAIRMKPHVAKRF 493
Db |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
497 RIKAASRQ--NSEASLPGEIDVDDKSCFEFVTEDLTPGLKVSIRAVCMRFLVSKRF 554
Qy 494 KETLRPDVMDVTEQYSAGHLDMCLKRIKSLQTRVDQILGKOITSKKREKIHAETH 553
Db ||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
555 KESLRPDVMDVTEQYSAGHLDMCLKRIKSLQSRVDQVGRGAITD-KDRTKGPAAEALP 613
Qy 554 DLSMLGRVVKVKOVOSTIESKLDCLDIYQQVLKGSASALALASFQIPPEC----- 607
Db ||:||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
614 EDPSMMGLKVBKQVLSMEKLFVNLMYO--RMG-----IPPTEBAYEGA 660
Qy 608 ---EOTSDYQSPVDSKDLGSAONSGCLRSTANSISRGLOFILTPNEFSQAFTVALSPT 664

Db	438	SLKDRV-FSSPRGVAAGKGSPOAQTVRRSPSADQSLSDSPSKVPKSWSGDRSRARQAF	496
Qy	434	RLKSSQPKPIDADTALGTDDVDEKCCQCDVSVEDLTPPLKTVIRAIRIMKEHVAKRKF	493
Db	497	RIKGAASRQNSE-EASLPGEDIVDDKSCPCFVTEDLTPGLKVSIRAVCMVRFVSKRKF	555
Qy	494	KETLRPYDVKDVIEOYSAGHLDMLCRISLQTRVDQILGKGQITSOKKREKITAHEHTT	553
Db	556	KESLRPYDVMDVIEQYSAGHLDMLSRKSLQSRVDQIVGRGPAITD-KORTKGPAEALP	614
Qy	554	DDLMLGRVVKVKQVQOSIESKLDCLDIYQQVLRKGSASALALASFOIPPFEC	607
Db	615	EDFSMMGRLGKVEKQVLSMEKLDLFLVWQ-RMG-----IPPTETAYFGA	661
Qy	608	---EQTSDYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTNEFSAQTFYALSPT	664
Db	662	KEPEPAPPYHSPEDSRE---HVDRHGCIIVKVRSSSTG-----QKNFSAPP--AAPP-	709
Qy	665	MHSQATQVPIQS-----DGSVAATNTIANQINTAPKPAAPTTLQI-----	706
Db	710	-----VQCPFSTWQPOSHPRQGHGTSFVGDHGSGLVRIPPPAPHERSLSAYGGNRASME	764
Qy	707	-----PP-----PLPAIKHLPRPETLHPNPAGLOESISDVTTCVLVASK	744
Db	765	FLRQEDTPGCRPPPEGNLRDSTISIPSDH---EELERSFSGF--SISQ-----SK	811
Qy	745	ENVQVAQS	752
Db	812	ENLDALNS	819

Search completed: April 8, 2005, 16:43:40
Job time : 48 secs

Brunner, B.
09/18/10796
Seq. ID 5

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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:23:30 ; Search time 180 Seconds
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Title: US-09-810-796-5

Perfect score: 4547

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Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4527.5	99.6	897	AAU09020	Human vol
4	4527.5	99.6	897	AAU09020	Human vol
5	4527.5	99.6	897	AAU09020	Human vol
6	4524.5	99.5	897	AAU09025	Human vol
7	4524.5	99.5	897	AAU09023	Human vol
8	4523.5	99.5	897	AAU09024	Human vol
9	4521.5	99.4	897	AAU09022	Human vol
10	4513.5	99.3	932	AAU09022	Human vol
11	4269.5	93.9	846	AAU09022	Human vol
12	1985	43.7	695	AAU09023	Human vol
13	1985	43.7	695	AAU09023	Human vol
14	1985	43.7	695	AAU09023	Human vol
15	1803.5	39.7	852	AAU09023	Human vol
16	1792	39.4	844	AAU09023	Human vol
17	1792	39.4	844	AAU09023	Human vol
18	1792	39.4	844	AAU09023	Human vol
19	1792	39.4	844	AAU09023	Human vol
20	1790.5	39.4	722	AAU09023	Human vol
21	1788.5	39.3	930	AAU09023	Human vol
22	1787.5	39.3	871	AAU09023	Human vol
23	1785	39.3	854	AAU09023	Human vol
24	1785	39.3	912	AAU09023	Human vol
25	1783	39.2	872	AAU09023	Human vol

ALIGNMENTS

RESULT 1

AAU09021	AAU09021	standard; protein; 888 AA.
XX	XX	AAU09021;
XX	XX	AC
XX	XX	AD
DT	18-DEC-2001	(first entry)
XX	XX	XX
DE	XX	Human voltage gated potassium channel hKCNQ5-2.
XX	XX	Human; voltage-gated potassium channel; hKCNQ5-2; nootropic; cerebrotective; neurotropic; analgesic; vision disorder; central nervous system disorder; epilepsy; migraine; hearing disorder; psychotic disorder; seizure; learning disorder; memory disorder; stroke; pain; gene therapy; splice variant.
KW	XX	Homo sapiens.
OS	XX	WO200170759-A1.
PN	XX	27-SEP-2001.
PD	XX	20-MAR-2001; 2001WO-US009328.
XX	XX	21-MAR-2000; 2000US-0190954P.
XX	XX	(ICAG-) ICAGEN INC.
XX	XX	Jegla TJ;
XX	XX	WPI; 2001-611467/70.
DR	XX	N-ESDB; AAS14653.
PT	XX	Polypeptides and polynucleotides of potassium channel KCNQ5 for identifying a compound modulating ion flux in eukaryotic cell or cell membrane expressing the protein, comprises KCNQ approximately alpha-subunits.
XX	XX	Claim 17; Page 64; 78pp; English.
XX	XX	The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in the scope of the invention are the nucleic acids encoding hKCNQ5 (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modelling to identify molecules that bind to a KCNQ containing


```

Db 301 ISFFALPAGILGSGFALKVQEQHQRKHFEKRNPAANLIQCVMRSYAADKSVSIATWKP 360
Qy 361 HLKALHTCSPT-----NQLSFKERVMSAPRGOSIKRSQASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPTKQGEASSQKLSFKERVMSAPRGOSIKRSQASVGDRRSPSTDITAE 420
Qy 412 GSPTKVKQSWSFNDTRFRPSLRKLSQPKPVIDADTALGTDDVYDKGQCQCVSVDLT 471
Db 421 GSPTKVKQSWSFNDTRFRPSLRKLSQPKPVIDADTALGTDDVYDKGQCQCVSVDLT 480
Qy 472 PPLKTVIRAIRMKFHVAKRFKFTLRPYDKVIEQYSAGHLMCLCRIKSLQTRVDQIL 531
Db 481 PPLKTVIRAIRMKFHVAKRFKFTLRPYDKVIEQYSAGHLMCLCRIKSLQTRVDQIL 540
Qy 532 KGQITSDKKSREKITAEHETDLSMLGRVVKVEKQVQSTESKLDCLLDIYQOVLKGS 591
Db 541 KGQITSDKKSREKITAEHETDLSMLGRVVKVEKQVQSTESKLDCLLDIYQOVLKGS 600
Qy 592 ASALALASFOIPPECEGTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPN 651
Db 601 ASALALASFOIPPECEGTSYQSPVDSKDLGSAQNSGCLSRSTSANISRGLOFILTPN 660
Qy 652 EFSAQTFVALSPTHSQAQVPIQSQDSGSAVAANTIANQINTAPKAAPTLQIPPLP 711
Db 661 EFSAQTFVALSPTHSQAQVPIQSQDSGSAVAANTIANQINTAPKAAPTLQIPPLP 720
Qy 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVQVQAQSNLTKDRSMRKSFDWGGETL 771
Db 721 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVQVQAQSNLTKDRSMRKSFDWGGETL 780
Qy 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESGSRGSDQFYPKWRRESKLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESGSRGSDQFYPKWRRESKLFITDEE 840
Qy 832 VGPEETETDTPDAAPQAPAREAFASDSLRTGRSRSSQICKAGESTALSIPHVKLK 888
Db 841 VGPEETETDTPDAAPQAPAREAFASDSLRTGRSRSSQICKAGESTALSIPHVKLK 897

RESULT 5
AAE16599 standard; protein; 897 AA.
XX AAE16599;
AC
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neuropsychological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antisense therapy;
KW synaptic transmission; electrical excitability.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 191..209
FT /note="Pore region"
FT Region 265..285
FT /note="S4 voltage sensor region"
XX
FN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US017314.

```

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XX
PR 26-MAY-2000; 2000US-0207389P.
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Dworetzky SI, Ramanathan CS, Trojnacki JT, Boissard CG;
XX Gribkoff VK;
XX
XX WPI; 2002-122069/16.
XX DR N-PSDB; AAD27192.
XX
XX Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
XX it, for diagnosing, treating and identifying modulators useful in
XX treating neurological, neuropsychological and neuropsychological
XX diseases.
XX
XX Claim 25; Fig 2; 128pp; English.
XX
XX The invention relates to potassium channel polypeptides referred to as
XX KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
XX polypeptides are useful for identifying compounds that modulate their
XX biological activity. The compounds identified and KCNQ5 polynucleotides
XX are useful for treating acute and chronic pain, migraine, acute stroke,
XX dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
XX multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
XX depression, bipolar disorders, sleep disorders, eating disorders,
XX addiction, myokymia, Alzheimer's disease, age-associated memory loss,
XX learning deficiencies, cognitive disorders and motor neuron diseases. The
XX nucleic acid molecules of the invention are further useful for treating
XX neuropsychological, neuropsychological disorders, asthma, neuron cell
XX death and brain tumours. They are also used in gene therapy and antisense
XX therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
XX excitability in the brain and are useful for generating antibodies. They
XX are also useful to affinity purify biological effectors from biological
XX materials e.g. disease tissues or cells. The present sequence is human
XX KCNQ5 protein
XX
XX Sequence 897 AA;
XX
Query Match 99.6%; Score 4527.5; DB 5; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;
Qy 1 MKDVESGRGRVLLNSAAARGDGLLLLTGTRATIGGGGGGLRESRRGQGRMSLLGKPLS 60
Db 1 MKDVESGRGRVLLNSAAARGDGLLLLTGTRATIGGGGGGLRESRRGQGRMSLLGKPLS 60
Qy 61 YTSQSCRRNVKVRVQNVLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
Db 61 YTSQSCRRNVKVRVQNVLYNVLERPRGWAFIYHAFVLLVFGCLILSVFSTIPEHTKL 120
Qy 121 ASSCLLILFVMIWVFGLEFIIRIWSAGCCCRVGMQGRLFARPKFCVIDTIVLIA 180
Db 121 ASSCLLILFVMIWVFGLEFIIRIWSAGCCCRVGMQGRLFARPKFCVIDTIVLIA 180
Qy 181 VSAKTOGNIFATLSALRSFLQLLRVMDRGGTWKLLGSAVVAHSELITAWYIGFL 240
Db 181 VSAKTOGNIFATLSALRSFLQLLRVMDRGGTWKLLGSAVVAHSELITAWYIGFL 240
Qy 241 VLIFFSFLVYLVEKDANKFSTVADALWWTGTTLTITIGYGDKTPLTWGLRLLSAGFALLG 300
Db 241 VLIFFSFLVYLVEKDANKFSTVADALWWTGTTLTITIGYGDKTPLTWGLRLLSAGFALLG 300
Qy 301 ISFFALPAGILGSGFALKVQEQHQRKHFEKRNPAANLIQCVMRSYAADKSVSIATWKP 360
Db 301 ISFFALPAGILGSGFALKVQEQHQRKHFEKRNPAANLIQCVMRSYAADKSVSIATWKP 360
Qy 361 HLKALHTCSPT-----NQLSFKERVMSAPRGOSIKRSQASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPTKQGEASSQKLSFKERVMSAPRGOSIKRSQASVGDRRSPSTDITAE 420
Qy 412 GSPTKVKQSWSFNDTRFRPSLRKLSQPKPVIDADTALGTDDVYDKGQCQCVSVDLT 471

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Db 661 EFSAQTFYALSPTHMSQATQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTTLQIPPLP 720
Qy 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOAQNLTQDRSMKSFDMGGETL 771
Db 721 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOAQNLTQDRSMKSFDMGGETL 780
Qy 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESGSGSGSQDFPKWRESKLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESGSGSGSQDFPKWRESKLFITDEE 840
Qy 832 VGPSETDTDFDAPQAPAREAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK 888
Db 841 VGPSETDTDFDAPQAPAREAFASDSLRTRGRSSQSIKAGESTDALSPLHVKLK 897

RESULT 8
AAU09024
ID AAU09024 standard; protein; 897 AA.
XX
AC AAU09024;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human voltage gated potassium channel hKCNQ5-1 variant #3.
XX
KW Human; voltage-gated potassium channel; hKCNQ5-1; nototropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; mutant; mutein.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 343..640
FT /label= Conserved region
FT /note= "This sequence is specifically claimed in claim
FT 13"
FT Misc-difference 446
FT /note= "Wild-type Ser substituted by Gly"
XX
PN WO200170759-A1.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US009328.
XX
PR 21-MAR-2000; 2000US-0190954P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2001-611467/70.
XX
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximately a- subunits.
XX
PS Disclosure; Page; 78pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic

CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a polymorphic variant of hKCNQ5-1. Note: The present
CC sequence does not appear in the specification but is based on hKCNQ5-1
CC sequence appearing as AAU09020
XX
SQ Sequence 897 AA;
Query Match 99.5%; Score 4523.5; DB 4; Length 897;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 886; Conservative 1; Mismatches 1; Indels 9; Gaps 1;
Qy 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRKQGAARMSLLGKPLS 60
Db 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRRKQGAARMSLLGKPLS 60
Qy 61 YTSQSCRRNVKRRVQNYLVNLERPRGWAFIYHAFVFLVFGCLLSVFSTIPEHTKL 120
Db 61 YTSQSCRRNVKRRVQNYLVNLERPRGWAFIYHAFVFLVFGCLLSVFSTIPEHTKL 120
Qy 121 ASSCLLILFVMIWVFGLEFIIRWSAGCCRYRGWQGRLEFRARFPFCVIDIVLIASTIA 180
Db 121 ASSCLLILFVMIWVFGLEFIIRWSAGCCRYRGWQGRLEFRARFPFCVIDIVLIASTIA 180
Qy 181 VVSATQGNIFATSALRSRFLQILRMVMDRRGGTWKLLGSVVVAHSKELITAWYIGFL 240
Db 181 VVSATQGNIFATSALRSRFLQILRMVMDRRGGTWKLLGSVVVAHSKELITAWYIGFL 240
Qy 241 VLIFFSFLVLEKDKANKEFSYADALWGGTTLTITIGYDKTPTLWGLLSAGFALLG 300
Db 241 VLIFFSFLVLEKDKANKEFSYADALWGGTTLTITIGYDKTPTLWGLLSAGFALLG 300
Qy 301 ISPFALPAGILGSGFALKVQEQHROKHFEKRRNPANLIQCVWRSYAADKSVSIATWKP 360
Db 301 ISPFALPAGILGSGFALKVQEQHROKHFEKRRNPANLIQCVWRSYAADKSVSIATWKP 360
Qy 361 HLKALHTCSPT-----NOKLSPKERVNRASPRGQSIKRSQASVGRDRSPSTDTAE 411
Db 361 HLKALHTCSPTKEQGEASSQKLSFKERVNRASPRGQSIKRSQASVGRDRSPSTDTAE 420
Qy 412 GSPTKVQKWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 471
Db 421 GSPTKVQKWSFNDRTRFRPSLRKSSQPKPVIDADTALGTDDVDYDEKGCQCDVSVEDLT 480
Qy 472 PPLKTVIRAIRIMKHFVAKGPKETLRPYDKDVIQYSGAGHLDMLCRKSLQTRVDQIL 531
Db 481 PPLKTVIRAIRIMKHFVAKGPKETLRPYDKDVIQYSGAGHLDMLCRKSLQTRVDQIL 540
Qy 532 GKQITSDKKSRKITAETHETDLSMLGHVVKVQVQVQVQVQVQVQVQVQVQVQVQVQV 591
Db 541 GKQITSDKKSRKITAETHETDLSMLGHVVKVQVQVQVQVQVQVQVQVQVQVQVQV 600
Qy 592 ASALALASFOIPPECEQTSYQSDVSDKLSGSAQNSGCLSRSTSANISRGLOFLTPN 651
Db 601 ASALALASFOIPPECEQTSYQSDVSDKLSGSAQNSGCLSRSTSANISRGLOFLTPN 660
Qy 652 EFSAQTFYALSPTHMSQATQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTTLQIPPLP 711
Db 661 EFSAQTFYALSPTHMSQATQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTTLQIPPLP 720
Qy 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOAQNLTQDRSMKSFDMGGETL 771
Db 721 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOAQNLTQDRSMKSFDMGGETL 780
Qy 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESGSGSGSQDFPKWRESKLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESGSGSGSQDFPKWRESKLFITDEE 840

Db 781 LSVCPMPKDLGKSLVONLIRSTEELNIQLSGSSGSRGSDQFPYKWRRESKLFITDEE 840
 Qy 832 VGPETETDTFDDAAPQAPAREAAAFASDSILRTGRSSOSICKAGESTDALSILPHVKLK 888
 Db 841 VGPETETDTFDDAAPQAPAREAAAFASDSILRTGRSSOSICKAGESTDALSILPHVKLK 897

RESULT 9

AAU09022
 ID AAU09022 standard; protein; 897 AA.

XX AAU09022;

DT 18-DEC-2001 (first entry)

XX Human voltage gated potassium channel hKCNQ5-1 variant #1.

XX Human; voltage-gated potassium channel; hKCNQ5-1; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
 KW pain; gene therapy; mutant; mutein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 36 /note= "Wild-type Gly substituted by Ala"

FT Region 343..640

FT /label= Conserved region

FT /note= "This sequence is specifically claimed in claim 13"

XX WO200170759-A1.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-US009328.

XX 21-MAR-2000; 2000US-0190954P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2001-611467/70.

XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ approximately alpha-subunits.

XX Disclosure; Page; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-
 CC subunit of a KCNQ potassium channel, with a subsequence having 65%
 CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
 CC and forms a KCNQ potassium channel having the characteristic of voltage-
 CC gating with at least an additional KCNQ alpha-subunit. Also included in
 CC the scope of the invention are the nucleic acids encoding hKCNQ5
 CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
 CC vectors encoding them, antibodies against them, the use of 3-dimensional
 CC computer modelling to identify molecules that bind to a KCNQ containing
 CC potassium channel and modulate ion flux through the channel. The KCNQ
 CC polypeptide is useful for identifying a compound that increases or
 CC decreases ion flux through a potassium channel expressed in an eukaryotic
 CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
 CC used in gene therapy) is useful as a pharmaceutical agent for treating
 CC diseases involving abnormal ion flux, such as disorders of the central
 CC nervous system, such as epilepsy, migraines, hearing and vision problems,
 CC psychotic disorders, seizures, learning and memory disorders, stroke and
 CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
 CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
 CC computer databases to find variants of the sequence which are associated

CC with disease states, is useful for screening mutations of KCNQ5. The
 CC present sequence is a polymorphic variant of hKCNQ5-1. Note: The present
 CC sequence does not appear in the specification but is based on hKCNQ5-1
 CC sequence appearing as AAU09020

XX Sequence 897 AA;

Query Match 99.4%; Score 4521.5; DB 4; Length 897;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 886; Conservative 1; Mismatches 1; Indels 9; Gaps 1;

Qy 1 MKDVESGGRVLLNSAARGDGLLLGTRAAATGGGGGGLRESRRGQGRMSLLGKPLS 60
 Db 1 MKDVESGGRVLLNSAARGDGLLLGTRAAATGGGGGGLRESRRGQGRMSLLGKPLS 60
 Qy 61 YTSQSCRRNVKVRVQNYLYNVLERPRGNWAFYHAFVLLVFGCLLSVFSFTPEHTKL 120
 Db 61 YTSQSCRRNVKVRVQNYLYNVLERPRGNWAFYHAFVLLVFGCLLSVFSFTPEHTKL 120
 Qy 121 ASSCLLILEFVMIVFGLFIIIRWSAGCCCRVGMQGRIFARFARKPCFVIDTIVLIASIA 180
 Db 121 ASSCLLILEFVMIVFGLFIIIRWSAGCCCRVGMQGRIFARFARKPCFVIDTIVLIASIA 180
 Qy 181 VVSAKTQGNIFATSALESRLFLQILRMVMDRGGTTWKLGLSVVYAHSKELITAWYIGFL 240
 Db 181 VVSAKTQGNIFATSALESRLFLQILRMVMDRGGTTWKLGLSVVYAHSKELITAWYIGFL 240
 Qy 241 VLIFFSPLVLYVEKDANKFSTYADALWMTITLTITIGYGDKTPLTWGLRLLSAGFALLG 300
 Db 241 VLIFFSPLVLYVEKDANKFSTYADALWMTITLTITIGYGDKTPLTWGLRLLSAGFALLG 300
 Qy 301 ISFFALPAGILGSGFALKVQEQHRQHFKEKRNPAAANLIQCVWRSYAADSKSVSIATWKP 360
 Db 301 ISFFALPAGILGSGFALKVQEQHRQHFKEKRNPAAANLIQCVWRSYAADSKSVSIATWKP 360
 Qy 361 HLKALHTCSPT-----NOKLSKERVMA SPRGSIKSRQASVGDRRSPSTDITAE 411
 Db 361 HLKALHTCSPTKKEQGEASSQKLSFKERVMA SPRGSIKSRQASVGDRRSPSTDITAE 420
 Qy 412 GSPTKVQKSWSFNDRTFRFRLSLKSKSQPKFVDADTALGTDVVDYDEKGCQCVSVDLT 471
 Db 421 GSPTKVQKSWSFNDRTFRFRLSLKSKSQPKFVDADTALGTDVVDYDEKGCQCVSVDLT 480
 Qy 472 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDKVDVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
 Db 481 PPLKTVIRAIRIMKHFVAKRKFKETLRPYDKVDVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
 Qy 532 GKQGITSDKKSRKITAHEHTTDDLSMLGRVVKVQVQVQSIKSLDCLLDIYQQLRKGS 591
 Db 541 GKQGITSDKKSRKITAHEHTTDDLSMLGRVVKVQVQVQSIKSLDCLLDIYQQLRKGS 600
 Qy 592 ASALALASFOIPPECEQTSQSDYQSPVDSKDLGSAQNSGCLSRSTSANSIRGLQFILTNP 651
 Db 601 ASALALASFOIPPECEQTSQSDYQSPVDSKDLGSAQNSGCLSRSTSANSIRGLQFILTNP 660
 Qy 652 EFSAQTFYALSPTMHSGAQTQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTLOIPPLP 711
 Db 661 EFSAQTFYALSPTMHSGAQTQVPIQSQSGSAVAANTNTIANQINTAPKPAAPTLOIPPLP 720
 Qy 712 AIKHLRPETLHPNAGLQESISDVTTCLVASKENVQVQVQVQVQVQVQVQVQVQVQVQVQV 771
 Db 721 AIKHLRPETLHPNAGLQESISDVTTCLVASKENVQVQVQVQVQVQVQVQVQVQVQVQV 780
 Qy 772 LSVCPMPVKDLGKSLVONLIRSTEELNIQLSGSSGSRGSDQFPYKWRRESKLFITDEE 831
 Db 781 LSVCPMPVKDLGKSLVONLIRSTEELNIQLSGSSGSRGSDQFPYKWRRESKLFITDEE 840
 Qy 832 VGPETETDTFDDAAPQAPAREAAAFASDSILRTGRSSOSICKAGESTDALSILPHVKLK 888
 Db 841 VGPETETDTFDDAAPQAPAREAAAFASDSILRTGRSSOSICKAGESTDALSILPHVKLK 897

RESULT 10

AAB86979
 ID AAB86979 standard; protein; 932 AA.
 XX
 AC AAB86979;
 XX
 DT 11-DEC-2001 (first entry)
 XX
 DE Human KCNQ5 protein.
 XX
 KW KCNQ5; potassium channel protein; human; neurological; cardiovascular;
 KW anticonvulsant; excitability modulator; membrane potential; neuron;
 KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
 KW screening; central nervous system disease; cardiovascular disease.
 XX
 OS Homo sapiens.
 XX
 FN DE10013732-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2000; 2000DE-01013732.
 XX
 PR 21-MAR-2000; 2000DE-01013732.
 XX
 PA (AVET) AVENTIS PHARMA DEUT GNEH.
 XX
 PI Steinmeyer K, Lerche C, Scherer C, Seeborn G, Busch AE;
 XX
 DR WPI: 2001-571700/65.
 XX
 DR N-PSDB; AAH49499.
 XX
 XX New DNA sequence encoding potassium channel KCNQ5, useful in screening
 PT for specific modulators, potential agents for treating central nervous
 PT system and cardiovascular diseases.
 XX
 PS Claim 1b; Page 10-14; 20pp; German.
 XX
 CC This invention describes a novel DNA sequence (I) encoding: (i) a
 CC polypeptide (ii) with potassium channel KCNQ5 activity; (ii) a
 CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
 CC the invention have neurological, cardiovascular and anticonvulsant
 CC activity and act as modulators of the voltage-dependent KCNQ5 potassium
 CC channel, a key regulator of membrane potential and modulator of
 CC excitability of electrically activated cells such as neurons and
 CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (ii)
 CC are used to screen for compounds that modulate the activity of KCNQ5,
 CC potentially useful for treating central nervous system (e.g. epilepsy)
 CC and cardiovascular diseases. This sequence represents the human potassium
 CC channel KCNQ5 protein described in the invention
 XX
 SQ Sequence 932 AA;
 Query Match 99.3%; Score 4513.5; DB 4; Length 932;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 885; Conservative 1; Mismatches 2; Indels 9; Gaps 1;
 QY 1 MKDVEGGRVLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQGARMSLGKPLS 60
 DB 36 MKDVEGGRVLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQGARMSLGSRLS 95
 QY 61 YTSSQSCRNVKRRVONYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 120
 DB 96 YTSSQSCRNVKRRVONYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 155
 QY 121 ASSCLILFVMIWVFGLEFIIRWSAGCCCRVWGQRLRFARPPFCVIDIVLIASIA 180
 DB 156 ASSCLILFVMIWVFGLEFIIRWSAGCCCRVWGQRLRFARPPFCVIDIVLIASIA 215
 QY 181 VVSAKTQGNIFATSALESRLFLQILRMVRMDRRGTTWKLGSVVVAHSELITAWYIGFL 240
 DB 216 VVSAKTQGNIFATSALESRLFLQILRMVRMDRRGTTWKLGSVVVAHSELITAWYIGFL 275
 QY 241 VLISSFLVYLVEKDANKFSTYADALWNGTITLTIGYDKTPTLWLGRLLSAGFALLG 300

DB 276 VLISSFLVYLVEKDANKFSTYADALWNGTITLTIGYDKTPTLWLGRLLSAGFALLG 335
 QY 301 ISFPALPAGILGSGFALKVQBOHQKHFKEKRRPAAANLIOCVRWSYAADSKSVSIATWKP 360
 DB 336 ISFPALPAGILGSGFALKVQBOHQKHFKEKRRPAAANLIOCVRWSYAADSKSVSIATWKP 395
 QY 361 HLKALHTCSPT-----NOKLSFKERVRMASPRGQSIKRSQASVGRSPSTDTIAE 411
 DB 396 HLKALHTCSPTKQGEASSQKLSFKERVRMASPRGQSIKRSQASVGRSPSTDTIAE 455
 QY 412 GSPTKVKQSWSFNDTRPRPSLRKSSQPFVIDADTALGTDYDEKGCOCDSVDELT 471
 DB 456 GSPTKVKQSWSFNDTRPRPSLRKSSQPFVIDADTALGTDYDEKGCOCDSVDELT 515
 QY 472 PPLKTVIRAIRIMKPHVAKRKFKETLRPYDVQVIEQVSAGHLDMLCRIKSLQTRVQIL 531
 DB 516 PPLKTVIRAIRIMKPHVAKRKFKETLRPYDVQVIEQVSAGHLDMLCRIKSLQTRVQIL 575
 QY 532 GKGQITSDKSKREKITAETHETDLSMLGRVVKVEKQVQSIKESKLDCLLDIYQVLRKGS 591
 DB 576 GKGQITSDKSKREKITAETHETDLSMLGRVVKVEKQVQSIKESKLDCLLDIYQVLRKGS 635
 QY 592 ASALALASFOIPPECEQTSYQSPVDSKDLSSAONSGCLSRSTSANISRGLOFILTPN 651
 DB 636 ASALALASFOIPPECEQTSYQSPVDSKDLSSAONSGCLSRSTSANISRGLOFILTPN 695
 QY 652 EFSAQTFVALSPTMHSQATQVPIQSODGSAVAANTIANQINTAPKPAAPTTLQIPPLP 711
 DB 696 EFSAQTFVALSPTMHSQATQVPIQSODGSAVAANTIANQINTAPKPAAPTTLQIPPLP 755
 QY 712 AIKHLPRPETHLPNAGLOESISDVTTCLVASKENVOVAOSNLTKDRSWRKSFDMGGSTL 771
 DB 756 AIKHLPRPETHLPNAGLOESISDVTTCLVASKENVOVAOSNLTKDRSWRKSFDMGGSTL 815
 QY 772 LSVCPMPVKDLCKSLSVQNLIRSTEELNQLSGSESSGSRGSDQFYPKWRSKLFTIDEE 831
 DB 816 LSVCPMPVKDLCKSLSVQNLIRSTEELNQLSGSESSGSRGSDQFYPKWRSKLFTIDEE 875
 QY 832 VGPEETETDTFDAAPQAPAREAAFPASDSLRTRGSRSSQSIKAGESTDALSLPHVKLK 888
 DB 876 VGPEETETDTFDAAPQAPAREAAFPASDSLRTRGSRSSQSIKAGESTDALSLPHVKLK 932
 RESULT 11
 AAB24241
 ID AAB24241 standard; protein; 846 AA.
 XX
 AC AAB24241;
 XX
 DT 07-FEB-2001 (first entry)
 XX
 DE Human KCNQ5 (KCN6q) protein sequence SEQ ID NO:3.
 XX
 KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
 KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
 KW Salla disease; ophthalmological; auditory; central nervous system;
 KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
 KW age-related macular degeneration; macular degeneration; deafness;
 KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
 KW gastrointestinal disorder.
 XX
 OS Homo sapiens.
 XX
 FN WO200061606-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 10-APR-2000; 2000WO-US009587.
 XX
 PR 14-APR-1999; 99US-0129274P.
 XX
 PA (MERI) MERCK & CO INC.

polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples and to identify mutations within them, and hence which patients may be in need of restorative therapy. They may also be used to study the expression and function of KCNQ4 polypeptides and their role in metabolism, for example through the production of transgenic animals. The KCNQ4 polypeptides may be used as antigens in the production of antibodies and to identify modulators (agonists and antagonists) of KCNQ4 expression and activity. The anti-KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate KCNQ4 expression and activity. They may be used in this way to treat tinnitus, loss of hearing (especially progressive hearing loss, neonatal deafness and presbycusis (deafness of the elderly)) and disease or adverse conditions of the central nervous system (CNS) such as affective disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative illness, cognitive deficits, compulsive behavior, dementia, depression, Huntington's disease, mania, memory impairment, memory disorders and dysfunctions, motion disorders, motor disorders, neurodegenerative diseases, Parkinson's disease, Parkinson-like motor disorders, phobias, Pick's disease, psychosis, schizophrenia, spinal cord damage, stroke and/or tremor. Conversely, antisense nucleic acid molecules may be administered to down regulate KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing their expression

Sequence 695 AA;

Sequence 695 AA;

Query Match	43.7%	Score	1985;	DB 3;	Length	695;			
Best Local Similarity	60.3%	Pred.	No. 1.1e-167;						
Matches	409;	Conservative	76;	Mismatches	101;	Indels	92;	Gaps	13;
QY	35	GGGGGLRESRRKQCARMSLLGKPL	-----SYTSSQCRNNVYRRVNYL	80					
DB	37	GGGGSFR	-----RLGLLGSPLPPGAPLPGPGSGSGACQGRSAAAHKRYRLQNW	87					
QY	81	YNYLERPRGWAIFYHAFVFLVFGCLLILSVFSTTPEHTKLASSCLLILFFWMLVFGLEF	140						
DB	88	YNYLERPRGWAIFYHFLVFGCLVLSVLSTIOEQHELANECLLILFFWMLVFGLEY	147						
QY	141	IIRIWAGAGCCYRGWQGRLFARPKFCVDTIVLIASIAVWSAKTQGNIFATSALRSR	200						
DB	148	IVRWAGAGCCYRGWQGRFFARPKFCVDFIVFVASVAVIAAGTQGNIFATSALRSR	207						
QY	201	FLQILRMVRMDRRGGTWWKLLGSVVYAHSGKELITAWYIGFLVLFSSFLVYLVEKDNKEF	260						
DB	208	FLQILRMVRMDRRGGTWWKLLGSVVYAHSGKELITAWYIGFLVLFASFVYLAEKDANSDF	267						
QY	261	STYADALWGTTLTITIGYGDKTPITWLGRLLSAGFALLGISFPALPAGILSGFPALKVQ	320						
DB	268	SSYADSLWGTTLTITIGYGDKTPITWLGRLVLAAGFALLGISFPALPAGILSGFPALKVQ	327						
QY	321	EQRHQHFKEKRRNPAANLIQCVRYSYAAD-EKSVSIATW	358						
DB	328	EQRHQHFKEKRRMPAANLIOAWRLYSTDMGRAYLTATWYYDSILSPFRELALLFHVQ	387						
QY	359	-----KPHLKAHT-----CSPTNOKLSFKERVMSASPRG	388						
DB	388	RARNGLRPLEVRRAPVDPGASRYPPVATCRPGSTSCFGESSRMGICDRIEMGSSQR	447						
QY	389	QSIKSRQ-ASVGDRLSPSTDTIABG-SPTKVQKSWSNDRTRRPSRLKSSQPKVID	445						
DB	448	RTGPSKQOLAPPTMPTSPSEQVGEATSPTKVQKSWSNDRTRFRASLRL-----KPTS	502						
QY	446	ADTALGTDDVYDEKGQCQDVSVEDLTPPLKTVIRAIRIMKEHVAKRKFETLAPYDKDV	505						
DB	503	AEDA-PSEEVAAEKSQYCELTVDIDINPAVKTVIRISIRILKELVAKRKFETLAPYDKDV	561						
QY	506	IEQYSAGHLDMLCRIKSLQTRVDQIILKGQITSDKKSR-----KITABHETTDLSMLGRV	562						
DB	562	IEQYSAGHLDWLGRIKSLQTRVDQIVGRG-PGDKAREKGDKGFSDAEVVDISMMGRV	619						
QY	563	VKVEKQVQSTESKLDCLDIYQQVLRKGSASALALASFOIPPECEOTSDYQSPVNSKDL	622						
DB	620	VKVEKQVQSTEHKLDLLGYSFCLRSRGTYA-----SLGAVQVPLFDPDITSHSPVDHEDI	677						

Qy	623	SGSAQNCSGLSRSTSANI	640
			:
			:
Db	678	SVSAQTLS-ISRVSVTNM	694
RESULT 13			
AAE16621			
ID	AAE16621	standard; protein;	695 AA.
XX	AC	AAE16621;	
XX	DT	09-APR-2002	(first entry)
XX	DE	Human potassium channel polypeptide	
XX	KW	Human; potassium channel polypeptid	
XX	KW	dementia; trauma; epilepsy; seizure	
XX	KW	multiplex sclerosis; MS; Parkinson's	
XX	KW	anxiety disorder; bipolar disorder;	
XX	KW	addition; myokymia; Alzheimer's di	
XX	KW	learning deficiency; cognitive disor	
XX	KW	neuropsychological disorder; neurops	
XX	KW	neuron cell death; brain tumour; ge	
XX	KW	synaptic transmission; electrical e	
XX	KW	hearing loss.	
XX	OS	Homo sapiens.	
XX	FN	WO200192526-A1.	
XX	XX	06-DEC-2001.	
XX	PD	24-MAY-2001;	2001WO-US017314.
XX	PF	26-MAY-2000;	2000US-0207389P.
XX	PR	(BRIM) BRISTOL-MYERS SQUIBB CO.	
XX	PA	Dworetzky SI, Ramanathan CS, Trof	
XX	PI	Griboff VK;	
XX	PI	WPI; 2002-122069/16.	
XX	DR	Novel potassium channel polypeptidi	
XX	PT	it, for diagnosing, treating and i	
XX	PT	treating neurological, neurophysio	
XX	PT	diseases.	
XX	PS	Disclosure; Fig 5; 129pp; English.	
XX	CC	The invention relates to potassium	
XX	CC	CKNQ5 and nucleic acid molecules en	
XX	CC	polypeptides are useful for identi	
XX	CC	biological activity. The compounds	
XX	CC	are useful for treating acute and	
XX	CC	dementia, trauma, epilepsy, seizur	
XX	CC	multiplex sclerosis (MS), Parkinso	
XX	CC	depression, bipolar disorders, slee	
XX	CC	addition, myokymia, Alzheimer's d	
XX	CC	learning deficiencies, cognitive d	
XX	CC	nucleic acid molecules of the inver	
XX	CC	neuropsychological, neuropsycholog	
XX	CC	death and brain tumours. they are	
XX	CC	therapy. KCNQ5 polypeptides modula	
XX	CC	excitability in the brain and are	
XX	CC	also useful to affinity purify	
XX	CC	materials e.g. disease tissues or	
XX	CC	KCNQ4 protein. Mutations in this p	
XX	CC	disease e.g. hearing loss	
XX	SQ	Sequence 695 AA;	

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Query Match 43.7%; Score 1985; DB 5; Length 695;
Best Local Similarity 60.3%; Pred. No. 1.1e-167;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

QY 35 GGGGLRESRRGKGARMSLLGKPL-----SYTSQSCRRNVKRVQNYL 80
DB 37 GGGGSPR-----RLGLGSLPPGAPLPGPGSGSGACGQRSSAAHKRYRLQNVW 87
QY 81 YNVLERPRGWAIFYHAFVFLLVFGCLLSVFTPIPTHTKLASSCLLILEFMVVFGLF 140
DB 88 YNVLERPRGWAIFYHAFVFLLVFGCLLSVFTPIPTHTKLASSCLLILEFMVVFGLF 147
QY 141 IIRTSAGCCCRVGMGRLEFARKPCVDITVILASIAVSVSAKTOGNIFATSALESRL 200
DB 148 IVRVMSAGCCCRVGMGRLEFARKPCVDITVILASIAVSVSAKTOGNIFATSALESRL 207
QY 201 FLQILRMVDRRGTTWKLGLSVVYAHSKELITAWYIGFLVLPSSFLVYLVEKDNKEF 260
DB 208 FLQILRMVDRRGTTWKLGLSVVYAHSKELITAWYIGFLVLPSSFLVYLVEKDNKEF 267
QY 261 STYADALWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGISFPALPGILGSGFALKVQ 320
DB 268 SSYADSLWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGISFPALPGILGSGFALKVQ 327
QY 321 EQRQKHFEKRRPAANLIQCVWSYAAD-EKSVSIATW----- 358
DB 328 EQRQKHFEKRRPAANLIQCVWSYAAD-EKSVSIATW----- 387
QY 359 -----KPHLKALHT-----CSPYNOKLSFKERVMAASPRG 388
DB 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCRPGSTSFCEGSSRMGIKDIRMSSQR 447
QY 389 QSTKSRQ--ASVGDRRSPSTIDITAEQ--SPTKVQKSWSFNDRTFRPSLRKSKOPKPVID 445
DB 448 RTGPSKQOLAPPTMPTSPSSEVGEATSPTKVQKSWSFNDRTFRPSLRKSKOPKPVID 502
QY 446 ADTALGCTDDVYDEKGCOCVSVDELTPPLKTVIRAIRIMKHFYAKRFKETLRPYDVQKV 505
DB 503 AEDA-PSEEAVERAEKSYOCYELTDDIMPAKTVIRISIRILFLVAKRFKETLRPYDVQKV 561
QY 506 IEQVSAGHLDMLCRKSLQTRVDQILGKGQITSDPKSKRE---KITABHETDLSMLGRV 562
DB 562 IEQVSAGHLDMLGRKSLQTRVDQILGKGQITSDPKSKRE---KITABHETDLSMLGRV 619
QY 563 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 622
DB 620 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 677
QY 623 SGSANQSGCLSRSTSANI 640
DB 678 SVSAQTLIS-ISRVSSTNM 694

RESULT 14
ADE31699
ID ADE31699 standard; protein; 695 AA.
XX AC ADE31699;
XX DT 29-JAN-2004 (first entry)
XX DE Human 32394 protein #SEQ ID 56.
XX KW Antiartherosclerotic; cardiast; vasotropic; antiinflammatory;
XX KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
XX KW cardiovascular; disorder; ischaemia; aortic bending;
XX KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;
XX KW angina; cardiomyopathy; cardiac death.
XX OS Homo sapiens.
XX PN W02003065984-A2.
XX
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PD 14-AUG-2003.
XX PF 29-JAN-2003; 2003WO-US0002571.
XX
PR 01-FEB-2002; 2002US-0353224P.
PR 15-MAR-2002; 2002US-0364529P.
PR 19-APR-2002; 2002US-0373861P.
PR 23-APR-2002; 2002US-0376287P.
PR 12-JUN-2002; 2002US-0388080P.
PR 24-JUN-2002; 2002US-0390971P.
PR 03-JUL-2002; 2002US-0394130P.
PR 10-JUL-2002; 2002US-0394797P.
PR 21-AUG-2002; 2002US-0404904P.
PR 23-AUG-2002; 2002US-0405450P.
PR 04-SEP-2002; 2002US-0408070P.
PR 06-NOV-2002; 2002US-0424300P.
PR 05-DEC-2002; 2002US-0431042P.
PR 05-DEC-2002; 2002US-0431079P.
XX (MILL-) MILLENNIUM PHARM INC.
PA Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
PI Stagliano N, Perodin J, Rodrigue-Way A;
XX WPI; 2003-731468/69.
DR N-PSDB; ADE31698.
XX
XX
PT Identifying a compound capable of treating a cardiovascular disorder
(e.g. atherosclerosis) comprises assaying the ability of the compound to
modulate the expression or activity of e.g. 1682, 6169 or 6193
polypeptide or nucleic acid.
XX
PS Disclosure; SEQ ID NO 56; 328pp; English.
XX
CC The invention relates to a method for identifying a compound capable of
treating a cardiovascular disorder. The present invention identifies the
differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
33276, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
43207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,
345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
6585 genes in cardiovascular disease states. The methods are useful in
diagnosing, preventing and treating cardiovascular disorders, such as
atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
stenosis, arterial inflammation, vascular wall remodeling, coronary
microembolism, tachycardia, bradycardia, pressure overload, aortic
bending, coronary artery ligation, vascular heart disease, valvular
disease, including but not limited to, valvular degeneration caused by
calcification, rheumatic heart disease, endocarditis, or complications of
artificial valves; atrial fibrillation, long-QT syndrome, congestive
heart failure, sinus node dysfunction, angina, heart failure,
hypertension, atrial fibrillation, atrial flutter, pericardial disease,
including but not limited to, pericardial effusion and pericarditis;
cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
cardiomyopathy, myocardial infarction, coronary artery disease, coronary
artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
cardiovascular developmental disorders. The methods may also be used for
identifying compounds that modulate cardiovascular disorders. Sequences
given in ADE31644-ADE31769 represent the genes and proteins that may be
regulated by a compound of the invention.
XX
SQ Sequence 695 AA;
Query Match 43.7%; Score 1985; DB 7; Length 695;
Best Local Similarity 60.3%; Pred. No. 1.1e-167;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;
QY 35 GGGGLRESRRGKGARMSLLGKPL-----SYTSQSCRRNVKRVQNYL 80
DB 37 GGGGSPR-----RLGLGSLPPGAPLPGPGSGSGACGQRSSAAHKRYRLQNVW 87
QY 81 YNVLERPRGWAIFYHAFVFLLVFGCLLSVFTPIPTHTKLASSCLLILEFMVVFGLF 140
DB 88 YNVLERPRGWAIFYHAFVFLLVFGCLLSVFTPIPTHTKLASSCLLILEFMVVFGLF 147
QY 141 IIRTSAGCCCRVGMGRLEFARKPCVDITVILASIAVSVSAKTOGNIFATSALESRL 200
DB 148 IVRVMSAGCCCRVGMGRLEFARKPCVDITVILASIAVSVSAKTOGNIFATSALESRL 207
QY 201 FLQILRMVDRRGTTWKLGLSVVYAHSKELITAWYIGFLVLPSSFLVYLVEKDNKEF 260
DB 208 FLQILRMVDRRGTTWKLGLSVVYAHSKELITAWYIGFLVLPSSFLVYLVEKDNKEF 267
QY 261 STYADALWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGISFPALPGILGSGFALKVQ 320
DB 268 SSYADSLWNGTITLTITGYGDKTPTLWGLRLLSAGFALLGISFPALPGILGSGFALKVQ 327
QY 321 EQRQKHFEKRRPAANLIQCVWSYAAD-EKSVSIATW----- 358
DB 328 EQRQKHFEKRRPAANLIQCVWSYAAD-EKSVSIATW----- 387
QY 359 -----KPHLKALHT-----CSPYNOKLSFKERVMAASPRG 388
DB 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCRPGSTSFCEGSSRMGIKDIRMSSQR 447
QY 389 QSTKSRQ--ASVGDRRSPSTIDITAEQ--SPTKVQKSWSFNDRTFRPSLRKSKOPKPVID 445
DB 448 RTGPSKQOLAPPTMPTSPSSEVGEATSPTKVQKSWSFNDRTFRPSLRKSKOPKPVID 502
QY 446 ADTALGCTDDVYDEKGCOCVSVDELTPPLKTVIRAIRIMKHFYAKRFKETLRPYDVQKV 505
DB 503 AEDA-PSEEAVERAEKSYOCYELTDDIMPAKTVIRISIRILFLVAKRFKETLRPYDVQKV 561
QY 506 IEQVSAGHLDMLCRKSLQTRVDQILGKGQITSDPKSKRE---KITABHETDLSMLGRV 562
DB 562 IEQVSAGHLDMLGRKSLQTRVDQILGKGQITSDPKSKRE---KITABHETDLSMLGRV 619
QY 563 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 622
DB 620 VKVEKQVQSIKSLDCLLDIYQVQLRKSASALAFQIPPECEQTSYQSGPVDKSL 677
QY 623 SGSANQSGCLSRSTSANI 640
DB 678 SVSAQTLIS-ISRVSSTNM 694

RESULT 14
ADE31699
ID ADE31699 standard; protein; 695 AA.
XX AC ADE31699;
XX DT 29-JAN-2004 (first entry)
XX DE Human 32394 protein #SEQ ID 56.
XX KW Antiartherosclerotic; cardiast; vasotropic; antiinflammatory;
XX KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
XX KW cardiovascular; disorder; ischaemia; aortic bending;
XX KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;
XX KW angina; cardiomyopathy; cardiac death.
XX OS Homo sapiens.
XX PN W02003065984-A2.
XX
```

Db 88 YNVLEPRGWAFFYHYFIFLLVFCVLSVLSSTIOHQELANECLLILEFVMIIVFGLEY 147
Qy 141 IIRWSAGCCCRVGRWGQRLRFARKPCFVIDTIVLIASIAVVSAAKTQGNIFATSLRSLR 200
Db 148 IVRWSAGCCCRVGRWGQRLRFARKPCFVIDFVVASVAVIAAGTQGNIFATSLRSMR 207
Qy 201 FLQILRMVRDRRGTTWKLGSVVVYAHSKELITAWYIGFLVLIFSSFLVLYVEKDANKEF 260
Db 208 FLQILRMVRDRRGTTWKLGSVVVYAHSKELITAWYIGFLVLIFASFLVLYAEKANDSF 267
Qy 261 STYADALWWTITLTIGYGDKTPLTWGLRLSAGFALLGISFPALPAGILGSGFALKVQ 320
Db 268 SSVYADSLWWTITLTIGYGDKTPLTWGLRLSAGFALLGISFPALPAGILGSGFALKVQ 327
Qy 321 EQRHKEHFEKRRNPAANLIQCVWRSYAAD-EKSVSIATW----- 358
Db 328 EQRHKEHFEKRRNPAANLIQAWEELYSTDMRAYLTATWYVYDSILPSFRELALFHVQ 387
Qy 359 -----KPHLKALHT-----CSPTNQKLSPKERVMA SPRG 388
Db 388 RARNGGLRPLEVRAPVDCAPSPYPVATCHRPGSTFCPGESSRMGIKDRIMGSSQR 447
Qy 389 OSIKSRO--ASVGRDRSPSTDAEG-SPTKVOKSWSFNDTRFRPSLRKSSQPKPVID 445
Db 448 RIGFSKQOLAPPTWPTSPSSQVGEATSPTKVOKSWSFNDTRFRASLRL-----KPRTS 502
Qy 446 ADTALGTDDVYDEKGCQCVSVEDLTPLTKTVIRAIRIMKHFVAKRKEKTLRPYDKOV 505
Db 503 AEDA-PSEVAEAKSYQCELTVDVDDIMPVAKTVIRAIRILKFLVAKRKEKTLRPYDKOV 561
Qy 506 IEQYSAGHLMCRKLSLOTVDVDDIILGKGQITSDKKSRE---KITASHETDDLSMLGRV 562
Db 562 IEQYSAGHLMGRKLSLOTVDVDDIILGKGQITSDKKSRE---PGDRKAREKDGKPSAEVVDLSNMGRV 619
Qy 563 VKVEKQVQSIKSLDCLLDIIYQVLRKGSASALALASFQIPPPCEOTSQSPVDSKDL 622
Db 620 VKVEKQVQSIKSLDCLLDIIYQVLRKGSASALALASFQIPPPCEOTSQSPVDSKHEDI 677
Qy 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLN-ISRVSSTNM 694

RESULT 15
ADSI17852
ID ADS17852 standard; protein; 852 AA.

AC ADS17852;

DT 02-DEC-2004 (first entry)

XX Rattus norvegicus KCNQ protein #2.

DE KCNQ; potassium channel; anxiety; insomnia; hyper-excitability disorder;
KW Alzheimer's disease; peripheral neuropathy; neurodegenerative disease;
KW neuroprotective; anticonvulsant; nootropic; tranquiliser; sedative;
KW norway rat.

OS Rattus norvegicus.

XX US2004175691-A1.

XX 09-SEP-2004.

XX 08-APR-2004; 2004US-00820307.

XX 03-DEC-1998; 98US-0110804P.

XX 03-DEC-1999; 99US-00454868.

XX (BROW/) BROWN B S.

XX (MCKI/) MCKINNON D.

PI Brown BS, McKinnon D;
XX WPI; 2004-6421119/62.
DR N-FSDB; ADS17851.
XX
PT Evaluating compound for utility in treating neurological disease such as
PT epilepsy and anxiety, involves contacting compound with cell co-
PT expressing KCNQ2 and KCNQ3 that form potassium channel, and measuring
PT activity of potassium channel.
XX
PS Disclosure; SEQ ID NO.9; 38pp; English.
XX
CC The present invention relates to a method of evaluating a compound for
CC utility in treating neurological diseases. The method involves contacting
CC a compound with a cell that co-expresses KCNQ2 and KCNQ3, where the KCNQ2
CC and KCNQ3 form a potassium channel and measuring the activity of the
CC potassium channel. The invention is useful for treating anxiety, insomnia
CC or other hyper-excitability disorders and Alzheimer's disease, peripheral
CC neuropathy or other neurodegenerative diseases. The present sequence is
CC the Rattus norvegicus KCNQ protein. This sequence is used to illustrate
CC the method of invention.
XX
XX Sequence 852 AA;

Query Match 39.7%; Score 1803.5; DB 8; Length 852;
Best Local Similarity 49.0%; Pred. No. 2.6e-151;
Matches 413; Conservative 96; Mismatches 193; Indels 141; Gaps 22;

Qy 17 AARGDGLLLGTRATLGGGGGLRESRRGKQGRMSLLGKPLSVTSQSQRNRYRRV 76
Db 34 STFDGALLIAGEAPK--RGSVLSPKRTGGAGA-----GKP-----PKRNAFYRKL 77
Qy 77 QNYLVNLEPRPGWAFIYHAFVFLVFCGLILSVFESTIPEHTKLASSCLLILEFVMIIVF 136
Db 78 QNFLYNLEPRPGWAFIYHAYVFLVFCGLVSVFESTIPEHTKLASSCLLILEFVMIIVF 137
Qy 137 GLEFIIRWSAGCCCRVGRWGQRLRFARKPCFVIDTIVLIASIAVVSAAKTQGNIFATSL 196
Db 138 GVEIFVRIWAAOCCCRVGRWGQRLRFARKPCFVIDTIVLIASIAVLAAGSQNVFATSL 197
Qy 197 RSLRFLQILRMVRDRRGTTWKLGSVVVYAHSKELITAWYIGFLVLIFSSFLVLYVEKDA 256
Db 198 RSLRFLQILRMVRDRRGTTWKLGSVVVYAHSKELITAWYIGFLVLIFASFLVLYAEKE 257
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Db	738	GNRASTFRLRLEGTACKRPSALRDS-----DTSISIPVDHEELERSFGFSISQSKE 792
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 Job time : 185 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:35:41 ; Search time 151 Seconds
(without alignments)
1952.408 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4547	100.0	923	16	US-10-803-268-2
4	4527.5	99.6	897	9	US-09-866-020-2
5	4527.5	99.6	897	9	US-09-810-796-4
6	4527.5	99.6	897	16	US-10-661-629-2
7	4527.5	99.6	897	17	US-10-948-493-2
8	4527.5	99.6	932	9	US-09-813-148-2
9	4300.5	94.6	854	16	US-10-661-629-7
10	1985	43.7	695	9	US-09-866-020-31
11	1985	43.7	695	9	US-09-810-796-15
12	1985	43.7	695	15	US-10-353-690-56
13	1985	43.7	695	16	US-10-661-629-6

14	1985	43.7	695	17	US-10-850-928-2	Sequence 2, Appli
15	1985	43.7	695	17	US-10-948-493-31	Sequence 31, Appl
16	1985	43.7	696	9	US-09-813-148-6	Sequence 6, Appli
17	1803.5	39.7	852	16	US-10-820-307-9	Sequence 9, Appli
18	1792	39.4	844	9	US-09-866-020-30	Sequence 30, Appl
19	1792	39.4	844	9	US-09-813-148-4	Sequence 4, Appli
20	1792	39.4	844	9	US-09-810-796-14	Sequence 14, Appli
21	1792	39.4	844	15	US-10-295-027-282	Sequence 282, App
22	1792	39.4	844	16	US-10-661-629-4	Sequence 4, Appli
23	1792	39.4	844	17	US-10-850-928-34	Sequence 34, Appl
24	1792	39.4	844	17	US-10-948-493-29	Sequence 29, Appl
25	1792	39.4	844	17	US-10-948-518-152	Sequence 152, App
26	1790.5	39.4	722	13	US-10-128-870-23	Sequence 23, Appl
27	1790.5	39.4	722	14	US-10-131-685-23	Sequence 23, Appl
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29	1787.5	39.3	871	13	US-10-128-870-3	Sequence 20, Appl
30	1787.5	39.3	871	14	US-10-131-685-20	Sequence 20, Appl
31	1783	39.2	872	14	US-10-345-680-17	Sequence 17, Appl
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33	1775	39.0	872	16	US-10-820-307-2	Sequence 3, Appli
34	1762	38.8	842	16	US-10-820-307-3	Sequence 3, Appli
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40	1587.5	34.9	872	14	US-10-096-578-7	Sequence 7, Appli
41	1587.5	34.9	872	16	US-10-661-629-5	Sequence 5, Appli
42	1587.5	34.9	872	17	US-10-850-928-35	Sequence 35, Appl
43	1587.5	34.9	872	17	US-10-948-493-30	Sequence 30, Appl
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ALIGNMENTS

RESULT 1
US-09-810-796-5
; Sequence 5, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICRG, Inc.
; TITLE OF INVENTION: KCNO5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNO5-2
US-09-810-796-5

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RESULT 2
US-09-825-147-2
; Sequence 2, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1: Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-825-147-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 923
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-803-268-2

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 876 TPDAAQPPAREAAAFASDSLRTGRSSQSICKAGESTDALSLPHVKLK 923

RESULT 4
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; Sequence 2, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-020-2

Query Match 99.6%; Score 4527.5; DB 9; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

Qy 1 MKDVESGRVLLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQARMILLGKPLS 60
Db 1 MKDVESGRVLLNSAAAGDGLLLGTRAAATLGGGGGLRESRRGKQARMILLGKPLS 60
Qy 61 YTSQSCRRNVKRRVQNYLVNLERPRGWAFVYHAFVLLVFGCLLSVFSTIPEHTKL 120
Db 61 YTSQSCRRNVKRRVQNYLVNLERPRGWAFVYHAFVLLVFGCLLSVFSTIPEHTKL 120
Qy 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRIRFARKPCFVIDTIVLIASIA 180
Db 121 ASSCLLILEFVMIWVFGLEFIIRWSAGCCCRVGMQGRIRFARKPCFVIDTIVLIASIA 180
Qy 181 VSAKTQGNIFATSALESRLFLQILRMVRMDRRGTTWKLGLSVVYAHSKELITAWYIGFL 240
Db 181 VSAKTQGNIFATSALESRLFLQILRMVRMDRRGTTWKLGLSVVYAHSKELITAWYIGFL 240
Qy 241 VLIFFSSFLVYLVEKDANKPESTYADALWNGTITLTTIGYGDKTPLTWGLSAGFALLG 300
Db 241 VLIFFSSFLVYLVEKDANKPESTYADALWNGTITLTTIGYGDKTPLTWGLSAGFALLG 300
Qy 301 ISPFALPAGILGSGFALKVQEOHQKHFKEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
Db 301 ISPFALPAGILGSGFALKVQEOHQKHFKEKRRNPAANLIQCVWRSYAADEKSVSIATWKP 360
```


Query Match 99.6%; Score 4527.5; DB 16; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

Qy 1 MKDVESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRRGKQARMSSLLGKPLS 60
Db 1 MKDVESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRRGKQARMSSLLGKPLS 60

Qy 61 YTSQSCRRNVKRRVQNYLVNLERPRGNAFIYHAFVLLVFGCLLSVFSPTIPEHTKL 120
Db 61 YTSQSCRRNVKRRVQNYLVNLERPRGNAFIYHAFVLLVFGCLLSVFSPTIPEHTKL 120

Qy 121 ASSCLLLEFVMIVVFGLEFIIRWSAGCCCRVGMQGRLFARFARKPCVDTIVILASIA 180
Db 121 ASSCLLLEFVMIVVFGLEFIIRWSAGCCCRVGMQGRLFARFARKPCVDTIVILASIA 180

Qy 181 VVSATQGNIFATSSALRSRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
Db 181 VVSATQGNIFATSSALRSRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy 241 VLIFSSFLVYLVEKDANKFSTYADALWGTITLTTIGYDKTPTLWGLRLLSAGFALLG 300
Db 241 VLIFSSFLVYLVEKDANKFSTYADALWGTITLTTIGYDKTPTLWGLRLLSAGFALLG 300

Qy 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360
Db 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360

Qy 361 HLKALHTCSPPT-----NOKLSFKERVMASSPGQSIKSRQASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPPT-----NOKLSFKERVMASSPGQSIKSRQASVGDRRSPSTDITAE 420

Qy 412 GSPTKVQKSWSPNDRTFRPSRLKSSQPKPVIDADTALGTDDVYDEKGCQCVSVDLT 471
Db 421 GSPTKVQKSWSPNDRTFRPSRLKSSQPKPVIDADTALGTDDVYDEKGCQCVSVDLT 480

Qy 472 PPLKTVIRAIRIMKPHVAKRKETLRYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 531
Db 481 PPLKTVIRAIRIMKPHVAKRKETLRYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy 532 GKQGITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 591
Db 541 GKQGITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 600

Qy 592 ASALALASFOIPPECEQTSYQSPVDSKOLSGSAQNSGCLSRSTSANISRGLOFILTNP 651
Db 601 ASALALASFOIPPECEQTSYQSPVDSKOLSGSAQNSGCLSRSTSANISRGLOFILTNP 660

Qy 652 EFSAQTFYALSPTHMSQATQVPIISQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 711
Db 661 EFSAQTFYALSPTHMSQATQVPIISQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720

Qy 712 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 771
Db 721 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 780

Qy 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQSGSESSGRSGSQDFYKWRKSLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQSGSESSGRSGSQDFYKWRKSLFITDEE 840

Qy 832 VGPETETDTFDAAPQAPARAAAFASDSLRTRGRSSQSIKAGBSTDALSLPHVKLK 888
Db 841 VGPETETDTFDAAPQAPARAAAFASDSLRTRGRSSQSIKAGBSTDALSLPHVKLK 897

RESULT 7

US-10-948-493-2
; Sequence 2, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S

APPLICANT: TROJNACKI, JOANNE T
APPLICANT: BOISSARD, CHRISTOPHER G
APPLICANT: GRIBKOFF, VALENTIN K
TITLE OF INVENTION: HUMAN KNO5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: D0023 DIV
CURRENT APPLICATION NUMBER: US/10/948,493
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: 60/207,389
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 897
TYPE: PRT
ORGANISM: Homo sapiens
US-10-948-493-2

Query Match 99.6%; Score 4527.5; DB 17; Length 897;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

Qy 1 MKDVESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRRGKQARMSSLLGKPLS 60
Db 1 MKDVESGRVLLNSAARGDGLLLGTRAAATLGGGGGLRESRRGKQARMSSLLGKPLS 60

Qy 61 YTSQSCRRNVKRRVQNYLVNLERPRGNAFIYHAFVLLVFGCLLSVFSPTIPEHTKL 120
Db 61 YTSQSCRRNVKRRVQNYLVNLERPRGNAFIYHAFVLLVFGCLLSVFSPTIPEHTKL 120

Qy 121 ASSCLLLEFVMIVVFGLEFIIRWSAGCCCRVGMQGRLFARFARKPCVDTIVILASIA 180
Db 121 ASSCLLLEFVMIVVFGLEFIIRWSAGCCCRVGMQGRLFARFARKPCVDTIVILASIA 180

Qy 181 VVSATQGNIFATSSALRSRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240
Db 181 VVSATQGNIFATSSALRSRFLQILRMVRMDRRGGTWKLLGSVVYAHSKELITAWYIGFL 240

Qy 241 VLIFSSFLVYLVEKDANKFSTYADALWGTITLTTIGYDKTPTLWGLRLLSAGFALLG 300
Db 241 VLIFSSFLVYLVEKDANKFSTYADALWGTITLTTIGYDKTPTLWGLRLLSAGFALLG 300

Qy 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360
Db 301 ISFPALPAGILGSFALKVQEOHROKHFEKERNPAANLIQCVWRSYAADKSUSIATWKP 360

Qy 361 HLKALHTCSPPT-----NOKLSFKERVMASSPGQSIKSRQASVGDRRSPSTDITAE 411
Db 361 HLKALHTCSPPT-----NOKLSFKERVMASSPGQSIKSRQASVGDRRSPSTDITAE 420

Qy 412 GSPTKVQKSWSPNDRTFRPSRLKSSQPKPVIDADTALGTDDVYDEKGCQCVSVDLT 471
Db 421 GSPTKVQKSWSPNDRTFRPSRLKSSQPKPVIDADTALGTDDVYDEKGCQCVSVDLT 480

Qy 472 PPLKTVIRAIRIMKPHVAKRKETLRYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 531
Db 481 PPLKTVIRAIRIMKPHVAKRKETLRYDVKDVIQYSAGHLDMLCRIKSLQTRVDQIL 540

Qy 532 GKQGITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 591
Db 541 GKQGITSDKKSREKITAETHETDLSMLGRVVKVQVQSIKSLDCLLDIYQOVLKRG 600

Qy 592 ASALALASFOIPPECEQTSYQSPVDSKOLSGSAQNSGCLSRSTSANISRGLOFILTNP 651
Db 601 ASALALASFOIPPECEQTSYQSPVDSKOLSGSAQNSGCLSRSTSANISRGLOFILTNP 660

Qy 652 EFSAQTFYALSPTHMSQATQVPIISQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 711
Db 661 EFSAQTFYALSPTHMSQATQVPIISQSGSAVAATNTIANQINTAPKPAAPTTLQIPPLP 720

Qy 712 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 771
Db 721 AIKHLPRPETLHPNAPAGLQESISDVTTCLVASKENVOVQASNLTKDRSMRKSFDMGGETL 780

QY 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDPFYPKWRESKLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDPFYPKWRESKLFITDEE 840
QY 832 VGPETETDTFDDAAPQAPAREAFASDSLRGSRSSQSIKAGESTDALSPLHVKLK 888
Db 841 VGPETETDTFDDAAPQAPAREAFASDSLRGSRSSQSIKAGESTDALSPLHVKLK 897

RESULT 8
US-09-813-148-2
; Sequence 2, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SERBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813.148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 932
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-148-2

Query Match 99.6%; Score 4527.5; DB 9; Length 932;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 887; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRGKGARMSLLGKPLS 60
Db 36 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRGKGARMSLLGKPLS 95
QY 61 YTSSQSCRNVKRYRVQNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 120
Db 96 YTSSQSCRNVKRYRVQNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 155
QY 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGRLPARKPFCVIDTIVILASIA 180
Db 156 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGRLPARKPFCVIDTIVILASIA 215
QY 181 VVSATQGNIFATSALESRLRFQILRMVMDRGGTWMKLLGSSVVAHSEKELITAWYIGFL 240
Db 216 VVSATQGNIFATSALESRLRFQILRMVMDRGGTWMKLLGSSVVAHSEKELITAWYIGFL 275
QY 241 VLIFFSFLVYLVEKDNKEFSTYADALWNGTITLTITIGYDKTPTLWGLRLLSAGFALLG 300
Db 276 VLIFFSFLVYLVEKDNKEFSTYADALWNGTITLTITIGYDKTPTLWGLRLLSAGFALLG 335
QY 301 ISFFALPAGILGSGFALKVQEOHQHFKERKRNPAANLIQCVWRSYAADKSVSTATWKP 360
Db 336 ISFFALPAGILGSGFALKVQEOHQHFKERKRNPAANLIQCVWRSYAADKSVSTATWKP 395
QY 361 HLKALHTCSP-----NOKLSFKERVASPRGQSIKSRQASVGDRRSPSDITAE 411
Db 396 HLKALHTCSP-----NOKLSFKERVASPRGQSIKSRQASVGDRRSPSDITAE 455
QY 412 GSPTKVQKWSFNDRTRFRPSLKLKSSQPKVIDADTALGTDVDEKCCQCDVSDVLT 471
Db 456 GSPTKVQKWSFNDRTRFRPSLKLKSSQPKVIDADTALGTDVDEKCCQCDVSDVLT 515

QY 472 PPLKTVIRAIRIMKHFVAKRKFETLRPYDVVKOVIROYISAGHLDMLCRIKSLQTRVDQIL 531
Db 516 PPLKTVIRAIRIMKHFVAKRKFETLRPYDVVKOVIROYISAGHLDMLCRIKSLQTRVDQIL 575
QY 532 GKGOITSDKSKREKITAHEHTTDDLSMLGRVVKVQVQSIKESKLDCLLDIYQOVLKRGK 591
Db 576 GKGOITSDKSKREKITAHEHTTDDLSMLGRVVKVQVQSIKESKLDCLLDIYQOVLKRGK 635
QY 592 ASALALASFOIPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSTANISRGLOFILTPTN 651
Db 636 ASALALASFOIPECEQTSYQSPVDSKDLGSAQNSGCLSRSTSTANISRGLOFILTPTN 695
QY 652 EFSAQTFYALSPPTWHSQATQVPISQSDGSAVAATNTIANQINTAPKPAATTIPIPPPLP 711
Db 696 EFSAQTFYALSPPTWHSQATQVPISQSDGSAVAATNTIANQINTAPKPAATTIPIPPPLP 755
QY 712 AIKHLPRPETHLPNAGLOESISDVTTCLVASKENVOVAQNSLTGKDRSMRKSFDMGGETL 771
Db 756 AIKHLPRPETHLPNAGLOESISDVTTCLVASKENVOVAQNSLTGKDRSMRKSFDMGGETL 815
QY 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDPFYPKWRESKLFITDEE 831
Db 816 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSGSQDPFYPKWRESKLFITDEE 875
QY 832 VGPETETDTFDDAAPQAPAREAFASDSLRGSRSSQSIKAGESTDALSPLHVKLK 888
Db 876 VGPETETDTFDDAAPQAPAREAFASDSLRGSRSSQSIKAGESTDALSPLHVKLK 932

RESULT 9
US-10-661-629-7
; Sequence 7, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNEL
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661.629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-629-7

Query Match 94.6%; Score 4300.5; DB 16; Length 854;
Best Local Similarity 98.8%; Pred. No. 1.1e-307;
Matches 841; Conservative 1; Mismatches 0; Indels 9; Gaps 1;

QY 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRGKGARMSLLGKPLS 60
Db 1 MKDVESGRVLLNSAAARGDGLLLGTRAAATLGGGGGLRESRGKGARMSLLGKPLS 60
QY 61 YTSSQSCRNVKRYRVQNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 120
Db 61 YTSSQSCRNVKRYRVQNYLVNLERPRGWAFIYHAFVFLVFGCLILSVFSTIPEHTKL 120
QY 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGRLPARKPFCVIDTIVILASIA 180
Db 121 ASSCLLILEFVMIWVFGLEFIIRIWSAGCCCRYRGWQGRLPARKPFCVIDTIVILASIA 180
QY 181 VVSATQGNIFATSALESRLRFQILRMVMDRGGTWMKLLGSSVVAHSEKELITAWYIGFL 240
Db 181 VVSATQGNIFATSALESRLRFQILRMVMDRGGTWMKLLGSSVVAHSEKELITAWYIGFL 240
QY 241 VLIFFSFLVYLVEKDNKEFSTYADALWNGTITLTITIGYDKTPTLWGLRLLSAGFALLG 300
Db 241 VLIFFSFLVYLVEKDNKEFSTYADALWNGTITLTITIGYDKTPTLWGLRLLSAGFALLG 300
QY 301 ISFFALPAGILGSGFALKVQEOHQHFKERKRNPAANLIQCVWRSYAADKSVSTATWKP 360

Db 301 ISFPALPAGILGSGFALKVQEQHQHFKHFKERNPAANLIQCVWRSYAADKSVSIATWKP 360
Qy 361 HLKALHTCSPT-----NQLSPKERVVMSAPRGOSIKSRQASVGDRRSPSTDTAE 411
Db 361 HLKALHTCSPTKKEQGEASQKLSFKERVVMSAPRGOSIKSRQASVGDRRSPSTDTAE 420
Qy 412 GSPTKVKQKSFNDRTFRPSRLKSSQPKVIDADTALGTDVVDYDEKGCOCVSVEDLT 471
Db 421 GSPTKVKQKSFNDRTFRPSRLKSSQPKVIDADTALGTDVVDYDEKGCOCVSVEDLT 480
Qy 472 PPLKTVIRAIRIMKHFVAKRKFETLRPDYDKVIEQYSAGHLDMLCRIKSLQTRVDQIL 531
Db 481 PPLKTVIRAIRIMKHFVAKRKFETLRPDYDKVIEQYSAGHLDMLCRIKSLQTRVDQIL 540
Qy 532 GKQITSDKSKREKITAHEHTTDLMLGRVVKVQKQVQIESKJCLLDIYQOVLKRG 591
Db 541 GKQITSDKSKREKITAHEHTTDLMLGRVVKVQKQVQIESKJCLLDIYQOVLKRG 600
Qy 592 ASALALASFOIPPECEQTSYQSPVDSKDLGSGAONSGCLSRSTSANISGLQFILTNP 651
Db 601 ASALALASFOIPPECEQTSYQSPVDSKDLGSGAONSGCLSRSTSANISGLQFILTNP 660
Qy 652 EFSAQTFYALSPTHSQAOTQVPIQSQDGSAAVAATNTIANQINTAPKPAAPTTLQIPPLP 711
Db 661 EFSAQTFYALSPTHSQAOTQVPIQSQDGSAAVAATNTIANQINTAPKPAAPTTLQIPPLP 720
Qy 712 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOVAQSNLTKDRSMKSPDMGGETL 771
Db 721 AIKHLPRPETLHPNAGLQESISDVTTCLVASKENVOVAQSNLTKDRSMKSPDMGGETL 780
Qy 772 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSQDFYPKWRESKLPITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTEELNIQLSGSESSGSGSQDFYPKWRESKLPITDEE 840
Qy 832 VGPEETETDTF 842
Db 841 VGPEETETDTF 851

RESULT 10
US-09-866-020-31
; Sequence 31, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DMORETSKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091051
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-020-31

Query Match 43.7%; Score 1985; DB 9; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

Qy 35 GGGGGLRESRGKQAGARMSLGKPL-----SYTSSQSCRNVKRYRVQNYL 80
Db 37 GGGGSPR-----RLGLLGSPLPFGALPUGPGSGSGSACGQSSAAHKRYRLQNWV 87
Qy 81 YNVLERPRGWAFTYHAFVLLVFGCLLSVFTPIETHKLASSCLLILEFVMIUVFGLF 140

Db 88 YNVLERPRGWAFTYHAFVLLVFGCLLSVFTPIETHKLASSCLLILEFVMIUVFGLF 147
Qy 141 IIRWSAGCCCRVGMQGRRLRFARKPCFVIDITVLIASIAVWSAKTQGNIFATSALRSR 200
Db 148 IVRWSAGCCCRVGMQGRRLRFARKPCFVIDIFVVASVAVIAAGTQGNIFATSALRSR 207
Qy 201 FLOILRVRMDRRGGTWKLLGSSVYVYAHSKELIATWYIGFLVLPSSFLVYLVEKANKEP 260
Db 208 FLOILRVRMDRRGGTWKLLGSSVYVYAHSKELIATWYIGFLVLPSSFLVYLVEKANKEP 267
Qy 261 STVADALWMTITLTITIGYDKTPTLWGLRLLSAGFALLIGISFPALPAGILGSGFALKVQ 320
Db 268 SSVADSLWMTITLTITIGYDKTPTLWGLRLLSAGFALLIGISFPALPAGILGSGFALKVQ 327
Qy 321 EHQHQRHFKERKRNPAANLIQCVWRSYAAD-EKSVSIATW----- 358
Db 328 EHQHQRHFKERKRNPAANLIQAAWRLYSTDMRAYLTATWYIYDSILPSPRELALLFEHVQ 387
Qy 359 -----KPHLKALHT----- 388
Db 388 RARNGGLRPLEVRAPVPDGPAPRYPPVATCHRPGSTSCFGESSRMGILKDIRMGSQR 447
Qy 389 QSIKSRQ--ASVGDRRSPSTDTAEQ--SPTKVOKSWSFNDRTFRPSRLKSSQPKVID 445
Db 448 RTGFSKQOLAPPTMPTSPSEQVEATSPTKVOKSWSFNDRTFRASRL-----KRTS 502
Qy 446 ADTALGTDDVYDKGQCQDVSVEDLTPPLKTVIRAIRIMKHFVAKRKFETLRPDYDKV 505
Db 503 AEDA-PSEEAEEKSYQCBELTVDDIMPVAVTVIRIRILKFLVAKRKFETLRPDYDKV 561
Qy 506 IEQYSAGHLDMLCRIKSLQTRVDQILKGQITSDKSKRE---KITAEHTTDDLMLGRV 562
Db 562 IEQYSAGHLDMLGRIKSLQTRVDQIVGRG--PGDRKAREKDGKPGSDAEVVEISMGRV 619
Qy 563 VKVEKQVQSTESKJCLLDIYQOVLKRGSAALASAFQIPPECEQTSYQSPVDSKDL 622
Db 620 VKVEKQVQSTESKJCLLDIYQOVLKRGSAALASAFQIPPECEQTSYQSPVDSKDL 677
Qy 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLIS-ISRVSSTNM 694

RESULT 11
US-09-810-796-15
; Sequence 15, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNQ4
US-09-810-796-15

Query Match 43.7%; Score 1985; DB 9; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;

Qy 35 GGGGGLRESRGKQAGARMSLGKPL-----SYTSSQSCRNVKRYRVQNYL 80

Db 37 GGGGSPR-----RLGLLSPLPFPGAPLPQPGSGSGSACQORSSAAHKRYRLQNWV 87
QY 81 YNVLPRGWAIFYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMVVFGLF 140
Db 88 YNVLPRGWAIFYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMVVFGLF 147
QY 141 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSLR 200
Db 148 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSLR 207
QY 201 FLOILMVRDRGGTWKLLGSSVVAHAKELITAWIGFLVLFSSFLVLYVEKDANKEF 260
Db 208 FLOILMVRDRGGTWKLLGSSVVAHAKELITAWIGFLVLFSSFLVLYVEKDANKEF 267
QY 261 STYADALWGGTITLTITIGYDGTPLTWGLRLLSAGFALLGISFPALPAGILSGFALKVQ 320
Db 268 SSYADSLWGGTITLTITIGYDGTPLTWGLRLLSAGFALLGISFPALPAGILSGFALKVQ 327
QY 321 EHQHKKHFKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 358
Db 328 EHQHKKHFKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 387
QY 359 -----KPHLKALHT-----KPHLKALHT-----KPHLKALHT----- 447
Db 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRGSTSCFGESSRMGIKDIRMGSSOR 447
QY 389 OSIKSRQ--ASVGDRRSPSTDTITAG-SPTKVQKSWSFNDRTFRPSLRLLKSSQPKVID 445
Db 448 RTGPSKQOLAPPTMTSPSSQVGEATSPTKVQKSWSFNDRTFRPSLRLLKSSQPKVID 502
QY 446 ADTALGTDDVDEKGCQCDVSEDLTPPLKTVIRAIRIMKHFHVAKEFKETLRYDVQKV 505
Db 503 AEDA-PSEVAEAEKSYQCELTVDIMPVAVKTVIRIRILKFLVAKKFKETLRYDVQKV 561
QY 506 IEQYSAGHLDMLCRISLQTRVQDILGKGOITSDKKSRE---KITAEHETDLSMLGRV 562
Db 562 IEQYSAGHLDMLCRISLQTRVQDILGKGOITSDKKSRE---KITAEHETDLSMLGRV 619
QY 563 VKVEQVQSIKSLDCLDIYQOVLKGSASALASPOIPPECEOTSDYQSPVDSKOL 622
Db 620 VKVEQVQSIKSLDCLDIYQOVLKGSASALASPOIPPECEOTSDYQSPVDSKOL 677
QY 623 SGASQNGCLSRSTSANI 640
Db 678 SVSAQTLIS-ISRVSNTNM 694
RESULT 12
US-10-353-690-56
; Sequence 56, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MF102-018PARNOMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 695
; TYPE: PR1
; ORGANISM: Homo Sapiens
; US-10-353-690-56
Query Match 43.7%; Score 1985; DB 15; Length 695;
Best Local Similarity 60.3%; Pred No. 3.2e-137;
Matches 409; Conservative 76; Mismatches 101; Indels 92; Gaps 13;
QY 35 GGGGGLRSERRKQGRMSLLGKPL-----SYTSSQSCRRNVKRYRQNYL 80
Db 37 GGGGSPR-----RLGLLSPLPFPGAPLPQPGSGSGSACQORSSAAHKRYRLQNWV 87
QY 81 YNVLPRGWAIFYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMVVFGLF 140
Db 88 YNVLPRGWAIFYHAFVLLVFGCLILSVFSTIPEHTKLASSCLLILEFVMVVFGLF 147
QY 141 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSLR 200
Db 148 IIRWSAGCCCRVWGQRLRFARKPCFVIDTIVLSTAVSAKTOGNIATSLRSLR 207
QY 201 FLOILMVRDRGGTWKLLGSSVVAHAKELITAWIGFLVLFSSFLVLYVEKDANKEF 260
Db 208 FLOILMVRDRGGTWKLLGSSVVAHAKELITAWIGFLVLFSSFLVLYVEKDANKEF 267
QY 261 STYADALWGGTITLTITIGYDGTPLTWGLRLLSAGFALLGISFPALPAGILSGFALKVQ 320
Db 268 SSYADSLWGGTITLTITIGYDGTPLTWGLRLLSAGFALLGISFPALPAGILSGFALKVQ 327
QY 321 EHQHKKHFKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 358
Db 328 EHQHKKHFKRRNPAANLIQCVWRSYAAD-EKSVSIATW-----KPHLKALHT----- 387
QY 359 -----KPHLKALHT-----KPHLKALHT-----KPHLKALHT----- 447
Db 388 RARNGGLRPLEVRAPVDPGAPSRYPVATCHRGSTSCFGESSRMGIKDIRMGSSOR 447
QY 389 OSIKSRQ--ASVGDRRSPSTDTITAG-SPTKVQKSWSFNDRTFRPSLRLLKSSQPKVID 445
Db 448 RTGPSKQOLAPPTMTSPSSQVGEATSPTKVQKSWSFNDRTFRPSLRLLKSSQPKVID 502
QY 446 ADTALGTDDVDEKGCQCDVSEDLTPPLKTVIRAIRIMKHFHVAKEFKETLRYDVQKV 505
Db 503 AEDA-PSEVAEAEKSYQCELTVDIMPVAVKTVIRIRILKFLVAKKFKETLRYDVQKV 561
QY 506 IEQYSAGHLDMLCRISLQTRVQDILGKGOITSDKKSRE---KITAEHETDLSMLGRV 562
Db 562 IEQYSAGHLDMLCRISLQTRVQDILGKGOITSDKKSRE---KITAEHETDLSMLGRV 619

[illegible]

RESULT 13
 US-10-661-629-6
 ; Sequence 6, Application US/10661629
 ; Publication No. US20040180405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JENTSCH, Thomas
 ; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
 ; FILE REFERENCE: 2815-0236P
 ; CURRENT APPLICATION NUMBER: US/10/661.629
 ; CURRENT FILING DATE: 2003-09-15
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 695
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-661-629-6

Query Match	43.7%	Score	1985;	DB	16;	Length	695;
Best Local Similarity	60.3%	Pred. No.	3.2e-137;				
Matches	409;	Conservative	76;	Mismatches	101;	Indels	92;
Gaps	13;						
Qy	35	GGGGGLRESRRGKGQARMSLLGKPL	-----SYTSSQSCRRNVKVRVNYL	80			
Db	37	GGGGSPR	-----RGLLGSPLPGCAPLPGGSGSGAGCGRSSAAHKRYRLQNW	87			
Qy	81	YNVLERPRGWAFIYHAFVFLVFLGCLILSVFSTIPEHTKLASSCLLILEFVMIYVFGLEF	140				
Db	88	YNVLERPRGWAFVYHVFIFFLVFSCVLVSVLSTIQEHQELANECLLILEFVMIYVFGLEY	147				
Qy	141	IIRIWSAGCCCRVRCWGQRLEFARKPCVIDTIVLIASIVVSAKTOGNFATSALESRL	200				
Db	148	IVRWSAGCCCRVRCWGQRFFARKPCVIDFIYFVASVAVIAAGTOGNFATSALESRL	207				
Qy	201	FLQILRMVRMDRRGCTWKLLGSSVYVAHSKELITAWYIGFLVLISSFLVYLVEKDANKEF	260				
Db	208	FLQILRMVRMDRRGCTWKLLGSSVYVAHSKELITAWYIGFLVLISSFLVYLAEKDANSDF	267				
Qy	261	STYADALWNGTITLTIGYGDKTELTWLGRLLSAGFALLGISFPFALPGILGSGFALKVQ	320				
Db	268	SSYADSLWNGTITLTIGYGDKTEHTWLGRVLAAGFALLGISFPFALPGILGSGFALKVQ	327				
Qy	321	EOHRQKHFEKRRNPAANLIQCWRSYAAD-EKSVSIATW	358				
Db	328	EOHRQKHFEKRRMPPAANLIQAANFLYSTDMSRAYLTATYYDYSILPSFRELALLFHVQ	387				
Qy	359	-----KPHLKALHT	-----CSPMTNOKLSFKRVRVMA SPRG	388			
Db	388	RARNGGLRPLEVRAPVDPGAPSYPPVATCHRPGSTSFCEGSSRMGIKDRINMGSSQR	447				
Qy	389	QSIKSRQ--ASVGDRRSPSTDITAEG-SPTKVQKSWSFNDRTFRPSLRLSKSPQKPVID	445				
Db	448	RTGPSKQQLAPPTWPTSPSBEQVEATSPTKVQKSWSFNDRTFRASLRL-----KPRTS	502				
Qy	446	ADTALGTDDVYDEKGCODVSVEDLTPLKTVIRAIRIMKHFVAKRKFETRLRYPDYKDV	505				
Db	503	AEDA-PSSEVAEAKSYCELTVDIMPAKTVIRSIIRILFLVAKRKFETRLRYPDYKDV	561				
Qy	506	IEQYSAGHLDMLCRIKSLQTRVDOILGKGQITSPDKKSR-----KITAEHTTDDLMLGRV	562				
Db	562	IEQYSAGHLDMLGRIKSLQTRVDOIVGRG--PGDKAREKGDQKPSDAEVVDELSMMGRV	619				
Qy	563	VKVEQVQSIESKLDCLLDITYQQVLRKGSASALAFQIPPPFCEQTSYQSPVDSKDL	622				

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Db      620 VKVEKQVQSIEHKLDLLLGFSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677
Qy      623 SGSAQNSGCLSRSTSANI 640
          |||||
          :|||:
Db      678 SVSNAQTLS-ISRVSVTNM 694

RESULT 14
US-10-850-928-2
; Sequence 2, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-928-2

```

Query Match	43.7%	Score 1985;	DB 17;	Length 695;
Best Local Similarity	60.3%;	Pred. No. 3.2e-137;		
Matches 409;	Conservative 76;	Mismatches 101;	Indels 92;	Gaps 13;
Qy	35	GGGGGLRESRRGQKGARMSLLGKPL-----SYTSSQSRNVKYYRRVQNYL	80	
Db	37	GGGGSPR-----RLGLLGSPLPGCAPLPGSGSGSACCQRSAAHKRRRLQNWV	87	
Qy	81	YNVLERPRGWAFYIYHAFVFLLVFGCLILSVFSTIPBHTKLASSCLLILEFVMIVFGLEF	140	
Db	88	YNVLERPRGWAFYVYVFIFFLVFSCVLVSLVSTIQEHQELANECLLILEFVMIVFGLEY	147	
Qy	141	IIRWSAGCCCRVRGQGRLFARFKPCVDTITVLJTASTAVSAKQGNIFATSALESLR	200	
Db	148	IVRWSAGCCCRVRGQGRFARFKPCVJDFIVFVASVAVIAGTQGNIFATSALESMR	207	
Qy	201	FLQILRMVRMDRRGGTWWKLGSVVYVYAHSKELITAWYIGFLVLIFSSFLVYLVEKDANKEF	260	
Db	208	FLQILRMVRMDRRGGTWWKLGSVVYVYAHSKELITAWYIGFLVLIFASFLVYLAEKDANSDF	267	
Qy	261	STADALWGWCTIITLTITIGYDKTPLTWLGRLLSAGFALLIGISFALPAGILGSGFALKVQ	320	
Db	268	SSYADSLWGWCTIITLTITIGYDKTPTHVWLGKVLAAAGFALLIGISFALPAGILGSGFALKVQ	327	
Qy	321	EQHRQKHFKERRRPAANLIQCVWRSYAAD-EKSVSIATW-----	358	
Db	328	EQHRQKHFKERRRPAANLIQAANRLYSTDMRSRAVLATATWYYYSILPSPRELALLPEHVQ	387	
Qy	359	-----KPHLKAHIT-----CSPNTQKLSFKERVVRMASPRG	388	
Db	388	RARNGGILRLPLEVRRAPVPDGPASRYFPVATCHRPGSTFCFGESSRMGKIDIRIMSSOR	447	
Qy	389	QSTKSRO--ASVGDGRSPSDITAEG-SPTKVQKSWSFNDRTRFPRSLRLKSSQPKRVID	445	
Db	448	RTGPSKQQLAPPMTPTSPSEQVEATSPTKVQKSWSFNDRTRFASRL-----KPRTS	502	
Qy	446	ADTALGTDDVYDRKGQCQDVSVEDLTPPLKTIVIRAIRMKFHVAKRKFETLRPYDKOV	505	
Db	503	AEDA-PSEEAEEKSYQCELTVDVIMPVAKTVIRISIRILKFLVAKRKFETLRPYDKOV	561	
Qy	506	IEQYSAGHLDMLCRIKSLQTRVDQIILGKQITSDKKSR-----KITAEHETTDLSMLGRV	562	
Db	562	IEQYSAGHLDMLCRIKSLQTRVDQIVGRG--PGRKAREKGDGPDSAAVVDISIMMGRV	619	
Qy	563	VKVEKQVQSTESKLDCLITDIYQVLRKGSASALALASFQIPPECEQTSYQSPVDSKOL	622	

Db 620 VKVEKQVQSIEHKLDLLLFYSRCLSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677
QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLS-ISRVSSTNM 694

RESULT 15
US-10-948-493-31
; Sequence 31, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-493-31

Query Match 43.7%; Score 1985; DB 17; Length 695;
Best Local Similarity 60.3%; Pred. No. 3.2e-137; Indels 92; Gaps 13;
Matches 409; Conservative 76; Mismatches 101;
QY 35 GGGGGLRESRRGKQAGMSLIGKPL-----SYTSSQSCRRNVKYRRVQNYL 80
Db 37 GGGGSPR-----RLGLLGSPLPGAPLPFGSGSGACGQRSSAAHKRYRRLQNVV 87
QY 81 YNVLEPRGMAFIYHAFVFLVFGCLILSVFSTIPEHTKLASSCLLILEFMIVVGLF 140
Db 88 YNVLEPRGMAFVHVFLVFLVFCVLSVLSVTIQEHQELANECLLILEFMIVVFGLEY 147
QY 141 IIRWSAGCCRYGQWQGLRFARKPCFVIDTIVLIASIAVVSATQCNIFATSALRSR 200
Db 148 IVRVWSAGCCRYGQWQGLRFARKPCFVIDFIVFVASVAVIAAGTQGNIFATSALRSR 207
QY 201 FLQILRMVMDRRGGTWWKLGSVVYVAHSHKELITAWYIGFLVLIFSSFLVYLVEKDNKEP 260
Db 208 FLQILRMVMDRRGGTWWKLGSVVYVAHSHKELITAWYIGFLVLIFASFLVYLAEKDANSDF 267
QY 261 STYDALWNGTITLTITIGYDKTFLTWGLLSAGFALLGIFPALPAGILGSGFALKVQ 320
Db 268 SSYADSLWNGTITLTITIGYDKTFLTWGLVLAAGFALLGIFPALPAGILGSGFALKVQ 327
QY 321 EQRHOKHFKERNPAANLIQCVRSYAAD-EKSVSIATW----- 358
Db 328 EQRHOKHFKERNPAANLIQAARLYSTDMRSAYLATATWYVYDSTLPSFRELALLFEHVQ 387
QY 359 -----KPHLKALHT-----CSPTNQKLSFKERVMSAPRG 388
Db 388 RARNGGLRPLEVRAPVPDGPAPRYPPVATCPGPGSTFCPGESSRMGKIRIRMGSSQR 447
QY 389 QSIKSRQ--ASVGDRESPTDITAEQ-SPTKVQKSWSFNDRFRFPSPRLKSSQPKVID 445
Db 448 RTGPSKQQLAPPTMTSPSEQVGEATSPTKVQKSWSFNDRFRFRASLRL-----KPRTS 502
QY 446 ADTALGTDVYDEKGCQCDVSVEDLTPPLKTVIRAIRIMKHFVAKRKFETLRPYDVKDV 505
Db 503 AEDA-PSEEAEBKSYQCELTVDVDDIMPAVKTVIRISIRILKFLVAKRKFETLRPYDVKDV 561

QY 506 IEQYSAGHDMLCRIKSLQTRVDQILKGQITSDKKSRE---KITAEHETDLSMLGRV 562
Db 562 IEQYSAGHDMLCRIKSLQTRVDQIVGRG--PGDRKAREKDGKPSDAEVDISMMGRV 619
QY 563 VKVEKQVQSIESKLDCLLDIYQOVLKGSASALALASFOIPPPPECEOTSDYQSPVDSKDL 622
Db 620 VKVEKQVQSIIEHKLDLLLFYSRCLRSGTSA--SLGAVQVPLFDPDITSDYHSPVDHEDI 677
QY 623 SGSAQNSGCLSRSTSANI 640
Db 678 SVSAQTLS-ISRVSSTNM 694

Search completed: April 8, 2005, 16:46:17
Job time : 155 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:32:30 ; Search time 50 Seconds
(without alignments)
1708.810 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGRVLNSAARG.....SICKAGESTDALSLPHVKLK 888

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1236.5	27.0	393	2 JC5275	voltage-gated pota
2	1226	27.0	744	2 T34116	voltage-gated pota
3	950	20.9	645	2 T27186	hypothetical prote
4	423.5	9.3	664	2 T28852	probable potassium
5	291.5	6.4	858	2 S31761	potassium channel
6	289	6.4	853	1 CHRT01	potassium channel
7	279	6.1	857	2 I56529	potassium channel
8	272	6.0	802	2 JH0535	potassium channel
9	248.5	5.5	528	2 T34417	delayed rectifier
10	248.5	5.5	924	2 B41359	potassium channel
11	245	5.4	484	2 T24238	hypothetical prote
12	245	5.4	581	2 S17150	potassium channel
13	242.5	5.3	490	2 T26983	potassium channel
14	242	5.3	613	2 A39402	hypothetical prote
15	242	5.3	624	2 S22703	potassium channel
16	241.5	5.3	344	2 E90564	voltage-gated pota
17	241	5.3	263	2 A12384	hypothetical prote
18	238	5.2	654	2 S11049	potassium channel
19	237	5.2	523	2 A38101	potassium channel
20	237	5.2	525	2 A43531	potassium channel
21	235.5	5.2	625	2 S13919	potassium channel
22	235.5	5.2	660	2 S24125	potassium channel
23	235	5.2	924	2 S12746	potassium channel
24	234	5.1	643	2 S00480	potassium channel
25	234	5.1	656	2 A39922	potassium channel
26	233.5	5.1	652	2 JH0133	potassium channel
27	232	5.1	528	2 I84205	potassium channel
28	231.5	5.1	769	2 I56546	Shaw type potassi
29	230	5.1	280	2 E75470	probable ion trans

RESULT 1
JC5275
voltage-gated potassium channel protein - human
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JC5275
R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A:Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific
A:Reference number: JC5272; MUID:97191543; PMID:9039501
A:Contents: neuroblastoma cell
A:Accession: JC5275
A:Molecule type: mRNA
A:Residues: 1-393 <YOK>
A:Cross-references: UNIPROT:O43526; DDBJ:D82346; NID:g1841341; PIDN:BAA11557.1; PID:d101

Query Match 27.0%; Score 1226.5; DB 2; Length 393;
Best Local Similarity 69.2%; Pred. No. 2.1e-73;
Matches 238; Conservative 33; Mismatches 56; Indels 17; Gaps 4;

QY 17 AARGDGLLLGTRAAATLGGGGGLRSGRRKQKQARMSSLLGKPLSYTSQSCRRNVKRRV 76
DB 34 STRDGALLIAGSPAK---RGSILSKPRAGAGA-----GKP-----PKRNAFRKL 77
QY 77 QNYLYNVLPRGMAFYHAFVFLVFGCLILSVFSTIPHTKLASSCLLILEFWMIVWF 136
DB 78 QNELYNVLPRGMAFYHAFVFLVFGCLILSVFSTIKEYKSSEGAIVLEIVTIWVF 137
QY 137 GLEFIRWSAGCCCRYRGHGRFARKPCFVIDITVLIASTAVVSATQGNIFATSAL 196
DB 138 GVEYFVRWIAAGCCCRYRGHGRFARKPCFVIDIMVLIASTAVLAAGSQGNVATSAL 197
QY 197 RSLRFLQILRMVMDRRGGTWKLLGSVVAHSELITAWYIGFLVLFSSFLVLYVEKDA 256
DB 198 RSLRFLQILRMVMDRRGGTWKLLGSVVAHSELITAWYIGFLVLFSSFLVLYVEKDA 257
QY 257 NKEFSTYADALWAGTITLTITIGYDKTPTLWGLRLSAGFALLGISFPALPAGILGSGFA 316
DB 258 NDHFDYADALWAGTITLTITIGYDKTPTLWGLRLSAGFALLGISFPALPAGILGSGFA 317
QY 317 LKVOEQRQHKFKRRNPANLIQCVWRSVADEKSVSI-ATWK 359
DB 318 LKVOEQRQHKFKRRNPANLIQSAWRFYATNLRTDLHSTWQ 361

RESULT 2
T34116
voltage-gated potassium channel klq-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T34116
R;Wilcox, L.

RESULT 4
T28852
probable potassium channel - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C/Accession: T28852

CHRTD1
potassium channel protein drk1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S05448; A44838
R;Frech, G.C.; Vandongen, A.M.J.; Schuster, G.; Brown, G.; Joho, R.H.
Nature 340, 642-645, 1989
A;Title: A novel potassium channel with delayed rectifier properties isolated from rat brain
A;Reference number: S05448; MUID:89365157; PMID:2770868
A;Accession: S05448
A;Molecule type: mRNA
A;Residues: 1-853 <PRE>
A;Cross-references: UNIPROT:P15387; EMBL:X16476; NID:957785; PIDN:CAA34497.1; PID:957786
A;Note: it is uncertain whether Met-1 or Met-17 is the initiator
R;Drewe, J.A.; Verma, S.; Frech, G.; Joho, R.H.
J. Neurosci. 12, 538-548, 1992
A;Title: Distinct spatial and temporal expression patterns of K+ channel mRNAs from different tissues in the developing rat brain
A;Reference number: A44838; MUID:92156897; PMID:1740690
A;Accession: A44838
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'MPAG', 1-571 <DRE>
A;Cross-references: GB:M81783; NID:G205038
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:81768)
C;Genetics:
A;Gene: drk1
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; ion channel; phosphoprotein; potassium channel; transmembrane
F;1-182/Domain: intracellular #status predicted <INT1>
F;183-204/Domain: transmembrane #status predicted <TM1>
F;225-245/Domain: transmembrane #status predicted <TM2>
F;256-276/Domain: transmembrane #status predicted <TM3>
F;291-312/Domain: transmembrane #status predicted <TM4>
F;327-348/Domain: transmembrane #status predicted <TM5>
F;389-410/Domain: transmembrane #status predicted <TM6>
F;411-853/Domain: intracellular #status predicted <INT2>
F;279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.4%; Score 289; DB 1; Length 853;
Best Local Similarity 19.7%; Pred. No. 5.8e-11;
Matches 176; Conservative 134; Mismatches 269; Indels 316; Gaps 37;

QY 80 LYNVLPRGWA---FIYHAFVLLVFGCLILSVFSTPEHTKL-----ASSCLLILE 129
DB 171 LWDLEKPNSSVAAKILAIISIMFVLSIALSL-NLPELQSLDFEQSDTNPQLAHVE 229
QY 130 FVMIVVFGLEFIIRWSAGCCCRYGQRLRPARKPCVIDTIVLIASIAVVSATQGN 189
DB 230 AVCIAWFTMEYLLRFLSSP-----KKW---KFFKGPLNAIDLAILPYVYV-----T 272
QY 190 IFATSAIRSL-----RFLQILRMVRMDRGGTWKLGSSVVAHSKEL-ITAW 235
DB 273 IFLTESNKSVLQFQNVRRVVOIFRIMRILRLKLAHSTGLQSLGFTLRSSYNELGLLIL 332
QY 236 YIGFLVLIFSSFLVYLVEKDA-NKEFTSYADALMWGTTITLTIGYGDKTPLTWIGRLISA 294
DB 333 FLAMGIMIFSS-LVFFAEKDEDTKFKSIPASFWMATITMTTVGYGDIYPKTLGKIVGG 391
QY 295 GFALLGISFPALPAGILGSGFALKVQEOHROKHFKEKRNPAANLIQCWRSYAADKSVS 354
DB 392 LCCIAGVLVIALPIPIIVNNFSEFYKQKOEKAIKRR-----MDIVVEKNG----- 429
QY 355 IATWPKHLKALTCSPNTOKLSFKERVMSRPGOSIKRSQASVGGDRRSPSTDITAEOSP 414
DB 430 -----EALREKENGIV----- 442
QY 415 TKVQKSWSFNDTRFRPSRLKSSQKPVVDADTALGTDDVDVEKGQCDVSDVDELTPPL 474
DB 443 -----SMNKDADFARSIEM-----MDIVVEKNG----- 465
QY 475 KTVIRAIRIMKHFVAKRKFKETLRPYVDVKDVIEQYSAGHLDMLCRIKSLQTRVDQILGKG 534
DB 444 -----BALERAKNGS----- 444

466 ESIAKKDKVDNHLSPNKKWKT-----KRALSTSSS-----KSFETK----- 503
QY 535 QITSDKKSKREKITAEHETDDLSMLGRVVKVEKQVQSTIESKLDCLDIYQOVLKRGASASA 594
DB 504 FQGSPEKARSSSSPQH-----LNVQLE-----DWSKMAKTSQSPI 540
QY 595 L---ALASFOIPIPPFCEQTSYQSPVDSKULSGAQNCGLSRSTSANISRGLOFILTPN 651
DB 541 LNTKEMAPQSPKPELEMS--MPSPVAPL-----PARTEGVIDMRSMSSID---SFISCAT 592
QY 652 EFSAOFTFVALSP--TMHSAQTQVPISQ-----SDGSAVAATNTIANQINT-----AP 696
DB 593 DPEETRFSSHSLASLSKAGSSTAPEVGVWGALGASGRLTETNPETSRSGFFVESP 652
QY 697 KPAAPTTLQIP-----PPLPAIKHLPRPETLHPNP-----AGLOEIS 734
DB 653 RSMKTNPNPLKRLKLVNFVEGDPTELLPSL---GLYHDPLENRGGAAAVAGL-ECAS 707
QY 735 DVTTCLVASKENVQVAQNLIKDRMRK-----SPDMG-----GETLLSYCP 776
DB 708 LLDKPVLSPESSIYTTASARTPPRSPKHTAFAFVGAHVHVIDTDDDEGQLLYSVDS 767
QY 777 WVPKDLGKLSVQNLIRSTEELNIQSGSESGSRGSDQFYPKWRKSLFITDEEVGPEE 836
DB 768 SPKSLHGSTPK-----FSTGAR----- 786
QY 837 TETDTFDAPOPAR-----EAFASDSLRTGRSRSSQISICKAGST--DALSLP 883
DB 787 TEKNHFESSPLTPSPKFLRPNVCVSEGL-TGKGPAQEKCKLENHTPPDVHMLP 840

RESULT 7
I56529
potassium channel protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56529
R;Pak, M.D.; Covarrubias, M.; Ratcliffe, A.; Salkoff, L.
J. Neurosci. 11, 869-880, 1991
A;Title: A mouse brain homolog of the Drosophila Shab K+ channel with conserved delayed-
A;Reference number: I56529; MUID:91162315; PMID:2002364
A;Accession: I56529
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-857 <RES>
A;Cross-references: UNIPROT:Q03717; GB:M64228; NID:G200975; PIDN:AAA40112.1; PID:G200976
C;Genetics:
A;Gene: Shab
C;Superfamily: potassium channel protein drk1

Query Match 6.1%; Score 279; DB 2; Length 857;
Best Local Similarity 20.4%; Pred. No. 2.7e-10;
Matches 181; Conservative 124; Mismatches 280; Indels 304; Gaps 37;

QY 80 LYNVLPRGWA---FIYHAFVLLVFGCLILSVFSTPEHTKL-----ASSCLLILE 129
DB 175 LWDLEKPNSSVAAKILAIISIMFVLSIALSL-NLPELQSLDFEQSDTNPQLAHVE 233
QY 130 FVMIVVFGLEFIIRWSAGCCCRYGQRLRPARKPCVIDTIVLIASIAVVSATQGN 189
DB 234 AVCIAWFTMEYLLRFLSSP-----KKW---KFFKGPLNAIDLAILPYVYV-----T 276
QY 190 IFATSAIRSL-----RFLQILRMVRMDRGGTWKLGSSVVAHSKEL-ITAW 235
DB 277 IFLTESNKSVLQFQNVRRVVOIFRIMRILRLKLAHSTGLQSLGFTLRSSYNELGLLIL 336
QY 236 YIGFLVLIFSSFLVYLVEKDA-NKEFTSYADALMWGTTITLTIGYGDKTPLTWIGRLISA 294
DB 337 FLAMGIMIFSS-LVFFAEKDEDTKFKSIPASFWMATITMTTVGYGDIYPKTLGKIVGG 395
QY 295 GFALLGISFPALPAGILGSGFALKVQEOHROKHFKEKRNPAANLIQCWRSYAADKSVS 354
DB 396 LCCIAGVLVIALPIPIIVNNFSEFYKQKOEKAIKRR-----BALERAKNGS----- 444

QY 242 LIFSSFLVYLVEK-----DANKEFSTYADALWNGTITLTITIGYGDKTPLTWLGRL 291
D 242 LIFAT-MIYAERVGAQNPDSASEHTQFNKIPGFVWVVTMTTLGYGDMYPQWGSGL 452
QY 292 LSAGFALLGISFFALPAGIL-----GSGFALKVQEQ-----HRQKH 331
D 453 VGALCALAGVLTITAMPVPVIVNFMGYSLAMAKQKLPKRKKHIPPAPLASSPTFCCKTE 512
QY 332 RNPAANIQ---CWMRYAADEKSVSIATWPKPHKALHTCSPT 371
D 513 LNMACNSTQSDTCGLKENLLEHNRVAS---TLEPMESTSOT 552

RESULT 13
T26983
hypothetical protein Y48A6B.6 - Caenorhabditis elegans
A;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T26983
R;Gardner, A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z20295
A;Accession: T26983
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-490 <WIL>
A;Cross-references: UNIPROT:Q9XXD1; EMBL:AL023844; PIDN:CAA19530.1; GSPDB:GN00021; CESP:
A;Experimental source: clone Y48A6B
C;Genetics:
A;Gene: CESP:Y48A6B.6
A;Map position: 3
A;Introns: 34/2; 94/1; 138/1; 175/3; 256/1; 282/1; 365/3; 410/2; 419/1; 429/1; 452/3
C;Superfamily: potassium channel protein drk1

Query Match 5.3%; Score 242.5; DB 2; Length 490;
Best Local Similarity 27.1%; Pred. No. 3e-08;
Matches 76; Conservative 63; Mismatches 110; Indels 31; Gaps 10;

QY 69 RNKYRRVQVNYLVNLERP-----RGWAFIYHAFVFLV-FGCLLSVFTSTIPHTKLASS 123
D 192 KTLRFGBIRRCWNIIEBPASSGKAQAFVCSVVFLISISGLVLSLPELQVATKQRNN 251
QY 124 -----CLLILEFMIIVFGLFIIRIWSAGCCCRVKGQRLR-----FARKP 166
D 252 LTGSEFTEMEPMTLGVIEYVCIWFTMEYGLKMLVS--AERSKTPRQLNIIDLLAILP 309
QY 167 FCVIDTIVLIASIAVSAKTQGNIFATSLRSLRFLQILRMVRMDRRGGTWKLGSVVYA 226
D 310 F-IIEMLLLIFGISTEQRLDLKGAPL--VIRILVLRVIRVLKGRYSSGLQMPFGTKLA 366
QY 227 HSKELITAWYIGFLVLIFFSFLVYLVEKD--ANKEFSTYADALWNGTITLTITIGYGDKTP 284
D 367 SFRQLGMWMMVMTGVIFSTLVVLFLEKDEPASK-FHSIPAAQWCVITMTTGVYGLTLP 425
QY 285 LTWIGRLLSAGFALLGISFPALPAGILGSGFALKVQEQHR 324
D 426 VTPVPGKLVGAIACGVLLALPITIIVDNE-MKVAETER 464

RESULT 14
A39402
potassium channel protein I1IA form 1, shaker-type - rat
A;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
A;Accession: A39402
R;McCormack, T.; Vega-Saenz de Miera, E.C.; Rudy, B.
Proc. Natl. Acad. Sci. U.S.A. 88, 4060, 1991
A;Reference number: A39402; MUID:91219512; PMID:2023956
A;Contents: erratum
A;Accession: A39402
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-613 <CC>
A;Cross-references: UNIPROT:P22462; GB:M34052; NID:g206913; PIDN:AAA42142.1; PID:g206914
C;Superfamily: potassium channel protein drk1

Query Match 5.3%; Score 242; DB 2; Length 613;
Best Local Similarity 24.1%; Pred. No. 4.5e-08;
Matches 83; Conservative 70; Mismatches 117; Indels 74; Gaps 14;

QY 35 GGGGLRESRRRGQAGMSL-----LQKPLSYTSSQSCRNVKRRVQVNYLVNLERP-- 87
D 176 GGDPGDDEDLGGK---RLGIEDAAGLGGPDG-----KSGRWKLPQRMWALFEDPYS 224
QY 88 -RGWAFIYHAFVFLVFG-----CL-----ILSVFSTIPHTKLASSCLLI 127
D 225 SRAARFIAPASLFFILVISITTFCTHEAFNIVKNTEPVTNGTSVAVLQEIETDPALTY 284
QY 128 LEFVMIVVFGLEFIIRIWSAGCCCRVKGQRLRFAKPFCDITIVLI-----ASIAVV 182
D 285 VEGCVVWFTFELVRIVES-----PNKLEFIKNLNIIDFVAILPFYLEVGLSGL 335
QY 183 SAKTQGNIFATSLRSLRFLQILRMVRMDRRGGTWKLGSVVVAHSKE-LITAWYIGFLV 241
D 336 SSRAAKDVL--GFLRVVRVRIILRIFKLTFRHFVGLRVLGHTLRASTNEFLLLIIFLALGV 393
QY 242 LIFSSFLVYLVEK-----DANKEFSTYADALWNGTITLTITIGYGDKTPLTWLGRL 291
D 394 LIFAT-MIYAERVGAQNPDSASEHTQFNKIPGFVWVVTMTTLGYGDMYPQWGSGL 452
QY 292 LSAGFALLGISFFALPAGIL-----GSGFALKVQEQ-----HRQKH 327
D 453 VGALCALAGVLTITAMPVPVIVNFMGYSLAMAKQKLPKRKKH 496

RESULT 15
S22703
voltage-gated potassium channel protein Rawl - rat
A;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-2001
C;Accession: S22703; A45292; S19099
R;Rettig, J.; Wunder, F.; Stocker, M.; Lichtinghagen, R.; Mastiaux, F.; Beckh, S.; Kues,
EMBO J. 11, 2473-2486, 1992
A;Title: Characterization of a shaw-related potassium channel family in rat brain.
A;Reference number: S22702; MUID:92331599; PMID:1378392
A;Accession: S22703
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-624 <RET>
A;Cross-references: EMBL:X62839; NID:g57650; PIDN:CAA44643.1; PID:g57651
R;Rudy, B.; Kentros, C.; Weiser, M.; Pruhling, D.; Serodio, P.; Vega-Saenz de Miera, E.;
Proc. Natl. Acad. Sci. U.S.A. 89, 4603-4607, 1992
A;Title: Region-specific expression of a K⁺ channel gene in brain.
A;Reference number: A45292; MUID:92262488; PMID:1374908
A;Accession: A45292
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 594-624 <RUD>
A;Note: sequence extracted from NCBI backbone (NCBIN:102300, NCBIP:102305)
C;Superfamily: potassium channel protein drk1
C;Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
F;230-248/Domain: transmembrane #status predicted <TM1>
F;282-303/Domain: transmembrane #status predicted <TM2>
F;315-335/Domain: transmembrane #status predicted <TM3>
F;347-365/Domain: transmembrane #status predicted <TM4>
F;382-401/Domain: transmembrane #status predicted <TM5>
F;452-473/Domain: transmembrane #status predicted <TM6>

Query Match 5.3%; Score 242; DB 2; Length 624;
Best Local Similarity 24.1%; Pred. No. 4.6e-08;
Matches 83; Conservative 70; Mismatches 117; Indels 74; Gaps 14;

QY 35 GGGGLRESRRRGQAGMSL-----LQKPLSYTSSQSCRNVKRRVQVNYLVNLERP-- 87
D 176 GGDPGDDEDLGGK---RLGIEDAAGLGGPDG-----KSGRWKLPQRMWALFEDPYS 224

Tue Apr 12 16:10:10 2005

88	QY	RGWAFIYHAFVLLVFG----	CL-----	ILSVFTIPBHTKCLASSCLI	127	
				:: :: ::		
225	Db	SRAARAFASLFFILSVITTF	CLEHAEFNIVKNKTEPINGS	SAVLQYIETDPALTY	284	
				:: :: ::		
128	QY	LEFVMIUVGLEFIIRWSAGCC	RYRGWGRLFARKEPCFVIT	LVL-----	ASIAVV	182
				:: :: ::		
285	Db	VEGVCCVWTFTEFLRVFS-----	PNKEFIKULLNIIDFVAIL	PFVLEVLSGL	335	
				:: :: ::		
183	QY	SAKTOGNIFATSALRSRFLQI	RMVMDRRGGTWWKLVGVV	YAHSEK-LITANIYGIFLV	241	
				:: :: ::		
336	Db	SSKAAKDVL--GFLRVRFVR	ILRIFKLTHFVGLRVLGLT	LEASNEFLLIIFLALGV	393	
				:: :: ::		
242	QY	LIFSFLAYLYEK-----	DANKEFSYADALMWGTIT	LITTCYGDGKPTPLTWGLR	291	
				:: :: ::		
394	Db	LIFAT-MIYAEVRCQAQNPDS	ASEHTQFNKPIGFVFWAV	VVTTLGYGDMYFQTWGML	452	
				:: :: ::		
292	QY	LSAGFALIGIFFPALPAGIL	-----	GSGFALKVQEQ-----	HRQXH	327
				:: :: ::		
453	Db	VGALCALAGVLTIAMPFVPI	VNNFGNMYSLAMAKOKL	PRKKHX	496	
				:: :: ::		

Search completed: April 8, 2005, 16:42:50
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 16:24:15 ; Search time 187 Seconds
(without alignments)
2431.692 Million cell updates/sec

Title: US-09-810-796-5
Perfect score: 4547
Sequence: 1 MKDVESGRGVILNSAARG.....SICKAGESTDALSLPHVHLK 888

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4527.5	99.6	897	1 C1Q5_HUMAN	Q9nr82 homo sapien
2	4227.5	93.0	878	1 C1Q5_MOUSE	Q9jk45 mus musculu
3	2655.5	58.4	572	2 Q8BSF6	Q8bsf6 mus musculu
4	1985	43.7	695	1 C1Q4_HUMAN	P56696 homo sapien
5	1930	42.4	427	2 Q86W40	Q86w40 homo sapien
6	1803.5	39.7	852	1 C1Q2_RAT	Q88943 rattus norv
7	1799.5	39.6	870	2 Q8R498	Q8r498 mus musculu
8	1783	39.2	872	1 C1Q2_HUMAN	Q43526 homo sapien
9	1754	38.6	759	1 C1Q2_MOUSE	Q9z351 mus musculu
10	1587.5	34.9	872	1 C1Q3_HUMAN	Q43525 homo sapien
11	1556.5	34.2	866	1 C1Q3_BOVIN	P58126 bos taurus
12	1556.5	34.2	873	2 Q8K3F6	Q8k3f6 mus musculu
13	1555.5	34.2	873	1 C1Q3_RAT	Q88944 rattus norv
14	1525.5	33.5	523	2 Q8C9Y6	Q8c9y6 mus musculu
15	1364.5	30.0	840	2 Q8IGU8	Q8iguh drosophila
16	1354	29.8	807	2 Q9V5H6	Q9v5h6 drosophila
17	1329.5	29.2	649	2 Q8IT87	Q8it87 drosophila
18	1321.5	29.1	992	2 Q9V5H7	Q9v5h7 drosophila
19	1226	27.0	692	2 Q967F8	Q967f8 caenorhabdi
20	1226	27.0	740	2 Q8MQC5	Q8mqc5 caenorhabdi
21	1198.5	26.4	459	2 Q7PP97	Q7pp97 anopheles g
22	1181	26.0	409	2 Q9BX08	Q9bx08 homo sapien
23	1145	25.2	621	2 Q9XWG9	Q9xwg9 caenorhabdi
24	1106.5	24.3	512	2 Q7QHB3	Q7qhb3 anopheles g
25	1102	24.2	676	1 C1Q1_HUMAN	P51787 homo sapien
26	1100.5	24.2	668	1 C1Q1_MOUSE	P37414 mus musculu
27	1097.5	24.1	669	1 C1Q1_RAT	Q9z0n7 rattus norv
28	1083.5	23.8	660	1 C1Q1_SQUAC	Q73925 squalus aca
29	1064.5	23.4	294	2 Q9BX07	Q9bx07 homo sapien
30	957.5	21.1	612	2 Q8K3P3	Q8k3p3 rattus norv
31	910.5	20.0	440	2 Q8CJG2	Q8cjg2 mus musculu

32	899.5	19.8	377	1 C1Q1_XENLA	P70057 xenopus lae
33	716	15.7	236	2 Q6DKP7	Q6dkp7 cavia porce
34	702	15.4	284	2 Q6DKP6	Q6dkp6 cavia porce
35	647	14.2	276	1 C1Q4_MOUSE	Q9jk97 mus musculu
36	591.5	13.0	172	1 C1Q1_FELCA	Q97531 felis silve
37	549.5	12.1	392	2 Q96A19	Q96a19 homo sapien
38	538.5	11.8	169	1 C1Q1_CAVPO	O70344 cavia porce
39	486.5	10.7	155	1 C1Q1_RABIT	Q9my86 oryctolagus
40	452.5	10.0	363	2 Q9BQU4	Q9bqu4 homo sapien
41	446.5	9.8	168	1 C1Q4_RAT	Q9jk96 rattus norv
42	441	9.7	145	2 Q6DKQ1	Q6dkq1 cavia porce
43	437	9.6	97	2 Q9CTU2	Q9ctu2 mus musculu
44	430	9.5	675	2 Q9GYM8	Q9gym8 caenorhabdi
45	424.5	9.3	399	2 Q9BQU5	Q9bqu5 homo sapien

ALIGNMENTS

RESULT 1
C1Q5_HUMAN STANDARD; PRT; 897 AA.
AC Q9NR82; Q9NRN0; Q9NYA6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 03-JUN-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 5 (Voltage-gated
DE potassium channel subunit Kv7.5) (Potassium channel alpha subunit
DE KvLQT5) (KQT-like 5).
GN Name=KCNO5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=20357367; PubMed=10787416; DOI=10.1074/jbc.M002378200;
RA Lerche C., Scherer C.R., Seebohm G., Derst C., Wei A.D., Busch A.E.,
RA Steinmeyer K.;
RT "Molecular cloning and functional expression of KCNQ5, a potassium
RT channel subunit that may contribute to neuronal M-current diversity."
RL J. Biol. Chem. 275:22395-22400(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain;
RX MEDLINE=20379054; PubMed=10816588; DOI=10.1074/jbc.M003245200;
RA Schroeder B.C., Hechenberger M., Weinreich F., Kubisch C.,
RA Jentsch T.J.;
RT "KCNQ5, a novel potassium channel broadly expressed in brain, mediates
RT M-type currents."
RN [3]
RP SEQUENCE FROM N.A.
RA Kananura C., Bivert B., Hechenberger M., Engels H., Steinlein O.K.;
RT "The new voltage gated potassium channel KCNQ5 and early infantile
RT convulsions."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 37-897 FROM N.A. (ISOFORM 1).
RC TISSUE=Brain, and Retina;
RA Knaizeva M., Han M.;
RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
RT is a candidate gene for retinal disorders."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE=21095345; PubMed=11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
RT mammalian cells."
RL Br. J. Pharmacol. 132:381-384(2001).
CC -!- FUNCTION: Probably important in the regulation of neuronal


```

Db 661 EFSAQTFVALSPTMHSQATQVPIQSOGSAVAANTNTANQINTAPKPAATTLQIPPLP 720
Qy 712 AIKHLPRPETHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGGTLL 771
Db 721 AIKHLPRPETHPNPAGLQESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGGTLL 780
Qy 772 LSVCPMPVKDLGKSLSVQNLIRSTRTEELNIQLSGSESSGSRGSDQFPYKWRKSLFITDEE 831
Db 781 LSVCPMPVKDLGKSLSVQNLIRSTRTEELNIQLSGSESSGSRGSDQFPYKWRKSLFITDEE 840
Qy 832 VGPETETDTFDAAPQAPAREAAAFASDSLRTGRSSSSQISCKAGSTDALSLPHVKLK 888
Db 841 VGPETETDTFDAAPQAPAREAAAFASDSLRTGRSSSSQISCKAGSTDALSLPHVKLK 897

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RESULT 2

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C105_MOUSE ID_C105_MOUSE STANDARD; PRT; 878 AA.
AC O9JK45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 5 (Voltage-gated
DE potassium channel subunit Kv7.5) (Potassium channel alpha subunit
DE KvLQTS) (KQT-like 5) (Fragment).
GN Name=Kcnd5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RA Kniازهva M., Han M.;
RT "A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5,
RT is a candidate gene for retinal disorders.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ3 to form a potassium channel
CC which contributes to m-type current, a slowly activating and
CC deactivating potassium conductance which plays a critical role in
CC determining the subthreshold electrical excitability of neurons.
CC May contribute, with other potassium channels, to the molecular
CC diversity of an heterogeneous population of M-channels, varying in
CC kinetic and pharmacological properties, which underly this
CC physiologically important current (By similarity).
CC -1- SUBUNIT: Heteromultimer with KCNQ3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -1- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.

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DR EMBL; AF263836; AAF73447.1; -.
DR HSSP; Q54397; 1JVM.
DR MGID; MGI:1924937; Kcnd5.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR003937; KCNQ channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF03520; KCNQ_channel; 1.

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DR PRINTS; PR00169; KCHANNEL.
KW Ion transport; Ionic channel; Multigene family; Potassium;
KW Potassium channel; Potassium transport; Transmembrane; Transport;
KW Voltage-gated channel.
FT NON_TER 1 1
FT TRANSMEM 72 92 Segment S1 (Potential).
FT TRANSMEM 103 123 Segment S2 (Potential).
FT TRANSMEM 147 167 Segment S3 (Potential).
FT TRANSMEM 176 198 Segment S4 (Potential).
FT TRANSMEM 213 233 Segment S5 (Potential).
FT TRANSMEM 272 292 Segment S6 (Potential).
FT DOMAIN 245 265 Segment H5 (pore-forming) (Potential).
FT SITE 257 262 Selectivity filter (By similarity).
SQ SEQUENCE 878 AA; 97029 MW; 3579F9C7D630F55 CRC64;

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Query Match 93.0%; Score 4227.5; DB 1; Length 878;
Best Local Similarity 94.3%; Pred. No. 4.4e-227;
Matches 827; Conservative 14; Mismatches 27; Indels 9; Gaps 1;

Qy 20 GDGLLLGTRAAVILGGGGGLRESRRKQKQARMSSLLGKPLSYTSSQSCRNVKRRVQNY 79
Db 1 GDGLLLGTRAAALGGGGGLRESRRKQKQARMSSLLGKPLSYTSSQSCRNVKRRVQNY 60
Qy 80 LYNVLERPRGMAFYHAFVFLVFGCLILSVFSTIPEHTKLASSCLLILFVMIIVFGLE 139
Db 61 LYNVLERPRGMAFYHAFVFLVFGCLILSVFSTIPEHTKLASSCLLILFVMIIVFGLE 120
Qy 140 FIIRWSAGCCCRYRGQGRRLRPFVCFVIDITVILIASIAVVSATQGNIFATSALRSL 199
Db 121 FIIRWSAGCCCRYRGQGRRLRPFVCFVIDITVILIASIAVVSATQGNIFATSALRSL 180
Qy 200 RFLQILRMVMDRRGGTGWLLGSSVVAHSHKELITAMVIGFLVLIFFSFLVLYVEKDANKE 259
Db 181 RFLQILRMVMDRRGGTGWLLGSSVVAHSHKELITAMVIGFLVLIFFSFLVLYVEKDANKE 240
Qy 260 FSTYADALWMTTLLTTTIGYGDKTPLTWLGRLLSAGFALLIGISFALPAGLGGSFALKV 319
Db 241 FSTYADALWMTTLLTTTIGYGDKTPLTWLGRLLSAGFALLIGISFALPAGLGGSFALKV 300
Qy 320 QEHRQKHFKERNPAAANLIQCVMRSVADEKSVSIATWPKHLKALHCTCSPT ----- 371
Db 301 QEHRQKHFKERNPAAANLIQCVMRSVADEKSVSIATWPKHLKALHCTCSPTKKEQGEAS 360
Qy 372 -NOKLSFKERVNRVWASPRGQSIKRSQASVGDRRSPSTDTAEGSPTKVQKSWFNDRTRFR 430
Db 361 SSQKLSFKERVNRVWASPRGQSIKRSQASVGDRRSPSTDTAEGSPTKVQKSWFNDRTRFR 420
Qy 431 PSURLKSSQPKPIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTIVAIRIMKHFVAK 490
Db 421 PSURLKSSQPKPIDADTALGTDDVYDEKGCQCDVSVEDLTPPLKTIVAIRIMKHFVAK 480
Qy 491 RPKFETLRPYDVKDVIQESAGHLDMLCRIKSLQTRVDDQILGKQITSDKKSREKITAHEH 550
Db 481 RPKFETLRPYDVKDVIQESAGHLDMLCRIKSLQTRVDDQILGKQITSDKKSREKITAHEH 540
Qy 551 ETTDDLSMLGRVVKVKEQVQSIKESKLDCLLDIYQQVLRKGSASALALASFOIPPFCEQOT 610
Db 541 ETTDDPSMLARVVKVKEQVQSIKESKLDCLLDIYQQVLRKGSASALALASFOIPPFCEQOT 600
Qy 611 SDYQSPVDSKDLGSGAQNCSLSRSTANSIRGLQFTLTPENEFSAQOTFYALSPTMHSAQT 670
Db 601 SDYQSPVDSKDLGSGAQNCSLSRSTANSIRGLQFTLTPENEFSAQOTFYALSPTMHSAQT 660
Qy 671 QVPISQSDGSAVAATNTIANQINTAPKPAATTLQIPPLPAIKHLPRPETHPNPAGLQ 730
Db 661 QVPMSQNDGSSVVAATNTIANQISAAKPAATTLQIPPLPAIKHLPRPETHPNPAGLQ 720
Qy 731 ESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGGTLLSVCPMPVKDLGKSLSVQ 790
Db 721 ESISDVTTCLVASKENVQVAQSNLTKDRSMRKSFDWGGTLLSVCPMPVKDLGKSLSVQ 780
Qy 791 LIPSTEELNIQLSGSESSGSRGSDQFPYKWRKSLFITDEEVPETETDTFDAAPAR 850
Db 781 LIPSTEELNIQLSGSESSGSRGSDQFPYKWRKSLFITDEEVPETETDTFDAAPAR 840

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DE KvLQ4 (KQT-like 4).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ON NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT DFNA2 SER-285.

RC TISSUE=Retina;

RX MEDLINE=99148276; PubMed=10025409; DOI=10.1016/S0092-8674(00)80556-5;

RA Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,

RA El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;

RT "KCQ4, a novel potassium channel expressed in sensory outer hair

RT cells, is mutated in dominant deafness.";

RL Cell 96:437-446(1999).

RN [2]

RP INHIBITION BY M1 MUSCARINIC RECEPTORS.

RX MEDLINE=20178300; PubMed=10713961;

RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,

RA Brown D.A.;

RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells

RT via M1 muscarinic acetylcholine receptors.";

RL J. Physiol. (Lond.) 522:349-355(2000).

RN [3]

RP PHARMACOLOGICAL CHARACTERIZATION, AND POSSIBLE FUNCTION.

RX MEDLINE=21143874; PubMed=11245603;

RA Soegaard R., Ljungstrom T., Pedersen K.A., Olesen S.-P.,

RA Jensen B.S.;

RT "KCQ4 channels expressed in mammalian cells: functional

RT characteristics and pharmacology.";

RL Am. J. Physiol. 280:C859-C866(2001).

RN [4]

RP VARIANTS DFNA2 SER-276; CVS-285 AND SER-321.

RX MEDLINE=99299248; PubMed=10369879; DOI=10.1093/hmg/8.7.1321;

RA Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schattman I.,

RA Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau F.,

RA Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,

RA Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,

RA Van Camp G.;

RT "Mutations in the KCNQ4 gene are responsible for autosomal dominant

RT deafness in four DFNA2 families.";

RL Hum. Mol. Genet. 8:1321-1328(1999).

RN [5]

RP VARIANT DFNA2 SER-281.

RX MEDLINE=20040027; PubMed=10571947;

RA DOI=10.1002/(SICI)1098-1004(199912)14:6<493::AID-HUMU8>3.0.CO;2-P;

RA Talebizadeh Z., Kelley P.M., Askew J.W., Beisel K.W., Smith S.D.;

RT "Novel mutation in the KCNQ4 gene in a large kindred with dominant

RT progressive hearing loss.";

RL Hum. Mutat. 14:493-501(1999).

RN [6]

RP VARIANT DFNA2 HIS-274.

RX MEDLINE=20389752; PubMed=109253378;

RA DOI=10.1002/1096-8628(20000731)93:3<184::AID-AJMG4>3.0.CO;2-5;

RA Van Hauwe P., Coucke P.J., Ensink R.J., Huygen P., Cremers C.W.R.J.,

RA Van Camp G.;

RT "Mutations in the KCNQ4 K+ channel gene, responsible for autosomal

RT dominant hearing loss, cluster in the channel pore region.";

RL Am. J. Med. Genet. 93:184-187(2000).

CC -1- FUNCTION: Probably important in the regulation of neuronal

CC excitability. May underlie a potassium current involved in

CC regulating the excitability of sensory cells of the cochlea. KCNQ4

CC channels are blocked by linopirdin, XE991 and bepridil, whereas

CC clofilium is without significant effect. Muscarinic agonist

CC oxotremorine-M strongly suppress KCNQ4 current in CHO cells in

CC which cloned KCNQ4 channels were coexpressed with M1 muscarinic

CC receptors.

CC -1- SUBUNIT: May form heteromultimers with KCNQ3.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Situated at the

CC basal membrane of cochlear outer hair cells (By similarity).

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=1;

CC IsoId=P56696-1; Sequence=Displayed;

CC Name=2;

CC IsoId=P56696-2; Sequence=VSP_001013;

CC TISSUE SPECIFICITY: Expressed in the outer, but not the inner,

CC sensory hair cells of the cochlea. Slightly expressed in heart,

CC brain and skeletal muscle.

CC -1- DOMAIN: The segment S4 is probably the voltage-sensor and is

CC characterized by a series of positively charged amino acids at

CC every third position (By similarity).

CC -1- DISEASE: Defects in KCNQ4 are a cause of nonsyndromic

CC sensorineural deafness type 2 (DFNA2) [MIM:600101], an autosomal

CC dominant form of progressive hearing loss.

CC -1- MISCELLANEOUS: Mutagenesis experiments were carried out by

CC expressing in Xenopus oocytes KCNQ4 mutants either individually

CC (homomultimers) or in combination with wild-type KCNQ4 (mut/wt

CC homomultimers) in a ratio of 1:1, to mimic the situation in a

CC heterozygous DFNA2 patient.

CC -1- SIMILARITY: Belongs to the potassium channel family. KQT

CC subfamily.

CC -1- DATABASE: NAME=Hereditary hearing loss homepage; NOTE=Gene page;

CC WWW="http://www.uia.ac.be/dnalab/hhh/".

CC -----

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CC or send an email to license@isb-sib.ch.

CC -----

CC EMBL; AF105202; AAD14680.1; -

CC EMBL; AF105216; AAD14681.1; -

CC EMBL; AF105203; AAD14681.1; JOINED.

CC EMBL; AF105204; AAD14681.1; JOINED.

CC EMBL; AF105205; AAD14681.1; JOINED.

CC EMBL; AF105206; AAD14681.1; JOINED.

CC EMBL; AF105207; AAD14681.1; JOINED.

CC EMBL; AF105208; AAD14681.1; JOINED.

CC EMBL; AF105209; AAD14681.1; JOINED.

CC EMBL; AF105210; AAD14681.1; JOINED.

CC EMBL; AF105211; AAD14681.1; JOINED.

CC EMBL; AF105212; AAD14681.1; JOINED.

CC EMBL; AF105213; AAD14681.1; JOINED.

CC EMBL; AF105214; AAD14681.1; JOINED.

CC EMBL; AF105215; AAD14681.1; JOINED.

CC HSP; Q54397; IJVM.

CC Genew; HGNC:6298; KCNQ4.

CC MIM; 603537; -

CC MIM; 600101; -

CC GO; GO:0005267; P:potassium channel activity; TAS.

CC GO; GO:0007605; P:perception of sound; TAS.

CC GO; GO:0006813; P:potassium ion transport; TAS.

CC InterPro; IPR005821; Ion trans.

CC InterPro; IPR001622; K-channel_pore.

CC InterPro; IPR003091; K channel.

CC InterPro; IPR003937; KCNQ channel.

CC InterPro; IPR005820; M-channel_nlg.

CC Pfam; PF00520; Ion trans; 1.

CC Pfam; PF03520; KCNQ channel; 1.

CC PRINTS; PR00169; KCHANNEL.

CC Alternative splicing; Deafness; Disease mutation; Ion transport;

CC Ionic channel; Multigene family; Potassium; Potassium channel;

CC Potassium transport; Transmembrane; Transport; Voltage-gated channel.

CC TRANSMEM 98 118 Segment S1 (Potential).

CC TRANSMEM 132 152 Segment S2 (Potential).

CC TRANSMEM 173 193 Segment S3 (Potential).

CC TRANSMEM 202 224 Segment S4 (Potential).

CC TRANSMEM 238 258 Segment S5 (Potential).

CC TRANSMEM 297 317 Segment S6 (Potential).

CC DOMAIN 271 292 Segment H5 (pore-forming) (Potential).

CC SITE 283 288 Selectivity filter (By similarity).

CC VARSPIC 378 431 Missing (In isoform 2).


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Db 156 ASSCLLLLEFWMVVGLEFIIRIWSAGCCRRGWRGRLPARKPCVDTIVILASIA 215
Qy 181 VWSAKTOGNIPATSAISSLRPLQILRMVRMDRRGGTWKLLGSVVVYAHSKELITAWYIGFL 240
Db 216 VWSAKTOGNIPATSAISSLRPLQILRMVRMDRRGGTWKLLGSVVVYAHSKELITAWYIGFL 275
Qy 241 VLISSFLVNLVEKDANKSESTYADALWNGTITLTITTYGDKTPLTWGLSNGFALLG 300
Db 276 VLISSFLVNLVEKDANKSESTYADALWNGTITLTITTYGDKTPLTWGLSNGFALLG 335
Qy 301 ISFPALPAGILGSGFALKVQEHQKHFEKRRNPAANLIQCVWRSYAADKSVSIATWKP 360
Db 336 ISFPALPAGILGSGFALKVQEHQKHFEKRRNPAANLIQCVWRSYAADKSVSIATWKP 395
Qy 361 HLKALHTCSPNTQK 374
Db 396 HLKALHTCSPNTKE 409

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RESULT 6

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C1Q2 RAT STANDARD; PRT; 852 AA.
AC O88943;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE potassium channel subunit Kv7.2) (Potassium channel alpha subunit
DE KvLOT2) (KQT-like 2).
GN Name=Kcnq2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RA Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=20493350; PubMed=11038262; DOI=10.1016/S0169-328X(00)00146-7;
RA Jow F., Wang K.-W.;
RT "Cloning and functional expression of rKCNQ2 K(+) channel from rat
RL brain."
RL Brain Res. Mol. Brain Res. 80:269-278(2000).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Sympathetic ganglion;
RX MEDLINE=21154288; PubMed=11230508;
RA Pan Z., Selyanko A.A., Hadley J.K., Brown D.A., Dixon J.E.,
RA McKinnon D.;
RT "Alternative splicing of KCNQ2 potassium channel transcripts
RT contributes to the functional diversity of M-currents."
RL J. Physiol. (Lond.) 531:347-358(2001).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=99055398; PubMed=9836639; DOI=10.1126/science.282.5395.1890;
RA Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT the M-channel."
RL Science 282:1890-1893(1998).
CC -I- FUNCTION: Probably important in the regulation of neuronal
CC excitability. Associates with KCNQ3 to form a potassium channel
CC with essentially identical properties to the channel underlying
CC the native M-current, a slowly activating and deactivating
CC potassium conductance which plays a critical role in determining
CC the subthreshold electrical excitability of neurons as well as the
CC responsiveness to synaptic inputs. KCNQ2 current is blocked by
CC barium and tetraethylammonium whereas 4-aminopyridine and

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CC charybdotoxin have no effect on KCNQ2 current. Tyrosine kinase
CC inhibitors genistein or herbimycin a markedly down-regulate KCNQ2
CC current. Muscarinic agonist oxotremorine-M suppress KCNQ2/KCNQ3
CC current in CHO cells in which cloned KCNQ2/KCNQ3 channels were
CC coexpressed with human M1 muscarinic receptors.
CC -I- SUBUNIT: Heteromultimer with KCNQ3.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=9;
CC Comment=Splice isoforms fell into three classes, those that
CC contain an in frame exon 16 (isoforms A-I) those that contain an
CC out-of-frame exon 16 due to an alternative splice junction in
CC exon 14 and those that terminate prematurely to exon 16. Only
CC the forms containing an in frame exon 16 are able to form
CC functional channels. A similar splice pattern is also produced
CC for splice variants that contain an out-of-frame exon 16. A wide
CC variety of different truncated isoforms were isolated for splice
CC variants that terminate prematurely to exon 16;
CC Name=A;
CC IsoId=O88943-1; Sequence=Displayed;
CC Name=B;
CC IsoId=O88943-2; Sequence=VSP_001009, VSP_001011;
CC Name=C;
CC IsoId=O88943-3; Sequence=VSP_001007;
CC Name=D;
CC IsoId=O88943-4; Sequence=VSP_001008, VSP_001010;
CC Name=E;
CC IsoId=O88943-5; Sequence=VSP_001008;
CC Name=F;
CC IsoId=O88943-6; Sequence=VSP_001007, VSP_001008, VSP_001010;
CC Name=G;
CC IsoId=O88943-7; Sequence=VSP_001011;
CC Name=H;
CC IsoId=O88943-8; Sequence=VSP_001007, VSP_001008;
CC Name=I;
CC IsoId=O88943-9; Sequence=VSP_001010;
CC -I- TISSUE SPECIFICITY: Expressed in brain and sympathetic ganglia. In
CC brain, expressed in cortex, hippocampus, and cerebellum. In
CC sympathetic ganglia, expressed at lower levels in celiac ganglia
CC and superior mesenteric ganglia than in superior cervical ganglia.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position (By similarity).
CC -I- MISCELLANEOUS: When coexpressed with KCNQ3 subunit in CHO cells or
CC Xenopus oocytes, isoform B was found to have significantly
CC different deactivation-activation kinetics. The kinetics was 2.5
CC times more slowly than the kinetics of other isoforms. The
CC presence of exon 15a in isoform B accounts for the slow
CC deactivation-activation kinetics. Alternative splicing of the
CC KCNQ2 gene may contribute to the variation in M-current kinetics
CC seen in vivo.
CC -I- SIMILARITY: Belongs to the potassium channel family. KQT
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF087453; AAC36722.1; -.
CC HSSP; Q54397; IJVM.
CC RGD; 621504; Kcnq2.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR01622; K+channel_pore.
CC InterPro; IPR003091; K channel.
CC InterPro; IPR003937; KCNQ channel.
CC InterPro; IPR005820; M+channel_nlg.
CC Pfam; PF00520; Ion trans; 1.
CC Pfam; PF03520; KCNQ channel; 1.
CC PRINTS; PR00169; KCHANNEL.

```

KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
KW Phosphorylation; Potassium; Potassium channel; Potassium transport;
KW Transmembrane; Transport; Voltage-gated channel;
FT TRANSMEM 92 112 Segment S1 (Potential).
FT TRANSMEM 123 143 Segment S2 (Potential).
FT TRANSMEM 167 187 Segment S3 (Potential).
FT TRANSMEM 198 221 Segment S4 (Potential).
FT TRANSMEM 232 252 Segment S5 (Potential).
FT TRANSMEM 292 312 Segment S6 (Potential).
FT DOMAIN 265 285 Segment H5 (pore-forming) (Potential).
FT SITE 277 282 Selectivity filter (By similarity).
FT MOD_RES 52 52 Phosphoserine (by PKA) (By similarity).
FT VARSPPLIC 373 382 Missing (in isoform C, isoform F and isoform H).
FT VARSPPLIC 416 416 S -> SKGRFCRCGLCGCRPHSS (in isoform D, isoform E, isoform F and isoform H).
FT VARSPPLIC 417 428 /FTid=VSP_001008.
FT VARSPPLIC 491 491 Missing (in isoform B).
FT VARSPPLIC 491 491 /FTid=VSP_001009.
FT VARSPPLIC 571 571 Missing (in isoform D, isoform F and isoform I).
FT VARSPPLIC 571 571 /FTid=VSP_001010.
FT VARSPPLIC 571 571 R -> RIDMIVGPPPPSTPRHKKYKPKGTPAPRSPPQVSP
FT VARSPPLIC 571 571 R (in isoform B and isoform G).
FT VARSPPLIC 571 571 /FTid=VSP_001011.
SQ SEQUENCE 852 AA; 93949 MW; 82A5PE42A5F259A CRC64;
Query Match 39.7%; Score 1803.5; DB 1; Length 852;
Best Local Similarity 49.0%; Pred. No. 4.4e-92;
Matches 413; Conservative 96; Mismatches 193; Indels 141; Gaps 22;
QY 17 AARGDGLLLGTRATLGGGGGLRSRRGKQARMSSLLGKPLSYTSSQSCRNVKRVV 76
DB 34 STRDGALLIAGEAPK---RGSVLSKPTGAGA-----GKP-----PKNAFYRKL 77
QY 77 QNYLYNVLERPRGWAFTYHAFVLLVFGCLLSVFTIPHTKLASSCLLILFVMIWVF 136
DB 78 QNFLYNVLERPRGWAFTYHAFVLLVFGCLLSVFTIPHTKLASSCLLILFVMIWVF 137
QY 137 GLEFIIRIWSAGCCCRYRQGRRLRFAKPCFVIDITVILIASIVAVSAKTQGNIFATSAL 196
DB 138 GVEYFVRIWAAGCCCRYRQGRRLRFAKPCFVIDITVILIASIVAVSAKTQGNIFATSAL 197
QY 197 RSLRFLQILNRVMDRGGTWKLGSSVYVYHAKSELITAWYIGFVLVFFSFLVYVEKDA 256
DB 198 RSLRFLQILNRVMDRGGTWKLGSSVYVYHAKSELITAWYIGFVLVFFSFLVYVEKGE 257
QY 257 NKEPSTYADALWGGTITLTIGYGDKTPLTWLGRLSAGFALLGISFPALPAGILGSGFA 316
DB 258 NDHPTDYADALWGGTITLTIGYGDKTPLTWLGRLSAGFALLGISFPALPAGILGSGFA 317
QY 317 LKVOEQRHOKHFERRRPAANLICOVRSVYAADEKSVSI-ATWK----- 359
DB 318 LKVOEQRHOKHFERRRPAANLICOVRSVYAADEKSVSI-ATWK----- 359
QY 360 -----PHLKALHTC-----SPTNQKLSFKERVRMASPRGOSIK 392
DB 378 TYGASRLIPPLNQLEMLRNLKSKSLTFRKEPQPEPSP-SQKVSLLKDRV-FSSPRGVAAK 435
QY 393 SRQASVGD--RRSPSTDIABGSPTKVOKSFSFNDRTRFRPSLRKLSQPKFVIDADATL 450
DB 436 GKGSPQAQTVRRSPSADQSLDSSPKVPSKFSFGDRSRARQAFRIKGAASRQNSEASLP 495
QY 451 GTDDVYDEKQCQDVSDVETLPPKLTIVIRIRIMKHFVAKRKFETLRPYDVKDVIQOYS 510
DB 496 GEDIVEDNKSNCHEFVTELLIPGLKVSIRAVCVMRFLVSKKFKESLRPYDMDVMDI 555
QY 511 AGHLDMLCRIKSLQTRVDQILKGQITSDKKSREKITAETHETDLSMLGRVWVKQVQ 570
DB 556 AGHLDMLCRIKSLQTRVDQILKGQITSDKKSREKITAETHETDLSMLGRVWVKQVQ 570
QY 571 SIESKLDCLLDIYQOVLKRGASALALASFOIIPPEC-----BQTSYQSPVDSKD 621

DB 615 SMEKKDLFLVSIYTO---RMG-----IPPAETAYFAKEPEPAPPVHSPEDSRD 661
QY 622 LSGSAQNSGC---LSRSTSANISRLGQILITPNEFSAQTFFVALSPTHMSQATQVPIQSOD 678
DB 662 ---HADKHCIIKIVRSISS-----TGORKYAAPFVM--PPAECPPSTS- 700
QY 679 GSAVAATNTIANQINTAPKPAATTLLQIPPPPLPAIKHLPRPETLHPNPAGLOESISDVTT 738
DB 701 -----WQSHQRHGTSPVGDHGLSVRIPPP-----PAH-ERLSAYSAG 737
QY 739 CLVASKENVOVAQSNLTK--DRSMKSFDMGGETLLSVCPMVPKDLGKSLSVQNLIIRSTE 796
DB 738 GNRASTEFLURLEGTACRPSEALRDS-----DTSISIPSDVHSELSRFSFGFSISQSK 792
QY 797 ELN 799
DB 793 NLN 795
RESULT 7
QY 8498 PRELIMINARY; PRT; 870 AA.
ID Q8R498
AC Q8R498; 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Potassium channel KCNQ2.
GN Name=Kcnq2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=12233552;
RA Wen H., Levitan I.B.;
RT "Calmodulin Is an Auxiliary Subunit of KCNQ2/3 Potassium Channels."
RL J. Neurosci., 22:7991-8001 (2002).
DR EMBL; AF490773; AAM09696.1; --
DR HSSP; Q54397; 1J95.
DR MGD; MGI:1309503; Kcnq2.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003947; KCNQ2 channel.
DR InterPro; IPR003937; KCNQ channel.
DR InterPro; IPR003091; K channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF03520; KCNQ channel; 1.
DR PRINTS; PR0169; KCHANNEL.
DR PRINTS; PR01461; KCNQ2CHANNEL.
DR PRINTS; PR01459; KCNQCHANNEL.
DR KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 870 AA; 95741 MW; 9C6106C27CE70C5F CRC64;
Query Match 39.6%; Score 1799.5; DB 2; Length 870;
Best Local Similarity 47.9%; Pred. No. 7.5e-92;
Matches 408; Conservative 96; Mismatches 195; Indels 153; Gaps 21;
QY 17 AARGDGLLLGTRATLGGGGGLRSRRGKQARMSSLLGKPLSYTSSQSCRNVKRVV 76
DB 34 STRDGALLIAGEAPK---RGSVLSKPTGAGA-----GKP-----PKNAFYRKL 77
QY 77 QNYLYNVLERPRGWAFTYHAFVLLVFGCLLSVFTIPHTKLASSCLLILFVMIWVF 136
DB 78 QNFLYNVLERPRGWAFTYHAFVLLVFGCLLSVFTIPHTKLASSCLLILFVMIWVF 137
QY 137 GLEFIIRIWSAGCCCRYRQGRRLRFAKPCFVIDITVILIASIVAVSAKTQGNIFATSAL 196
DB 138 GVEYFVRIWAAGCCCRYRQGRRLRFAKPCFVIDITVILIASIVAVSAKTQGNIFATSAL 197

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QY 197 RSLRFLQILRMVDRGGTCKLLGSSVYAHKSLITAWYIGFLVLIFFSFLVLYVEKDA 256
Db 198 RSLRFLQILRMVDRGGTCKLLGSSVYAHKSLITAWYIGFLVLIFFSFLVLYVEKGE 257
QY 257 NKFSFTYADALWMTITLTTIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILGSGFA 316
Db 258 NDHEDTYADALWGLITLTTIGYDGTPLTWLGRLLSAGFALLGISFPALPAGILGSGFA 317
QY 317 LKVOEQRHQHFKEKRNPAANLQCVWRSYAAD-----EKSVSIATW----- 358
Db 318 LKVOEQRHQHFKEKRNPAANLQCVWRSYAAD-----EKSVSIATW----- 377
QY 359 -----KHLKALHTCSP---TNOKL 375
Db 378 TYGASRLIPLINOLELRLNLSKSLGTLFRKEPOEPSKGRPCGCLCGCCGHSSQKV 437
QY 376 SFKERVMAFPRGOSIKRSQASVGD--RRSPSTDTITAEGSTPKVQKSWFNDRTRFPSSL 433
Db 438 SLKDRV-FSSPRGMAAKGSPQAQTVRRSPADQSLDPSFKVPSWFGDRSRTRQAF 496
QY 434 RLKSSQPKVIDATLGTDDVDYDEKGCQCDVSVEDLTPLKTVIRAIRIMKHFVAKRKF 493
Db 497 RIKGAASRQNSEASLPGEDIVEDNKSNCNCFVTEDLTPGLKVSIRAVCMVRFVLSKRF 556
QY 494 KETLRPYDKVDVIOYSAGHLMCRISLQTRVDQILKGQITSDKKSREKITAHEHTT 553
Db 557 KESLRPYDKVDVIOYSAGHLMCRISLQTRVDQILKGQITSDKKSREKITAHEHTT 615
QY 554 DDLISMLGRVVKVQKQVQKQIESKLDCLDIYQVLRKGSASALALASFOIPPFEC----- 607
Db 616 EDSMGRGLKVKQVLSMEKLDLFLVSIYQ--RMG-----IPASTEAYFGA 662
QY 608 ---EOTSQYSPVDSKDLGSAQNSGC---LSRSTSANISRGQLFILTNPNEFSAQTFYAL 661
Db 663 KEPEPAPYHSPEDSRD---HADKHGCIKIVRSTSS-----TGQRNYAA 704
QY 662 SPTMHSQATQVPSQSDGSAVAATNTIANQINTAPKPAATTIQLIPPLFA----- 712
Db 705 PPA-----IPPAQCPS--TSWQSHQRHGTSPVGDHGLSVLRIPPP-PAHERSLSAYG 754
QY 713 -----IKHLRPETLHPNAGLOESIDVTTCVLVASKENVOVQASNLTKDRSMKSF 764
Db 755 GGNRASTEFRLGTPACRPFSEALRSDTSISIPSV-DHEELERSFGFSISQS-KENL 812
QY 765 DMCGETLLSVCP 776
Db 813 DALGSCVAAP 824

RESULT 8
C1Q2 HUMAN STANDARD; PRT; 872 AA.
AC O4356; O43796; O75580; O95845; Q96459; Q99454;
DT 16-OCT-2001 (Rel. 40, Created)
DT 18-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 2 (Voltage-gated
DE potassium channel subunit Kv7.2) (Neuroblastoma-specific potassium
DE channel alpha subunit KvLQT2) (KQT-like 2).
GN Name=KCNQ2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RC TISSUE=Neuroblastoma;
RX MEDLINE=97191543; PubMed=9039501;
RA Yokoyama M., Nishi Y., Yoshii J., Okubo K., Matsubara K.;
RT "Identification and cloning of neuroblastoma-specific and nerve
RT tissue-specific genes through compiled expression profiles.";
RL DNA Res. 3:311-320(1996).
```

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RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS BPNC1 CYS-284 AND
RP THR-306.
RC TISSUE=Brain, Fetal brain, and Temporal cortex;
RX MEDLINE=9805864; PubMed=9425895;
RA Singh N.A., Charlier C., Stauffer D., DuPont B.R., Leach R.J.,
RA Melis R., Ronen G.M., Bjerre I., Quattlebaum T., Murphy J.V.,
RA McHarg M.L., Gagnon D., Rosales T.O., Peiffer A., Anderson V.E.,
RA Leppert M.;
RT "A novel potassium channel gene, KCNQ2, is mutated in an inherited
RT epilepsy of newborns.";
RL Nat. Genet. 18:25-29(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=fetal brain;
RX MEDLINE=9805252; PubMed=9430594; DOI=10.1126/science.279.5349.403;
RA Biervert C., Schroeder B.C., Kubisch C., Berkovic S.F., Propping P.,
RA Jentsch T.J., Steinlein O.K.;
RT "A potassium channel mutation in neonatal human epilepsy.";
RL Science 279:403-406(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RX MEDLINE=99055398; PubMed=9836639; DOI=10.1126/science.282.5395.1890;
RA Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT the M-channel.";
RL Science 282:1890-1893(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 5).
RX MEDLINE=99043242; PubMed=9827540; DOI=10.1016/S0014-5793(98)01296-4;
RA Tinel N., Lauritzen I., Chouabe C., Lazdunski M., Borsotto M.;
RT "The KCNQ2 potassium channel: splice variants, functional and
RT developmental expression. Brain localization and comparison with
RT KCNQ3.";
RL FEBS Lett. 438:171-176(1998).
RN [6]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=21114072; PubMed=11160379;
RA Smith J.S., Iannotti C.A., Dargatzis P.G., Christian E.P., Aiyar J.;
RT "Differential expression of KCNQ2 splice variants: implications to M
RT current function during neuronal development.";
RL J. Neurosci. 21:1096-1103(2001).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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FT	TRANSMEM	292	312	Segment S6 (Potential).
FT	DOMAIN	265	285	Segment H5 (pore-forming) (Potential).
FT	SITE	277	282	Selectivity filter (By similarity).
FT	MOD_RES	52	52	Phosphoserine (by PKA) (By similarity).
FT	VARSPPLIC	310	338	GILGSGPALVQQRHPEKREKRNPAAG -> VSPAHLPT LEMGLVLEAHKAWPWTCSL (in isoform 11). /FTid=VSP_000991.
FT	VARSPPLIC	339	759	Missing (in isoform 11). /FTid=VSP_000992.
FT	VARSPPLIC	342	349	SAWRFYAT -> GOVRCAGH (in isoform 9). /FTid=VSP_000993.
FT	VARSPPLIC	350	759	Missing (in isoform 9). /FTid=VSP_000994.
FT	VARSPPLIC	342	347	SAWRFY -> VSLSPC (in isoform 10). /FTid=VSP_000995.
FT	VARSPPLIC	348	759	Missing (in isoform 10). /FTid=VSP_000996.
FT	VARSPPLIC	372	372	Y -> YSSQTQTVGAS (in isoform 7). /FTid=VSP_000997.
FT	VARSPPLIC	406	463	SQVSLKDRVFSSPRGMAAKGKSPQAQTVRRSPSADQSLD DSPSKPKVSGFGRDR -> RSVPPASSRPGVCTCHALL SLCIHHSWGRATMGPCVCFYQVQTVPCGTPTRVTSQL (in isoform 7 and isoform 8). /FTid=VSP_000998.
FT	VARSPPLIC	464	759	Missing (in isoform 7 and isoform 8). /FTid=VSP_000999.
FT	VARSPPLIC	407	418	Missing (in isoform 3). /FTid=VSP_001000.
FT	VARSPPLIC	562	596	IDMTVGPFPSTPRDKKPYTKGPTAPSRSPQVSP -> QE PLPVQSGHEQGPQNGQAWKHGQGLGD (in isoform 2). /FTid=VSP_001001.
FT	VARSPPLIC	562	597	Missing (in isoform 4). /FTid=VSP_001002.
FT	VARSPPLIC	562	570	IDMTVGPFP -> SCDMRGVLA (in isoform 5). /FTid=VSP_001003.
FT	VARSPPLIC	571	759	Missing (in isoform 5). /FTid=VSP_001004.
FT	VARSPPLIC	562	623	IDMTVGPFPSTPRDKKPYTKGPTAPSRSPQVSPRVDHIV GRGPTTIDKDKTKGPAETELP -> QEPPLVQSGHEQGPFG QNGAWKHGQGLGRCACQGGQQLMWSLPTLLASCCLFLCF HTVCF (in isoform 6). /FTid=VSP_001005.
FT	VARSPPLIC	624	759	Missing (in isoform 6). /FTid=VSP_001006.
FT	CONFLICT	125	125	A -> P (in Ref. 1; BAA37161).
FT	CONFLICT	326	326	P -> Q (in Ref. 1; BAA37161).
FT	SEQUENCE	759 AA;	84450 NW;	CID12DBFF3979D3F CRC64;
QY	Query Match	38.6%;	Score 1754;	DB 1; Length 759;
Db	Best Local Similarity	51.9%;	Pred. No. 2,1e-89;	
QY	Matches 387;	Conservative 73;	Mismatches 149;	Indels 136; Gaps 18
QY	17	AARGDGLLLGTRATLGGGGGLRESRGKGARMSLLGKPLSVTSSQSCRNVKRYRV	76	
Db	34	STRDCALLIAGSEAPK---RGSVLSPKPTGGAGA-----GKP-----PKRNAFYRKL	77	
QY	77	QNYLVNVLPRPGWAFIVHAFVFLVFGCLILSVSTIPEHTKCLASSCLILIEFVMIVVF	136	
Db	78	QNYLVNVLPRPGWAFIVHAYFLVFLVFCCLVSVSTIPEHTKCLASSCLILIEFVMIVVF	137	
QY	137	GLEFIRIWSACCCRYRGWGLRFARKPFCVIDTIVLIASIVVSAKTQNI FATSL	196	
Db	138	GVEYFVRIWAACCCRYRGWGLRFARKPFCVIDTIVLIASIVVSAKTQNI FATSL	197	
QY	197	RSRLRFLQILRWYRMDRGCTWKLGSVVYAHSKELITAWYIGFLVLI PSEFLVILVEKDA	256	
Db	198	RSRLRFLQILRWYRMDRGCTWKLGSVVYAHSKELITAWYIGFLVLI PSEFLVILVEKDE	257	
QY	257	NKEFSTYADALWNGTITLTITIGYDKTPTLWTLGRLLSAGFALLGISFFPALPAGILGSGFA	316	
Db	258	NHDFDTYADALWNGTITLTITIGYDKYPTQWNGRLLAATFTLIGVSFFPALPAGILGSGFA	317	

RT responsible for an inherited idiopathic epilepsy.";
J. Biol. Chem. 273:19419-19423(1998).
[4]
RP INVOLVEMENT IN M-LIKE CURRENT.
RX MEDLINE=99410758; PubMed=10479678;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Delmas P.,
Buckley N.J., London B., Brown D.A.;
RT "Two types of K(+) channel subunit, Erg1 and KCNQ2/3, contribute to
the M-like current in a mammalian neuronal cell.";
J. Neurosci. 19:7742-7756(1999).
[5]
RP ASSOCIATION WITH KCNE2.
RX MEDLINE=20487128; PubMed=11034315; DOI=10.1016/S0014-5793(00)01918-9;
RA Tinel N., Diocot S., Lauritzen I., Barhanin J., Lazdunski M.,
Borsotto M.;
RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
subunit.";
FEBS Lett. 480:137-141(2000).
[6]
RP SURFACE EXPRESSION OF HETEROMERS.
RX MEDLINE=20250883; PubMed=10786442; DOI=10.1074/jbc.275.18.13343;
RA Schwake M., Pusch M., Kharkovets T., Jentsch T.J.;
RT "Surface expression and single channel properties of KCNQ2/KCNQ3, M-
type K+ channels involved in epilepsy.";
J. Biol. Chem. 275:13343-13348(2000).
[7]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20150152; PubMed=10694873;
RA Shapiro M.S., Roche J.P., Kaftan E.J., Cruzblanca H., Mackie K.,
Hille B.;
RT "Reconstitution of muscarinic modulation of the KCNQ2/KCNQ3 K(+) channels that underlie the neuronal M current.";
J. Neurosci. 20:1710-1721(2000).
[8]
RP INHIBITION BY M1 MUSCARINIC RECEPTORS.
RX MEDLINE=20178300; PubMed=10713961;
RA Selyanko A.A., Hadley J.K., Wood I.C., Abogadie F.C., Jentsch T.J.,
Brown D.A.;
RT "Inhibition of KCNQ1-4 potassium channels expressed in mammalian cells
via M1 muscarinic acetylcholine receptors.";
J. Physiol. (Lond.) 522:349-355(2000).
[9]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20368587; PubMed=10908292;
RA Main M.J., Cryan J.E., Dupre J.R., Cox B., Clare J.J., Burbidge S.A.;
RT "Modulation of KCNQ2/3 potassium channels by the novel anticonvulsant
retigabine.";
Mol. Pharmacol. 58:253-262(2000).
[10]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20411474; PubMed=10953053;
RA Wickenden A.D., Yu W., Zou A., Jegla T., Wagoner P.K.;
RT "Retigabine, a novel anti-convulsant, enhances activation of KCNQ2/Q3
potassium channels.";
Mol. Pharmacol. 58:591-600(2000).
[11]
RP ACTIVATION BY RETICABINE.
RX MEDLINE=20180045; PubMed=10713399; DOI=10.1016/S0304-3940(00)00865-1;
RA Rundfeldt C., Netzer R.;
RT "The novel anticonvulsant retigabine activates M-currents in Chinese
hamster ovary-cells transfected with human KCNQ2/3 subunits.";
Neurosci. Lett. 282:73-76(2000).
[12]
RP CHARACTERIZATION, AND ACTIVATION BY RETICABINE.
RX MEDLINE=21095345; PubMed=11159685;
RA Wickenden A.D., Zou A., Wagoner P.K., Jegla T.;
RT "Characterization of KCNQ5/Q3 potassium channels expressed in
mammalian cells.";
Br. J. Pharmacol. 132:381-384(2001).
[13]
RP VARIANT BFNC2 ARG-309.
RX MEDLINE=20309392; PubMed=10852552;
DOI=10.1002/1531-8249(200006)47:6<822::AID-ANAL9>3.3.CO;2-O;
Hirose S., Zenri F., Akiyoshi H., Fukuma G., Iwata H., Inoue T.,
Yonekani M., Tsutsumi M., Muranaka H., Kurokawa T., Hanai T., Wada K.,
Kaneko S., Mitsudome A.;
RT "A novel mutation of KCNQ3 (c.925T-->C) in a Japanese family with
benign familial neonatal convulsions.";
Ann. Neurol. 47:822-826(2000).
CC -I- FUNCTION: Probably important in the regulation of neuronal
excitability. Associates with KCNQ2 or KCNQ5 to form a potassium
channel with essentially identical properties to the channel
underlying the native M-current, a slowly activating and
deactivating potassium conductance which plays a critical role in
determining the subthreshold electrical excitability of neurons as
well as the responsiveness to synaptic inputs.
CC -I- SUBUNIT: Heteromultimer with KCNQ2 or KCNQ5. May associate with
KCNE2.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Predominantly expressed in brain.
CC -I- DOMAIN: The segment S4 is probably the voltage-sensor and is
characterized by a series of positively charged amino acids at
every third position (By similarity).
CC -I- DISEASE: Defects in KCNQ3 are the cause of benign familial
neonatal convulsions type 2 (BFNC2) [MIM:121201]; also known as
epilepsy, benign neonatal type 2 (BBN2). BFNC2 is an autosomal
dominant form of epilepsy in the newborn that clears spontaneously
after a few weeks and is followed by normal psychomotor
development.
CC -I- MISCELLANEOUS: Mutagenesis experiments were carried out in Xenopus
oocytes by coexpression of either KCNQ3(mut) and KCNQ2 at the ratio
of 1:1, or of KCNQ3(mut), KCNQ3(wt) and KCNQ2 at the ratio
of 1:1:2, to mimic the situation in a heterozygous patient with
BFNC2 disease.
CC -I- SIMILARITY: Belongs to the potassium channel family. KQT
subfamily.

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or send an email to license@isb-sib.ch).

CC EMBL; AF071491; AAC96101.1; JOINED.
CC EMBL; AF071478; AAC96101.1; JOINED.
CC EMBL; AF071479; AAC96101.1; JOINED.
CC EMBL; AF071480; AAC96101.1; JOINED.
CC EMBL; AF071481; AAC96101.1; JOINED.
CC EMBL; AF071482; AAC96101.1; JOINED.
CC EMBL; AF071483; AAC96101.1; JOINED.
CC EMBL; AF071484; AAC96101.1; JOINED.
CC EMBL; AF071485; AAC96101.1; JOINED.
CC EMBL; AF071486; AAC96101.1; JOINED.
CC EMBL; AF071487; AAC96101.1; JOINED.
CC EMBL; AF071488; AAC96101.1; JOINED.
CC EMBL; AF071489; AAC96101.1; JOINED.
CC EMBL; AF071490; AAC96101.1; JOINED.
CC HSSP; Q54397; 1JVM.
CC Genew; HGNC:6297; KCNQ3.
CC MIM; 602232; -
CC MIM; 121201; -
CC GO; GO:0008076; C:voltage-gated potassium channel complex; TAS.
CC GO; GO:0005249; F:voltage-gated potassium channel activity; TAS.
CC GO; GO:0006813; P:potassium ion transport; TAS.
CC GO; GO:0007268; P:synaptic transmission; TAS.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR003091; K+channel.
CC InterPro; IPR003937; KCNQ channel.
CC InterPro; IPR005820; M+channel_nlg.
CC Pfam; PF00520; Ion trans; 1.
CC Pfam; PF03520; KCNQ channel; 1.
CC PRINTS; PR00169; KCHANNEL.

Disease mutation; Epilepsy; Ion transport; Ionic channel;
Multigene family; Potassium; Potassium channel; Potassium transport;
Transmembrane; Transport; Voltage-gated channel.
TRANSMEM 122 142 Segment S1 (Potential).
FT TRANSMEM 153 173 Segment S2 (Potential).
FT TRANSMEM 197 217 Segment S3 (Potential).
FT TRANSMEM 226 247 Segment S4 (Potential).
FT TRANSMEM 262 282 Segment S5 (Potential).
FT TRANSMEM 331 351 Segment S6 (Potential).
FT TRANSMEM 304 324 Segment S5 (pore-forming) (Potential).
FT DOMAIN 13 24 Poly-Gly.
FT SITE 316 321 Selectivity filter (By similarity).
FT VARIANT 309 309 W -> R (in BFN2).
FT VARIANT 310 310 G -> V (in BFN2; about 50% reduction of
wild-type heteromeric current; ratio of

Query Match 34.9%; Score 1587.5; DB 1; Length 872;
Best Local Similarity 42.8%; Pred. No. 4.8e-80;
Matches 386; Conservative 106; Mismatches 244; Indels 165; Gaps 28;

Qy 3 DVESGRVLLNSAARGDGLLILGTRAAATLGGGGGLRESRKGKOGARMSLLGK-PLSY 61
Db 49 DVEQ---VTALGAGADKDGTL---EGGGDEGGRTPQG--IGLLAKTPLSR 95
Qy 62 TSSQSCRRNVKRRVQNYLVNLERPRGMAFIVHAFVFLVFLVGLLILSVFSTIPEHTKLA 121
Db 96 PVK---RNNAKYRIQIYDALERPRGMALLYHALVFLVFLVGLLILAVLTTFKEYETVS 152
Qy 122 SSCILLIEFVMVVGLEFIIRIWSAGCCRYRGWQRLRPAPKPFVVIDTIVLIASIV 181
Db 153 GDWLLLETFEFAIFGAEFALRIWAAGCCRYKGRGLKFAKPLCMLDFVLIASVPV 212
Qy 182 VSAQTQNIATFALSRLSIFLOILRMVMDRRGTWKLGSVVVYHAKELITAWYIGFLV 241
Db 213 VAVNGQNVLAIS--LRSRLFQILRLMDRRGTWKLGSALCAHAKELITAWYIGFLT 271
Qy 242 LIFSSFLVYLVEKDA-----NKEFSTYDALMWGITITLTIGYDKTFLTWLGR 291
Db 272 LILSSFLVYLVEKDVPEVDAQBEEMKEEFYDALMWGITITLTIGYDKTFLTWBGR 331
Qy 292 LSAGFALLIGTFPAPGILGSGFALKVQOHQKHEKRNPAANILQCVWSYAADEK 351
Db 332 IAATFSLIGVSFFPAPGILGSGFALKVQOHQKHEKRNPAANILQCVWSYAADEK 391
Qy 352 SVS-IATWK-----PHLKALTCGPTNOKLSFKERVMSRPGQSIKRSQASVGD 402
Db 392 RIDIVATWRFVSVSPFPFKEQLEASQKGLLDRLVLSNPRGNTK-----OKLF 445
Qy 403 SPSTDTITAGSPTKVQKSWSFNDRTRFRPSLRK-----SSQPKVIDADTALGTDDVY 456
Db 446 TPLNVDAIEESPSKEPKPVGLNNKRFRTAFMKAYAFQSSSE-----DAGTG---DPMA 497
Qy 457 DEKGQCDVSVEDLTPPLKTVIRAIRIMKHFVAKKETLRPPVDKVDVTEQYSAGHLD 516
Db 498 EDRGNGNDFFIEDIMPTLKAIRAVRILQFLRYKKFKETLRPPVDKVDVTEQYSAGHLD 557
Qy 517 LCRIKSLQTRVDQILGKQITSDKKSR-----EKITABHETT--DDLS 557
Db 558 LSRKYLQTRIDMTFTPPPTTPKHKSKQSAFTFPQQSPRNPVYVAREPSTSEIEDQS 617
Qy 558 MLGRVVKVEKQVQIESKCLDCLLDIYQVLR-----KGSASALALASFOI PPP 605
Db 618 MMGRFVKVERQVDMGKKLDELVDMMHQMHERLQVQVTEYYPTKTGTS-----PA 667
Qy 606 ECEQTSQVQSPVDSKDLSSAQNCSLSRSANISRLGLQILTPNFFSAOTFFVALSPTM 665
Db 668 EAERKEDNRYIS-DUKTIICNSETGPPPPYFHH-----QVITDKVSPGVGFADHP-- 717
Qy 666 HSQATQVPIISDGSAAVATNTIANQINATPKPAAPTTLQIPPLPAIKHLPRPETLHPN 725
Db 718 ----VNLPRGGSSGKVQAT-----PPSSATTVERPTVLTILTLLDSRVSCH-S 762

Qy 726 PAGLQESISDVTTCLVASKENVQVQASNLTKDRSMRKSFGMGGETILLSVCVMPVKDLGKS 785
Db 763 QADLQCPYSD-----RISPRQ-----RSITRSDTPLSL----- 792
Qy 786 LSVQNLIRSTELNQLGSSSGSGRGSDQFVP-----KWRESKLITDEEVGPETETDT 841
Db 793 MSVNH-----EELERSPSGFSIQDRDDVYVFGPNGGSSWMREKRYLAE--GETDTIDP 844
Qy 842 F 842
Db 845 F 845

RESULT 11
C1Q3_BOVIN STANDARD; PRT; 866 AA.
AC P58126;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated
potassium channel subunit Kv7.3) (Potassium channel alpha subunit
Kv7.3) (KQT-like 3).
DE Name=KCNQ3;
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rae J.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Probably important in the regulation of neuronal
excitability. Associates with KCNQ2 to form a potassium channel
with essentially identical properties to the channel underlying
the native M-current, a slowly activating and deactivating
potassium conductance which plays a critical role in determining
the subthreshold electrical excitability of neurons as well as the
responsiveness to synaptic inputs.
CC -!- SUBUNIT: Heteromultimer with KCNQ2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
characterized by a series of positively charged amino acids at
every third position (By similarity).
CC -!- SIMILARITY: Belongs to the potassium channel family. KQT
subfamily.
CC
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or send an email to license@isb-sib.ch).
CC
DR HMBP; AF325548; AAK11221.1; -
DR HSBP; Q54397; 1JVM.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003937; KCNQ_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion trans; 1.
DR Pfam; PF03520; KCNQ channel; 1.
DR PRINTS; PR00169; KCHANNEL.
DR Ion transport; Ionic channel; Multigene family; Potassium;
Potassium channel; Potassium transport; Transmembrane; Transport;
Voltage-gated channel.
KW TRANSMEM 122 142 Segment S1 (Potential).
FT TRANSMEM 153 173 Segment S2 (Potential).
FT TRANSMEM 197 217 Segment S3 (Potential).
FT TRANSMEM 226 247 Segment S4 (Potential).

FT	TRANSMEM	262	282	Segment S5 (Potential).
FT	TRANSMEM	331	351	Segment S6 (Potential).
FT	DOMAIN	304	324	Segment H5 (pore-forming) (Potential).
FT	DOMAIN	13	24	Poly-Gly.
FT	SITE	316	321	Selectivity filter (By similarity).
SQ	SEQUENCE	866 AA;	95644 MW;	43996161E07A0424 CRC64;

Query Match		34.2%;	Score 1556.5;	DB 1;	Length 866;
Best Local Similarity		41.6%;	Pred. No. 2.5e-78;		
Matches 384;		Conservative 99;	Mismatches 258;	Indels 181;	Gaps 299;
Qy	3 DVESGRGVLLNSAARGDGLLLGTRAAATLGGGGGLRESRKGQGNRMSLLGK-PLSY 61				
Db	49 DVEQ---VTLAGAGADKDGTLGL-----EGGRDEGQRTPQG---IGLLAKTPLSR 95				
Qy	62 TSSQSCRNVKRYQVNYLVNLRPRGWAIFYHAFVFLVFGCLLSVFTIPEHTKLA 121				
Db	96 PVK---RNNAKYRIQIYLYDALSRPRGWALLYHALVFLVVGCLLAVLTFFREYTVS 152				
Qy	122 SSCILLIEFVMVVGLEFIIRIWSAGCCRYRGQGRLFARPKPCFVIDTIVLIASIAV 181				
Db	153 GDMWLLLETFATIFGAEFALRIWAAGCCCRKYGWGRGLKFAKPLCMLDIFVLIASVPV 212				
Qy	182 VSAKTOGNI FATSALRSRFLQIILRMVMDRGCTWKLGLSVVVAHSEKELITANYIGFLV 241				
Db	213 VAVGNQGNVLATS--LRSLRFLQIILRMVMDRGCTWKLGLSGAISCAHSEKELITAWYIGFLT 271				
Qy	242 LIFSFLVLYVEKDA-----NKEFSTYADALMWGTTTLTIGYGDKTPLTWLGR 291				
Db	272 LISSFLVLYVEKDVPEVDAQCEEMKEFEFYADALMWGLTLTATIGYGDKTPTWGR 331				
Qy	292 LSAGFALLGHSFFPALPAGILGSGFALKVQEOHRQKHFEKRENPAANLIQCVRYSAADEK 351				
Db	332 IAAFFSLIGVSFFPALPAGILGSGLALKVQEOHRQKHFEKRPAAELIQAARWYATNP 391				
Qy	352 SVS-IATWK-----PHLKALHTCPTNOKLSFKERVNRVMSRPGSIKSRQASVGDRR 402				
Db	392 RIDLVATWRFYVESVSPFFPKQEQLDPAASOKGLDLRVLSNPRGSNTK-----GKLF 445				
Qy	403 SPSTDITAEGSPTKVQKSWSPNDRTFRPSLRK-----SSQPKPVIDADTALGTDDVY 456				
Db	446 TPLNVDAIESPSKEPKVGSNNKREFTAFMKAYAPWQSE-----DAGTG---DPTA 497				
Qy	457 DEKCQCQDVSDIEDTLPKTVIRAIRIMKFAVRKPKETLRPYDVKDVIQYSAGHLDM 516				
Db	498 EDRGYGNDFLIEDMIPTLKAAIRAVRILQPLRYKKKFKETLRPYDVKDVIQYSAGHLDM 557				
Qy	517 LCRIKSLQTRVDQLGKGQITSDKKS-----EKITAHEH-----TDLS 557				
Db	558 LSRIKYQLQTRIDMIFTPGPPSPTHKKSQRGAFTYPSQSPRNEPVYAREPSTSETDQS 617				
Qy	558 MLGRVVKVEKQVQIESKLDCLLDIYQVLR-----XGSASALASAFQPPFP 605				
Db	618 MMGFVKEVQVHDMGKKLDFVDMHLQHMRLQVHVGAFSPSGASS-----PA 667				
Qy	606 ECEQTSYQSPVDSKDLSSGAQNSGCLSRSTSANISRLQFILTPNPFSAOTFYALSP 665				
Db	668 EAEQED--RRADLKTICNVSETG-----APDA 695				
Qy	666 HSQATQVPIQSOGSAAVNTNIANQINTAPKAAPTTLQTPPLPAIKHLPRPETHLPN 725				
Db	696 PYSFQHPVDK-----VGPYGFFAHD-----PVNL-----PLGG---PSSGKGHAT 733				
Qy	726 PAGIQESISDVTTCLVA--SKENVVAQSNLTKDR---SMRKSFDWGGETLLSVCPMPVKD 781				
Db	734 PYAERPTVLPFLTLLDRSGSVRSQVELHGPCDSVSPRQRSEITRDSDTPLSL----- 786				
Qy	782 LGKSLSVQNLIIRSTEELNIQLSGSESGSRGSQDFYP-----KWRESKLFIDEVGPPEET 837				
Db	787 ----MSVNH-----EELERSPSGFSISQDRDDYAFGSGGSSWREKRYLAE-----GET 832				
Qy	838 ETDTFDAAPOAREAAAFASDSL 859				

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Db 393 RLDELVATWREYEVSVPPFRKQLEAAASQKGLLDRVLSNPRGSNTK-----GKLF 446
Cc
Cc
Cc 403 SPSTDTAEGSPKVKQKSMFNDRTFRPSLRUK-----SSQPKVVIDADTALGTDDVY 456
Cc
Cc 447 TPLNDAIEESPKEPKPVGLNKKERFRTAFRMKAVAFWQSS-----DAGTG---DPWA 498
Cc
Cc 457 DEKGCQDVVEDLTPPLKTVIRAIRIMKPHVAKRKFETLRDYVDKDVIEQVSAGHLDM 516
Cc
Cc 499 EDRGYGNDFLIEDIMPTLKAAIRAVRILQPLRYKKFKETLRDYVDKDVIEQVSAGHLDM 558
Cc
Cc 517 LCRIKSLQTRVDQITLKGQITSDKKREK-----ITAHEHTTDDLS 557
Cc
Cc 559 LSRKYLQTRIDMLFTPGPSTPKHKKSQKSAFTVPSQSPNEPVPVAAATSETDQS 618
Cc
Cc 558 MLGRVVKVEQVQIESKLCCLDITVQVLRKGSASALASQIIPPFCEQTSQSPV 617
Cc
Cc 619 MMGRFVVERQVDMGKGLFLVDMHOMHER-----LQVHVTEYPTKGASSPA 668
Cc
Cc 618 D-----SKDLGSAQNSGCLSRSTSANISRGLOFILTP-NEPSAQTFFVALSPTMHSQATQVP 673
Cc
Cc 669 EGEKKENRNSDLKTIICINSETGPPDPFPPFQVPIDRVGPYGFPAHD-----VK 720
Cc
Cc 674 ISQDGSAAVATNTIANQINTAPKAAPTTLQIPPLPAIKHLPRPETHLPNPAQLOESI 733
Cc
Cc 721 LTRGGRSSTKAQNLPS-----SGSTVAERPTVLPILTLDDSCVSVH-----762
Cc
Cc 734 SDVTTCLVASKENVOVAQSNLTKDRSMKSFDMGGETLLSVCPMPKDLGKSLSVONLIR 793
Cc
Cc 763 -----SQTELQGYPSDHISPR-QRRSITRSDTPLSL-----MSVNH---798
Cc
Cc 794 STEELNIQLSGSESGSGSGODFP-----KWRESKLFITDEEVGPEETETDTF 842
Cc
Cc 799 --EELERSPSGFSISQDRDDVFGPSGSSWMREKRYLAE---GETDITDTPF 846

RESULT 13
C103 RAT STANDARD; PRT; 873 AA.
AC O88944; Q92240;
AT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium voltage-gated channel subfamily KQT member 3 (Voltage-gated
DE potassium channel subunit Kv7.3) (Potassium channel alpha subunit
DE Kv1QT3) (KQT-like 3).
GN Name=Kcnq3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Derst C., Preisig-Mueller R., Hennighausen A., Daut J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=99055398; PubMed=9836339; DOI=10.1126/science.282.5395.1890;
RA Wang H.-S., Pan Z., Shi W., Brown B.S., Wymore R.S., Cohen I.S.,
RA Dixon J.E., McKinnon D.;
RT "KCNQ2 and KCNQ3 potassium channel subunits: molecular correlates of
RT the M-channel.";
RL Science 282:1890-1893 (1998).
Cc
Cc -!- FUNCTION: Probably important in the regulation of neuronal
Cc excitability. Associates with KCNQ2 to form a potassium channel
Cc with essentially identical properties to the channel underlying
Cc the native M-current, a slowly activating and deactivating
Cc potassium conductance which plays a critical role in determining
Cc the subthreshold electrical excitability of neurons as well as the
Cc responsiveness to synaptic inputs.
Cc -!- SUBUNIT: Heteromultimer with KCNQ2.
Cc -!- SUBCELLULAR LOCATION: Integral membrane protein.
```

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Cc
Cc -!- ALTERNATIVE PRODUCTS:
Cc Event=Alternative splicing; Named isoforms=2;
Cc Name=1;
Cc IsoId=O88944-1; Sequence=Displayed;
Cc Name=2;
Cc IsoId=O88944-2; Sequence=VSP_001012;
Cc Note=No experimental confirmation available;
Cc -!- TISSUE SPECIFICITY: Expressed in brain and sympathetic ganglia. In
Cc brain, expressed in cortex, hippocampus and at much lower levels
Cc in cerebellum. In sympathetic ganglia, expressed at approximately
Cc equal levels in both superior cervical ganglia and prevertebral
Cc ganglia.
Cc -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
Cc characterized by a series of positively charged amino acids at
Cc every third position (By similarity).
Cc -!- SIMILARITY: Belongs to the potassium channel family. KQT
Cc subfamily.
Cc
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Cc or send an email to license@isb-sib.ch).
Cc
Cc -----
Cc EMBL; AF087454; AAC36723.2; -;
Cc EMBL; AF091247; AAC79846.1; -;
Cc HSSP; O54397; LJVM.
Cc RGD; 69222; Kcnq3.
Cc InterPro; IPR005821; Ion trans.
Cc InterPro; IPR001622; K-channel_pore.
Cc InterPro; IPR003091; K channel.
Cc InterPro; IPR003937; KCNQ channel.
Cc InterPro; IPR005820; M-channel_nlg.
Cc Pfam; PF00520; Ion trans; 1.
Cc Pfam; PF03520; KCNQ_channel; 1.
Cc PRINTS; PR00169; KCHANNEL.
Cc KW Alternative splicing; Ion transport; Ionic channel; Multigene family;
Cc Potassium channel; Potassium transport; Transmembrane;
Cc Transmem; 123 143 Segment S1 (Potential).
Cc Transmem; 154 174 Segment S2 (Potential).
Cc Transmem; 198 218 Segment S3 (Potential).
Cc Transmem; 227 248 Segment S4 (Potential).
Cc Transmem; 263 283 Segment S5 (Potential).
Cc Transmem; 332 352 Segment S6 (Potential).
Cc Transmem; 305 325 Segment H5 (pore-forming) (Potential).
Cc DOMAIN 13 25 Poly-Gly.
Cc SITE 317 322 Selectivity filter (By similarity).
Cc VARSPLIC 1 83 MGLKARRAAGAGGGGGGGGGGGGAGNANPAGDSAVAGDEE
Cc RKVGLAPGVQVTLALGTGADKDGTLLEGGREGGQRRT
Cc P -> MALEFPGLQPPPPRPTPSAPSSRSSSGEGEAPSG
Cc /FTId=VSP_001012.
Cc CONFLICT 654 654 H -> R (in Ref. 2).
Cc SEQUENCE 873 AA; 96897 MW; D77AF808051E15 CRC64;
Cc
Cc Query Match 34.2%; Score 1555.5; DB 1; Length 873;
Cc Best Local Similarity 42.1%; Pred. No. 2.9e-78;
Cc Matches 376; Conservative 106; Mismatches 262; Indels 149; Gaps 25;
Cc
Cc QY 3 DVESGRGVLLNSAARGDGLLLIGTLTAATLGGGGGLRESREGKQARMSLAGK-PLSY 61
Cc DB 50 DVEQ---VTIALGTGADKDGTLLE-----EGGREGGQRTPG--IGLIAKPLSR 96
Cc
Cc QY 62 TSSQSCRNVKRYRVQVLYNVLPRGWFVIFHAFVLLVFGCLILSVFSTPIETKLA 121
Cc DB 97 PVK---RNAKYRIQTLIYDALERGWALLYHALVFLVIGCLILAVLTTFKEVETVS 153
Cc
Cc QY 122 SSCLLILFVMIYVVGLEFIIRIWSAGCCCRYGQGLRFAFKPFCVIDTIVILASIV 181
Cc DB 154 GDWLLLETFALITFGAEFALRIWAAGCCCRYGWRGLKFAFKPLCLMDFVLIASVPV 213
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Db 787 CDESTEDTALLQCART 803

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Job time : 192 secs

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